

**GENETIC ANALYSIS OF YIELD AND YIELD COMPONENTS
OF MUNGBEAN [*Vigna radiata* (L.) Wilczek]**

BY
N. VARADARAJULU NAIDU
M.Sc. (Ag)



THESIS SUBMITTED TO THE
ANDHRA PRADESH AGRICULTURAL UNIVERSITY
IN PARTIAL FULFILMENT OF THE REQUIREMENTS
FOR THE AWARD OF THE DEGREE OF
Doctor of Philosophy (Agriculture)
IN GENETICS AND PLANT BREEDING

ANGRAU
Central Library
Hyderabad



DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE
ANDHRA PRADESH AGRICULTURAL UNIVERSITY
RAJENDRANAGAR, HYDERABAD -500 030

1989

CERTIFICATE

Mr.N.VARADARAJULU NAIDU has satisfactorily prosecuted the course of research and that the thesis entitled **GENETIC ANALYSIS OF YIELD AND YIELD COMPONENTS OF MUNGBEAN [Vigna radiata (L.) Wilczek]** submitted by him is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that the thesis or part thereof has not been previously submitted by him for a degree of any University.

Date: **19.12.89**

A. Satyanarayana
(Dr. A. SATYANARAYANA)
Major Advisor

CERTIFICATE

This is to certify that the thesis entitled **GENETIC ANALYSIS OF YIELD AND YIELD COMPONENTS OF MUNGBEAN [Vigna radiata (L.) Wilczek]** submitted in partial fulfilment of the requirements for the degree of **Doctor of Philosophy in Agriculture** of the Andhra Pradesh Agricultural University, Hyderabad is a record of the bonafide research work carried out by **Mr.N.VARADARAJULU NAIDU** under my guidance and supervision. The subject of the thesis has been approved by the Students' Advisory Committee.

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

A. Satyanarayana
(Dr.A.SATYANARAYANA)

Chairman of the Advisory Committee

Thesis approved by the Student Advisory Committee.

Chairman : (Dr.A.SATYANARAYANA) **A. Satyanarayana**
Senior Scientist (Pulses)
Regional Agricultural Research Station
Lam, Guntur

Member : (Dr.HABIBUDDIN AHMED KHAN) **HABIBUDDIN**
Associate Professor
Dept. of Genetics & Plant breeding
College of Agriculture
Rajendranagar, Hyderabad

Member : (Dr.K.ANANTASAYANA) **K A**
Sunflower Breeder and Head
Sunflower project
Agricultural Research Institute
Rajendranagar, Hyderabad

Member : (Dr.D.V.MADHUSUDAN RAO) **D.V.M.**
Co-ordinator
Planning and Monitoring Cell
Andhra Pradesh Agricultural University
Rajendranagar, Hyderabad

Member : (Dr.G.NAGESWARA RAO) **G.N.**
Professor and Head
Dept. of Mathematics & Statistics
College of Agriculture
Rajendranagar, Hyderabad

LIST OF CONTENTS

Chapter	Title	Page No.
I	INTRODUCTION	1-8
II	REVIEW OF LITERATURE	9-67
III	MATERIALS AND METHODS	68-109
IV	RESULTS	110-275
V	DISCUSSION	276-355
VI	SUMMARY	356-365
	LITERATURE CITED	366-400
	APPENDICES	401-431
	VITA	432.

LIST OF FIGURES

Figure No.	Title	Page No.
1.	Area, production and productivity of pulses in India	3
2.	Area, production and productivity of mungbean in India	16
3.	Area, production and productivity of mungbean in Andhra Pradesh	17
4.	Stability parameters plotted against mean performance of individual genotype - days to 50% flowering	148
5.	Stability parameters plotted against mean performance of individual genotype - days to maturity	151
6.	Stability parameters plotted against mean performance of individual genotype - days to plant height	155
7.	Stability parameters plotted against mean performance of individual genotype - number of branches per plant	158
8.	Stability parameters plotted against mean performance of individual genotype - number of clusters per plant	161
9.	Stability parameters plotted against mean performance of individual genotype - number of pods per plant	163
10.	Stability parameters plotted against mean performance of individual genotype - pod length	168
11.	Stability parameters plotted against mean performance of individual genotype - number of seeds per pod	171

Contd..

Contd..

Figure No.	Title	Page No.
12.	Stability parameters plotted against mean performance of individual genotype - 1000 seed weight	174
13.	Stability parameters plotted against mean performance of individual genotype - shoot dry weight	177
14.	Stability parameters plotted against mean performance of individual genotype - seed protein	180
15.	Stability parameters plotted against mean performance of individual genotype - shoot nitrogen	184
16.	Stability parameters plotted against mean performance of individual genotype - grain yield	187
17.	ML 267 - Stable genotype	189
18.	LGG 450 - Good general combiner	252
19.	PDM 54 - Good general combiner	252
20.	Pusa 105- Good general combiner	253
21.	LGG 410 - Good general combiner	253
22.	Pusa 105 x LGG 410 - Good specific combiner	254
23.	Pusa 105 x LGG 450 - Good specific combiner	254
24.	ML 267 x LGG 450 - Good specific combiner	255
25.	K 851 x LGG 410 - Good specific combiner	255

LIST OF TABLES

TABLE NO.	TITLE	PAGE NO.
2.1	Variability in Mungbean.	19
2.2	Available literature on heritability and genetic advance in Mungbean.	23
2.3	Summary of univariate stability statistic.	34
2.4	Review of literature on gene action for various characters in Mungbean.	47
3.1	Characteristics of the genotypes used in the study.	69
3.2	Details of the experiment on genetic divergence.	77
3.3	Details of environments and genotypes used in genotype environment studies.	80
3.4	Details of the experiment on combining ability studies.	81
3.5	Analysis of variance and mean sum of squares in simple lattice design.	87
3.6	General form of environment wise analysis of variance and expected mean squares in a randomized block design.	94
3.7	Analysis of variance of multi-environmental data and mean sum of squares according to Eberhart and Russell model (1966).	95
3.8	Analysis of variance with parents and crosses in RBD.	103
3.9	ANOVA for line x tester analysis.	104
4.1	Mean, variability, heritability and genetic advance for yield and its components of Mungbean in <u>kharif</u> 1988 (El).	111

Contd..

Contd.

TABLE NO.	TITLE	PAGE NO.
4.2	Mean, variability, heritability and genetic advance for yield and yield components of Mungbean in <u>rabi</u> upland 1987-88 (E2).	112
4.3	Mean, variability, heritability and genetic advance for yield and yield components in <u>rabi</u> rice fallows 1987-88 (E3).	113
4.4	Clustering pattern of 49 genotypes of Mungbean on the basis of genetic divergence in E1 (<u>kharif</u> , 1988).	122
4.5	Clustering pattern of 49 genotypes of Mungbean on the basis of genetic divergence in E2 (<u>rabi</u> uplands, 1987-88)	123
4.6	Clustering pattern of 49 genotypes of Mungbean on the basis of genetic divergence in E3 (<u>rabi</u> rice fallows, 1987-88).	124
4.7	Average inter and intra cluster D^2 values among 14 clusters of Mungbean under <u>kharif</u> , 1988 (E1).	126
4.8	Average inter and intra cluster D^2 values among 11 clusters of Mungbean under <u>rabi</u> uplands, 1987-88 (E2).	127
4.9	Average inter and intra cluster D^2 values among 8 clusters in Mungbean under <u>rabi</u> rice fallows, 1987-88 (E3).	128
4.10	Cluster means for various characters of Mungbean in E1 (<u>kharif</u> , 1988).	130
4.11	Cluster means for various characters of Mungbean in E2 (<u>rabi</u> uplands, 1987-88).	131
4.12	Cluster means for various characters of Mungbean in E3 (<u>rabi</u> rice fallows, 1987-88).	132

Contd.

TABLE NO.	TITLE	PAGE NO.
4.13	Mean sum of squares in pooled analysis for different characters of Mungbean in genotype x environment interaction studies.	141
4.14	Relative contribution of linear and non linear portion of Genotype x Environment interaction for different characters of Mungbean.	143
4.15	Environmental index (EI) for various characters of Mungbean in Genotype x Environment interaction studies.	145
4.16	Stability parameters of Mungbean Genotypes for days to 50% flowering.	147
4.17	Stability parameters of Mungbean genotypes for days to maturity.	150
4.18	Stability parameters of Mungbean genotypes for plant height (cm).	154
4.19	Stability parameters of Mungbean genotypes for number of branches per plant.	157
4.20	Stability parameters of Mungbean genotypes for number of clusters per plant.	160
4.21	Stability parameters of Mungbean genotypes for number of pods per plant.	163
4.22	Stability parameters of Mungbean genotypes for pod length (cm).	167
4.23	Stability parameters of Mungbean genotypes for number of seed per pod.	170
4.24	Stability parameters of Mungbean genotypes for 1000 seed weight (g).	173
4.25	Stability parameters of Mungbean genotypes for shoot dry weight (g).	176

Contd..

Contd.

TABLE NO.	TITLE	PAGE NO.
4.26	Stability parameters of Mungbean genotypes for seed protein (%).	179
4.27	Stability parameters of Mungbean genotypes for shoot nitrogen (%).	183
4.28	Stability parameters of Mungbean genotypes for grain yield(kg/ha).	186
4.29	Correlation coefficients among stability parameters for different characters.	190
4.30	Phenotypic and Genotypic correlation coefficients between yield and yield components in E1 (kharif, 1987).	192
4.31	Phenotypic and Genotypic correlation coefficients between yield and yield components in E2(rabi uplands, 1987-88).	193
4.32	Phenotypic and Genotypic correlation coefficients between yield and yield components in E3 (rabi rice fallows, 1987-88).	194
4.33	Phenotypic and Genotypic correlation coefficients between yield and yield components in E ₄ (kharif, 1988).	195
4.34	Phenotypic and Genotypic correlation coefficients between yield and yield components in E ₅ (rabi uplands, 1988-89).	196
4.35	Phenotypic and Genotypic correlation coefficients between yield and yield components in E ₆ (rabi rice fallows, 1988-89).	197
4.36	Genotypic path coefficient analysis for grain yield in E1 (kharif, 1987).	201
4.37	Phenotypic path coefficient analysis for grain yield in E1 (kharif, 1987).	202

Contd..

Contd.

TABLE NO.	TITLE	PAGE NO.
4.38	Genotypic path coefficient analysis for grain yield in E2 (<u>rabi</u> uplands, 1987-88).	203
4.39	Phenotypic path coefficient analysis for grain yield in E2 (<u>rabi</u> uplands, 1987-88).	204
4.40	Genotypic path coefficient analysis for grain yield in E3 (<u>rabi</u> rice fallows, 1987-88).	205
4.41	Phenotypic path coefficient analysis for grain yield in E3 (<u>rabi</u> rice fallows, 1987-88).	206
4.42	Genotypic path coefficient analysis for grain yield in E ₄ (<u>kharif</u> , 1988).	207
4.43	Phenotypic path coefficient analysis for grain yield in E ₄ (<u>kharif</u> , 1988).	208
4.44	Genotypic path coefficient analysis for grain yield in E ₅ (<u>rabi</u> uplands, 1988-89).	209
4.45	Phenotypic path coefficient analysis for grain yield in E ₅ (<u>rabi</u> uplands, 1988-89).	210
4.46	Genotypic path coefficient analysis for grain yield in E ₆ (<u>rabi</u> rice fallows, 1988-89).	211
4.47	Phenotypic path coefficient analysis for grain yield in E ₆ (<u>rabi</u> rice fallows, 1988-89).	212
4.48	Mean performance of Mungbean parents for yield and yield components in a line x tester programme.	216
4.49	Mean performance of Mungbean F ₁ hybrids (L x T programme) for yield and yield components.	217

Contd.

Contd.

TABLE NO.	TITLE	PAGE NO.
4.50	Mean performance of Mungbean F_2 (L x T programme) for yield and yield components.	218
4.51	Estimates of heterosis in Mungbean over mid parent (MP) and better parent (BP) in per cent.	219
4.52	Inbreeding depression in per cent in F_2 generation.	221
4.53	ANOVA for combining ability (mean squares) for grain yield and its components in F_1 generation.	236
4.54	ANOVA for combining ability (mean squares) for grain yield and its components in F_2 generation.	237
4.55	Estimates of general combining ability (gca) effects of parents in F_1 generation.	239
4.56	Estimates of general combining ability (gca) effects of parents in F_2 generation.	240
4.57	Estimates of specific combining ability (sca) effects of crosses of F_1 generation.	241
4.58	Estimates of specific combining ability (sca) effects of crosses in F_2 generation.	242
4.59	Phenotypic and Genotypic correlation coefficients between yield and yield components in parents.	257
4.60	Phenotypic and Genotypic correlation coefficients between yield and yield components in F_1 generation.	259
4.61	Phenotypic and Genotypic correlation coefficients between yield and yield components in F_2 generation.	262

Contd...

Contd.

TABLE NO.	TITLE	PAGE NO.
4.62	Genotypic path coefficient analysis for grain yield in parents.	267
4.63	Phenotypic path coefficient analysis for grain yield in parents.	268
4.64	Genotypic path coefficient analysis for grain yield in F_1 generation.	270
4.65	Phenotypic path coefficient analysis for grain yield in F_1 generation.	271
4.66	Genotypic path coefficient analysis for grain yield in F_2 generation.	273
4.67	Phenotypic path coefficient analysis for grain yield in F_2 generation.	274
5.1	Good general combiners for yield and yield components in Mungbean.	341

LIST OF APPENDICES

S.NO.	TITLE	PAGE NO.
I.	Area, Production and Productivity of pulses in India (1968-87).	
II.	Area, Production and Productivity of Mungbean in India (1968-87).	
III.	Area, Production and Productivity of Mungbean in Andhra Pradesh (1971-1989).	
IV.	Meteorological data during crop period	
V.	Mean sum of squares for 13 characters in simple lattice under E1 (<u>kharif</u> , 1988).	
VI.	Mean sum of squarres for 13 characters in simple lattice under E2 (<u>rabi</u> , 1987-88, uplands).	
VII.	Mean sum of squares for 13 characters in simple lattice under F ₃ (<u>rabi</u> , 1987-88, Rice fallows).	
VIII.	Average intra and inter clusters D values (D^2) among 14 cluster of mungbean under E1	
IX.	Average intra and inter clusters D values (D^2) among 11 cluster of mungbean under E2 (rabi uplands, 1987-88)	
X.	Average intra and inter clusters D values (D^2) among 8 cluster of mungbean under E3 (rabi rice fallows 1987-88)	
XI.	Analysis of variance for 13 characters of mungbean in genotype x environment interaction studies.	
XII.	Mean performance of Mungbean genotypes for days to 50% flowering under six environments.	

Contd..

Contd..

S.NO.	TITLE	PAGE NO.
XIII.	Mean performance of Mungbean genotypes for days to maturity under six environments.	
XIV.	Mean performance of Mungbean genotypes for plant height under six environments.	
XV.	Mean performance of Mungbean genotypes for number of branches per plant under six environments.	
XVI.	Mean performance of Mungbean genotypes for number of clusters per plant under six environments.	
XVII.	Mean performance of Mungbean genotypes for number of pods per plant under six environments.	
XVIII.	Mean performance of Mungbean genotypes for pod length under six environments.	
XIX.	Mean performance of Mungbean genotypes for number of seeds per pod under six environments.	
XX.	Mean performance of Mungbean genotypes for 1000 seed weight (g) under six environments.	
XXI.	Mean performance of Mungbean genotypes for shoot dry weight (g) under six environments.	
XXII.	Mean performance of Mungbean genotypes for seed protein (%) under six environments.	
XXIII.	Mean performance of Mungbean genotypes for shoot nitrogen (%) under six environments.	
XXIV.	Mean performance of Mungbean genotypes for seed yield per plant (g) under six environments.	

Contd..

S.NO.	TITLE	PAGE NO.
XXV.	Mean performance of Mungbean genotypes for seed yield (kg/ha) under six environments.	
XXVI.	Analysis of variance of parents and crosses at F_1 generation.	
XXVII.	Analysis of variance of parents and crosses in F_2 generation.	

ACKNOWLEDGEMENTS

I would like to express my deep sense of gratitude to **Dr. A. Satyanarayana**, Senior Scientist (Pulses) and Major Advisor, Regional Agricultural Research Station, Andhra Pradesh Agricultural University, Lam, Guntur for providing the requisite genetic material and all other facilities and constant guidance and encouragement, valuable suggestions and constructive criticism throughout the course of this research work.

I am highly thankful to **Dr. Habibuddin Ahmad Khan**, Associate Professor, Department of Genetics and Plant Breeding, College of Agriculture, Rajendranagar; **Dr.K.Anantasayana**, Sunflower Breeder and Head, Sunflower Breeding Scheme, ARI, Rajendranagar, **Dr.D.V.Madhusudana Rao**, Co-ordinator, Planning and Monitoring Cell, Andhra Pradesh Agricultural University and **Dr. G. Nageswara Rao**, Professor and Head, Department of Mathematics and Statistics, College of Agriculture, Rajendranagar who were kind enough to offer their valuable advice, encouragement and constructive criticism during the course of investigation and preparation of this thesis.

I am also grateful to **Dr. M. Shiva Shantha Reddy**, Professor and Head, Department of Genetics and Plant Breeding, College of Agriculture, Rajendranagar

and **Dr.C.A.Jagadish**, Senior Scientist (OS) and ex-Professor and Head, Hyderabad for providing the necessary facilities and encouragement.

I am extremely thankful to **Dr. I.V. Subba Rao**, the then Associate Director of Research, RARS Lam and the present Director of Research, Andhra Pradesh Agricultural University and to **Dr. M. Rama Rao**, Associate Director of Research, RARS, Lam for allowing me to carry out the research work at the RARS, Lam and Rice Fallow Pulses Experimental Centre, Munipalle.

I would like to express my thanks to **Mr.P.Seenaiah**, **Sri S. Sreemannarayana Murthy**, **Mr. D. Kondanda Ramaiah** and **Mrs. B. Pramila Rani**, Assistant Research Officers, RARS, Lam for their constant encouragement.

I am especially thankful to **Mr. G. Rosaiah**, Senior Research Fellow, CSIR, Nagarjuna University, **Miss.A.Rohini**, Senior Research Fellow, ICAR, Adhoc Scheme on Preharvest sprouting resistance in Mungbean and **Mr. A. Narsi Reddy**, Assistant Research Officer (Millets), RARS, Lam, **Dr. A.R.G. Ranganath**, Scientist, Directorate of Oilseeds Research, Rajendranagar, Hyderabad for their help in the preparation of the thesis.

I am also thankful to Mr.K.Ramaprasad, Technical Assistant, Computer Centre, Directorate of Rice Research, Rajendranagar for statistical assistance and the staff of Prasa Computer Centre, Premavatipet, Rajendranagar for aid in typing the thesis.

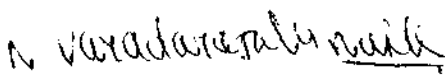
I am indebted to my wife Mrs.V.Raja Rajeswari, Assistant Research Officer (Plant Physiology) RARS, Lam for her encouragement and assistance during the course of my studies.

B. Venkatakrishnaiah
19/12/89

DECLARATION

I, **N.VARADARAJULU NAIDU**, hereby declare that the thesis entitled **GENETIC ANALYSIS OF YIELD AND YIELD COMPONENTS OF MUNGBEAN [Vigna radiata (L.) Wilczek]** is a result of the original research work done by me. I, further, declare that the thesis or any part thereof has not been published earlier elsewhere in any manner.

Date : 14-12-1989


(**N.VARADARAJULU NAIDU**)

Name of the student : N.VARADARAJULU NAIDU
Title of the thesis : GENETIC ANALYSIS OF YIELD AND
YIELD COMPONENTS OF MUNGBEAN
[Vigna radiata (L.) Wilczek]
Degree to which : DOCTOR OF PHILOSOPHY IN
it is submitted AGRICULTURE
Major field of study : GENETICS AND PLANT BREEDING
Major Advisor : Dr.A.SATYANARAYANA
Name of the University : ANDHRA PRADESH AGRICULTURAL
UNIVERSITY
Year of submission : 1989

ABSTRACT

To understand the genetic architecture of yield and its components in mungbean, detailed investigations were undertaken to study systematically the pattern of genetic variability and diversity over three environments, Genotype x Environment interactions over six environments and combining ability using F_1 and F_2 populations by line x tester analysis during 1987 to 1989.

Wider genetic variability was recorded for number of branches number of clusters, number of pods, shoot dry weight and grain yield. Higher variability and heritability coupled with higher genetic advance was observed for branches, plant height, clusters, number of pods, shoot dry weight, and grain yield.

D^2 statistic indicated the presence of considerable genetic diversity in the genotypes. Clustering pattern was influenced by the environments with 14 clusters during kharif, followed by 11 in rabi uplands and 8 in rabi rice fallows. The pattern of distribution into clusters was random irrespective of the parentage. Relation between geographic diversity and genetic diversity was not observed. Plant height, number of pods, shoot dry weight, shoot nitrogen and grain yield influenced the clustering pattern. Based on the yield performance and inter cluster distances LGG 421, LGG 429, LGG 442, LGG 487-3 and DC 1 x DC 2 - 4SB-SB in kharif; LGG 410, LGG 418, LGG 424, LGG 437, LGG 441, and LGG 442 in rabi uplands and LGG 424, LGG 446

and LGG 449 in rabi rice fallows were found genetically diverse.

A substantial portion of the G X E interaction was linear for plant height, branches, clusters, number of pods, pod length, seeds per pod, 1000 seed weight, shoot dry weight, shoot nitrogen and grain yield, whereas, non linear portion was predominant for days to 50% flowering and maturity. Kharif, 1988 was found to be the favourable environment, whereas rabi rice fallows was observed as unfavourable environment. The genotypes were classified as stable - K 851, PDM 54, PDM 84-145 and ML 267; suitable for favourable environments - LGG 410, LGG 407, ML 131 and LGG 426; and suitable for unfavourable environments - Pusa 105, LGG 450 and LGG 403.

Based on the variance components ('gca' and 'sca'), degree of dominance and heritability, it was found that maturity, plant height, clusters, number of pods, 1000 seed weight, shoot dry weight, seed protein and grain yield were governed by additive gene action. Number of branches was found to be governed by non-additive gene action. Days to 50% flowering, pod length, number of seeds per pod and shoot nitrogen were found to be governed by both additive and non additive gene action.

Among the lines Pusa 105 and K 851 and among the testers PDM 54, LGG 410 and LGG 450 were found to be the good general combiners. Seven crosses viz., Pusa 105 x PDM 54 (H x H), Pusa 105 x LGG 410 (H x H), Pusa 105 x LGG 450 (H x H), ML 267 x LGG 410 (L x H), ML 267 x LGG 450 (L x H), K 851 x LGG 410 (H x H) and K 851 x LGG 450 (H x H) recorded significant 'sca' effects with high mean yield. The H x H general combiner combinations may be advanced through pedigree breeding for improving yield per se. While the L x H combinations may be advanced after biparental mating or diallel selective mating in the initial stages so as to combine additive as well as non additive gene action.

Association analysis over six environments with 20 genotypes and with different populations (parents, F_1 , F_2) in a single environment indicated that number of clusters, pods, 1000 seed weight, shoot dry weight and shoot nitrogen were found to have consistent positive correlation with grain yield while branches was found to have negative associations. Path analysis indicated that shoot dry weight was found to have maximum direct effect on grain yield followed by number of clusters, number of pods per plant. Number of pods,

1000 seed weight and shoot nitrogen also exerted indirect effect on grain yield through shoot dry weight. Number of branches showed negative direct effect on grain yield.

From the present investigations it is evident that wider genetic variability is present in the mungbean. Higher estimates of heritability coupled with high genetic advance were recorded for number of clusters, pods, shoot dry weight and grain yield. Consistently positive association of clusters, pods, 1000 seed weight, shoot nitrogen and shoot dry weight and the negative association of branches with grain yield, coupled with the high direct effect of the shoot dry weight followed by pods on grain yield indicates that a plant type with tall habit, less branching coupled with higher number of bearing nodes and pods may lead to higher productivity in mungbean.

...

INTRODUCTION

CHAPTER I

INTRODUCTION

Mungbean (Vigna radiata (L) Wilczek), also popularly known as green gram, is a diploid ($2n = 22$) and a self pollinated grain legume crop. It is an important Asiatic Vigna grown in India for its dry beans, which are excellent source of easily-digestible protein of low flatulence and complementary to the staple rice diet. It is consumed as dhal, bean sprouts, noodles, boiled beans, Moong Vada, Moong dosa etc. in different parts of the world. Mungbean, like other pulse crops, play an important role in Indian agriculture because of its amenability to various cropping systems, nitrogen fixing ability and high nutritive value.

Annual world Mungbean production is about 1.4 million tonnes from about 3.4 million hectares (Anon, 1984). India produces more than 70 per cent of total world output (Shanmugasundaram and Poehlman, 1988). Andhra Pradesh is one of the major Mungbean growing states of India and is grown over an area of 5.14 lakhs ha, producing 1.69 lakh tonnes during 1988-89.

The area and production of Mungbean in the world, India and Andhra Pradesh during 1987-88 are given below.

	Area (Lakh ha.)		Production (Lakh tonnes)	
	Total pulses	Mung bean	Total pulses	Mung bean
World	686.88	38.38	533.45	18.19
India	227.73	28.50	111.76	11.54
A.P.	15.00	5.14	6.72	1.69*

Source : RAPA Publication 1988/13

*Directorate of Agriculture, Government of Andhra Pradesh, 1988-89.

The Area and Production of Pulses in India, has remained almost stagnant over the past two decades (Fig.1). With increasing population, this has resulted in an appreciable decline in per capita availability. Borlaug (1973) rightly called pulse crops as 'slow runners', since they failed to take the advantage of the Green Revolution. However, the situation with Mungbean is considerable better, with an increase of 58% and 85% in area and production, respectively during the same period in India. It is a short duration legume, maturing in 60-70 days, therefore, fits well in various cropping systems involving cereals, and commercial crops under rainfed as well as irrigated

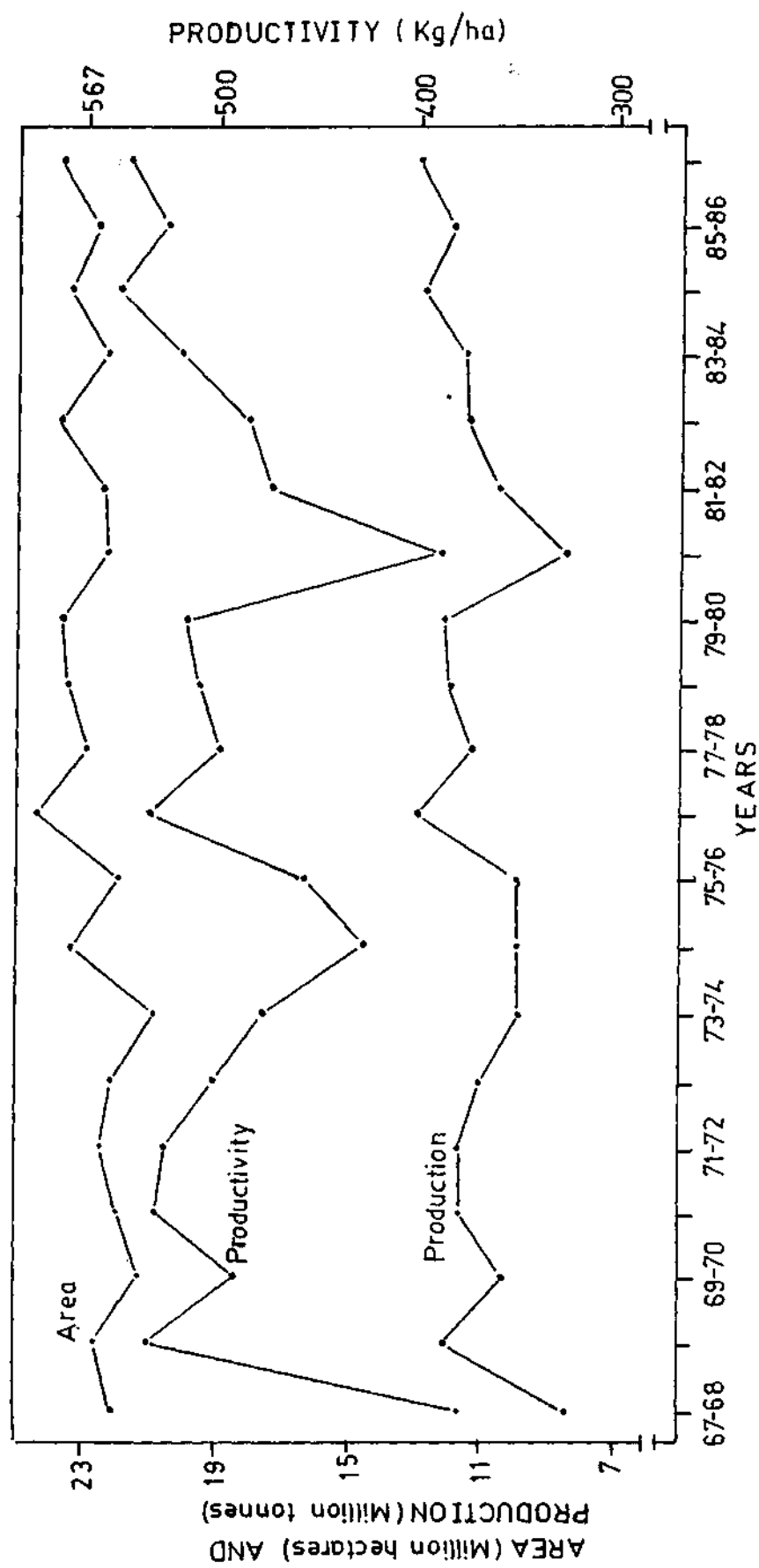


Fig.1. ALL INDIA AREA, PRODUCTION AND PRODUCTIVITY OF PULSES

conditions. However, the problem of low and uncertain productivity still persists in different agroclimatic niches. The constraints for low productivity have been analysed and some of the factors limiting the breakthrough in Mungbean are (i) low yield potential of the present day cultivated types (ii) lack of yield stability and narrow adaptability (iii) susceptibility to major diseases like Yellow mosaic virus and Powdery mildew (iv) susceptibility to abiotic stresses like drought, heat and salinity and (v) non-synchronous pod maturity, pod shattering and field weathering.

Hence, the objective of Mungbean improvement programme is to develop stable high yielding Mungbean varieties. To accomplish this objective, the understanding of the genetic architecture of yield and yield components and their response to various environments is essential.

Generation of variability and selection of superior recombinants among the variants is the major objective of any plant breeding programme. One of the major constraints noticed for the lack of breakthrough in Mungbean productivity has been the lack of genetic variability for high yield potential (Ramanujam, 1978). However, all the studies reported so far indicated considerable variability for yield and yield components

traits. It indicates that the variability present in the crop could not be properly understood or was not easily usable. Classification of variability available and selection of diverse parents belonging to distinct groups might lead to a wide spectrum of recombinations for quantitatively inherited traits. Hence, studies on the genetic diversity are of considerable importance to classify the available genotypes into discrete classes so that parents belonging to diverse groups could be selected. However, it has not been adequately utilised in Mungbean improvement programmes.

Genotype x environment interactions are known to interfere with the evaluation of genotypes and reduces the progress of selection in a plant breeding programme (Comstock and Moll, 1963 and Allard and Bradshaw, 1964). Hence, estimation of the nature and magnitude of G x E interactions for yield and its component traits is essential. Mean performance coupled with regression coefficient and deviations from regression (Eberhart and Russell, 1966) are used as parameters of stability and the range of adaptability. Though, information on G x E interactions has been adequately worked out in cereal crops, such information on Mungbean is limited (Imrie et al., 1981).

The Mungbean is predominantly a self pollinated crop. Identification of superior pure lines from the variation created through hybridization or mutation is the primary objective in breeding self pollinated crops. Pedigree method, Bulk method, Back cross method are usually employed for improving Mungbean (Joshi, 1979), which helps to attain homozygosity quickly. The breeding methods listed above can exploit only the additive type (fixable) of gene action governing a trait. In recent years, however, biparental matings and diallel selective mating enabled accumulation of favourable genes and exploitation of additive as well as additive x additive effects (Jensen, 1970). Therefore, to select an appropriate breeding methodology for the improvement of any trait, knowledge on the nature of gene action governing the quantitative trait is essential. Combining ability analysis has been used to get an insight into the inheritance through the predominance of general combining ability (gca) over specific combining ability (sca) variances and vice-versa. It also helps to identify the parents with good 'gca' and crosses for better 'sca' effects. Combining ability analysis helps the plant breeder to select the parents

and the appropriate breeding methodology to achieve the objective quickly and reliably.

In the present investigations therefore, an attempt has been made to understand the genetic nature of yield and yield components through different studies, viz., (a) studies on the genetic variability and diversity with the help of 49 diverse genotypes (b) studies on the genotype x environment interactions with the help of 20 genotypes over 6 environments and (c) the line x tester analysis, utilizing 4 lines and 5 testers, with the following objectives.

1. To understand the nature and magnitude of genetic variability, heritability and Genetic advance for yield and yield attributes.
2. To classify the Mungbean genotypes into discrete classes using D_2 - statistic .
3. To study the nature and magnitude of genotype x environment interactions for yield and yield component traits.
4. To identify superior parents and crosses through combining ability analysis

5. To understand the nature of gene actions governing the inheritance of yield and its component characters and to choose appropriate breeding methodology.
6. To understand the character association between yield and yield component traits of Mungbean.

...

REVIEW OF LITERATURE

CHAPTER II

REVIEW OF LITERATURE

The available literature on mungbean is reviewed under the following sub heads.

1. Taxonomy 2. Breeding methods followed and varietal improvement 3. Variability, Heritability and Genetic advance 4. Genetic divergence 5. Genotype x Environment interaction 6. Heterosis and inbreeding depression 7. Combining ability and Gene action 8. Correlations and 9. Path coefficient analysis.

2.1 TAXONOMY

The mungbean, Vigna radiata (L.) wilczek (basionym Phaseolus radiatus L.; Syn. Phaseolus aureus Roxb.) is a diploid with $2n = 2x = 22$ chromosomes (Marechal, 1970; Sarbhoy 1977 and 1978) belongs to the family Fabaceae (Leguminosae). Wilczek (1954) transferred the mungbean to the genus Vigna from phaseolus based on two distinct characters viz. Stipules produced under the insertion and a beak prolonging the style beyond the stigma. Verdcourt (1970), Lackey (1971), cowell (1978), subramanian (1979) and Jain and Mehra (1980) supported and confirmed wilczek's conclusions.

Verdcourt (1970) considered mungbean and urdbean as variants of one species but recommended that the two species be kept distinct until monographed. Otoul (1975) detected different free dipeptides on the seeds.

----- glutamyl-s-methyl cysteine and its sulfoxide
in vigna radiata

----- glutamyl methyl cysteine and its sulfoxide in
vigna mungo

Watt and Marechal (1977) demonstrated the existence of incompatibility barriers when the two taxa were crossed. Suman sahai and Rana (1980) have also suggested that these species should be kept or considered as distinct based on cytological studies.

Vigna radiata Var-sublobata (Roxb) Verdc. is considered to be the wild ancestor of mungbean (verdcourt, 1970; Arora et al. 1973; Singh et al., 1974; Jain and Mehra, 1980 and Lukoki et al. (1980). It has a wide distributed area centered around the Indian Ocean. In India, Himachal Pradesh and the Western ghats are noted to be the centres of diversity of the wild mung (Chandel, 1981). According to Vavilov (1926) mungbean originated in India.

Vigna radiata var. sublobata is indeterminate in habit with long inter nodes and broader leaflets, and sub lobed/deeply lobed leaflets with large and rhomboid stipules, large cream colored yellow flowers with incurved keel, long linear and thin cylindrical and cuneate pods turning black at maturity, densely pubescent when immature which upon maturity dehisce voluntarily along the sutures. Seeds are brown or tan.

Lawn and Ahn (1985) described the morphology of mungbean as follows. Mungbean is a branching erect or semi-spreading herbaceous annual between 25 and 125 cm. tall. Leaf is mostly entire, but some lobed types occur sporadically. Flowers large yellow or greenish yellow with five to fifteen clustered at the top of each peduncle. Flowers are bisexual and primarily self fertilized. Pods are long slender and straw, tan, black or brown at maturity. Pod length is quite variable ranging from 4 to 10 cm. with variable beaks. The seed colour shows a wide variation from yellow, greenish yellow, black, brown, mottled with black, light green, dark green and dull green. Hilum is white and may be flat or convex. Mean seed weight ranged from 20-80 mg. and seeds are globose or elliptical in shape.

2.2. BREEDING METHODS FOLLOWED AND VARIETAL IMPROVEMENT

Mungbean is a self pollinated crop and cleistogamy is some times present (Narasimham, 1929; Purseglove, 1968). Natural out crossing of 4 to 5 per cent was reported by van Rheenen (1964). The principal breeding approach is selection among available germplasm for direct release or use as parents and hybridization followed by pedigree selection. Type 1 was the first greengram variety developed from Muzzaffarpur (Bihar) during 1948 through selection (AVRDC, 1988). Shining mong No.1 was developed from a single plant selection in 1962 from a sample obtained from china (Singh 1982). Scientists of IARI pursued the new concept of short duration cum photo insensitive character in their breeding programmes and isolated from T 44 an early maturing variety, pusa baisakhi mung maturing in 65 days during 1962. Later on a number of promising selections: S8 (Mohini), PS-7, PS-10, PS-16 were developed from cross BR-2 x T-2. (Jeswani, 1986). Many of these varieties failed to make any impact on productivity due to their limited adaptability, indeterminate growth habit, photoperiod sensitivity, late and non synchronous maturity, susceptibility to lodging, pod shattering and to pests and diseases.

More than 80 varieties of mungbean were identified/developed so far through selection, intervarietal hybridization and mutation breeding (AVRDC, 1988). Of these, about 50 varieties were released by State and Central variety release committees in India (DPR, 1986). More than 30 varieties were developed through hybridization (Viz. MLI, ML5, ML131, K851, Pant moong No.1, Pantmoong No.3, ML267, Pusa 105, UPM 79-3-4, UPM 79-1-2, Sabarmati (PIMS4), Jawahar 45, Hyb 12-4 (Sujatha), and Hyd-43 (Jyothi) etc.). The remaining by pureline selection (eg.: G65, Co-3, PBM, LGG 127) and mutation breeding (eg.Dhauli, CO-4, TAP7, Pant moong-2, TAU-1 etc.). Most of the varieties were developed through selection from local types (viz. Kopergaon, khargaon 1, Krishna-11, Gujarat-1 and 2, Amrit, PDM 11, PDP 71-1, PDM 54 etc.).

Backcross method of breeding is also currently being used in introducing specific traits such as higher methionine level and tolerance to seed weathering into desirable recurrent parents. Diallel selective mating system approach (Jensen, 1970), or intermating of selected F2 progenies is followed at AVRDC to enable the accumulation of fixable components of genetic variability (Additive and Additive x Additive gene

effects) and breakage of unfavourable repulsion phase linkage groups (Fernandez and Shanmugasundaram (1988).

Physical mutagens were used more frequently than chemical mutagens in inducing viable mutants for utilization in mutation breeding (Jebaraj and Marappan 1981). Interspecific hybridization between greengram and blackgram is also performed to transfer the methionine content, (AVRDC, 1979) and genes resistance to pod shattering (Singh, et al., 1975), Mungbean yellow mosaic virus (Gill et al., 1983); powdery mildew (AVRDC, 1974), cercospora leafspot and bruchids (AVRDC, 1977 and 1979), and yield (Sree Rangaswamy et al., 1988) from Urdbean to Mungbean.

Biotechnology methods such as embryo culture and anther culture are currently being utilized to accomplish the transfer of pest and diseases resistance genes from Vll60 into AVRDC mungbean cultivars (Fernandez and Shanmugasundaram, 1988).

The successful development and release of new, improved high yielding disease resistant varieties have made a tremendous impact on area and production of mungbean. The area and production of mungbean showed the linear increase during the period from 1964-65 to 1985-86. The increase in area during this period was observed as 43.70% whereas in production it was as high as 75% and in productivity the increase was 21.5 per

cent (Fig.2). However, there has been phenomenal growth after 1980-81 both in production and productivity mainly due to development of early maturing and synchronous genotypes with fairly good level of resistance to yellow mosaic virus (DPR, 1988) which helped to fit it into various cropping systems. In Andhra Pradesh both area and production of mungbean increased by 78 and 98 per cent from 1974-75 to 1987-88 inspite of a decrease in area by 0.24 per cent (Government of Andhra Pradesh, 1988) and is shown in Fig.3.

2.3 VARIABILITY, HERITABILITY AND GENETIC ADVANCE

2.3.1 Variability

Variability forms the basis for all plant improvement programmes. Yield and yield component characters are quantitative characters and are polygenically inherited which are greatly influenced by environment. The phenotype of a character is the resultant of interaction between genotype and environment. Partitioning of observed variability into heritable and non heritable components is essential to get a true indication of the genetic variation of the trait. Genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance (GA) are

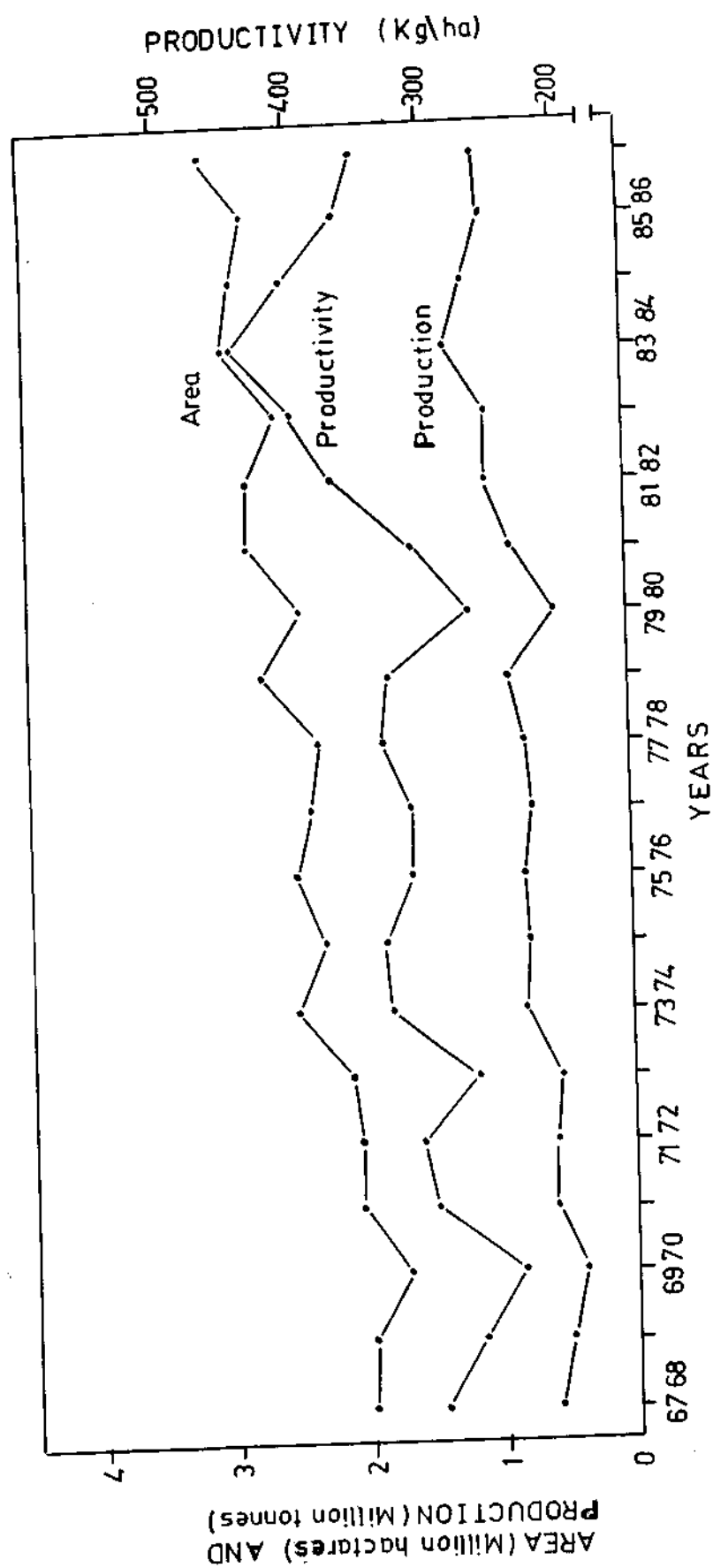


Fig.2. ALL INDIA AREA, PRODUCTION AND PRODUCTIVITY OF MUNGBEAN

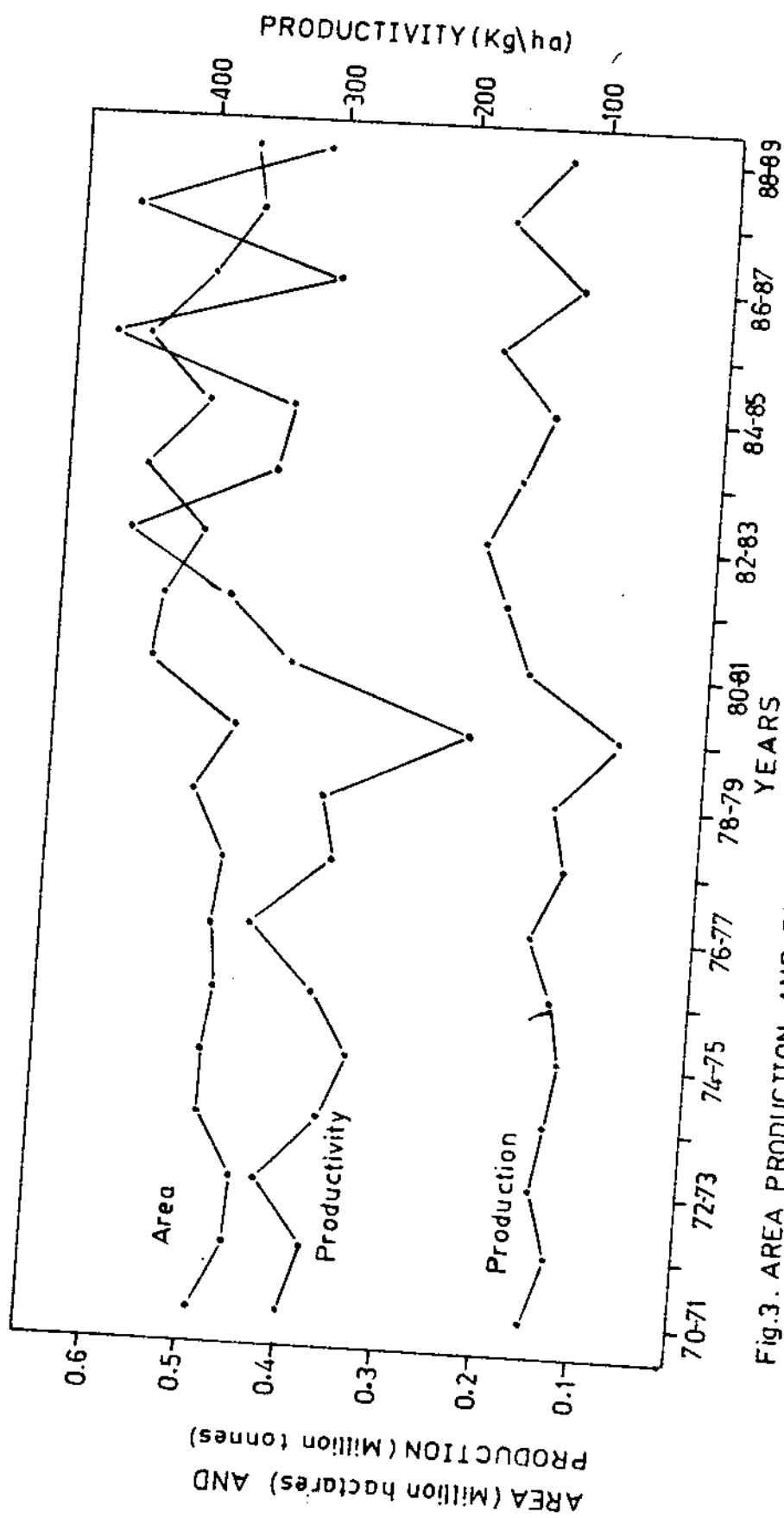


Fig.3. AREA PRODUCTION AND PRODUCTIVITY OF MUNGBEAN IN ANDHRA PRADESH

commonly used in describing the variability and genetics of a character.

The published literature on the variability in the yield and yield components traits of Mungbean indicate wider variability for all the traits studied based on the PCV and GCV estimates and is furnished in Table 2.1 for ready reference.

2.3.2 HERITABILITY AND GENETIC ADVANCE

The degree of success in a selection programme depends on the magnitude of heritability. Heritability (h^2) measures the relative amount of the heritable portion of variability. High heritability is always not an indication of high genetic gain (Swarup and Chagle 1962). Characters which show high h^2 coupled with wider variability would be successfully improved by direct selection (Paul, 1978). Genetic advance (GA) helps to measure the amount of progress that could be obtained with selection in a characters at particular selection intensity.

The available literature on heritability and genetic advance in mungbean is presented in a concise form in table 2.2 for ready reference.

Table 2.1: Variability studies in mungbean.

S.No.	Character	Wider genetic variability	Narrow genetic variability
1.	Days to 50% flowering	Singh and Malhotra (1970b), Giriraj (1973), Veeraswamy <u>et al.</u> (1973), Sandhu <u>et al.</u> (1979) and Tickoo <u>et al.</u> (1988)	Paramasivan and Rajasekharan (1980), Medhi <u>et al.</u> (1980) and Ramana and Singh (1987)
2.	Days to maturity	Singh and Malhotra (1970b), Sandhu <u>et al.</u> (1979), Tickoo <u>et al.</u> (1988) and Xianghuai He <u>et al.</u> (1988)	Bhargava <u>et al.</u> (1966), Veeraswamy <u>et al.</u> (1973), Joshi and Kabaria (1973), Medhi <u>et al.</u> (1980), Ramana and Singh (1987) and Rosaiah <u>et al.</u> (1987)
3.	Plant height	Bhargava <u>et al.</u> (1966), Chowdhury <u>et al.</u> (1972), Giriraj (1973), Veeraswamy <u>et al.</u> (1973), Yohe and Pehlman (1972), Siddaraju 1987, Rosaiah <u>et al.</u> (1987), Ramana and Singh (1987) and Xianghuai He <u>et al.</u> (1988)	—

Contd..

S.No.	Character	Wider genetic variability	Narrow genetic variability
4.	Number of branches per plant	Bhargava <u>et al.</u> (1966), Gupta and Singh (1969), Krishnaswamy <u>et al.</u> (1973), Veeraswamy <u>et al.</u> (1973), Sandhu <u>et al.</u> (1979), Siddaraju (1987), and Sandhu <u>et al.</u> (1988)	—
5.	Number of clusters per plant	Bhargava <u>et al.</u> (1966), Singh and Malhotra (1970b), Veeraswamy <u>et al.</u> (1973), Sandhu <u>et al.</u> (1979), Pandey <u>et al.</u> (1979), Singh and Sharma (1981) Rosaiah <u>et al.</u> (1987), Ramana and Singh (1987), and Sandhu <u>et al.</u> (1988)	—
6.	Number of pods per plant	Bhargava <u>et al.</u> (1966), Gupta and Singh (1969), Singh and Malhotra (1970b), Chowdhury <u>et al.</u> (1971), Veeraswamy <u>et al.</u> (1973), Giriraj (1973), Sandhu <u>et al.</u> (1979), Singh and Sharma (1981b) Misra and Sahu (1985), Siddaraju (1987), Rosaiah <u>et al.</u> (1987), Ramana and Singh (1988) Sandhu <u>et al.</u> (1988) and Tickoo <u>et al.</u> (1988)	—

Contd..

Contd..

S.No.	Character	Wider genetic variability	Narrow genetic variability
7.	Pod length	Gupta and Singh (1970), Giriraj (1973), Sandhu <u>et al.</u> (1979), and Paramasivan and Rajasekaran (1980)	Bhargava <u>et al.</u> (1966), Singh and Malhotra (1970b), Chowdhury <u>et al.</u> (1971), Rosaiah <u>et al.</u> (1987)
8.	Seeds per pod	Gupta and Singh (1969), Veeraswamy <u>et al.</u> (1973), Sandhu <u>et al.</u> (1979), Virmani <u>et al.</u> (1983), Siddaraju (1987), and Tickoo <u>et al.</u> (1988)	Singh and Malhotra (1970b), Giriraj (1973), Joshi and Kabaria (1973), Chowdhury <u>et al.</u> (1982), Rosaiah <u>et al.</u> (1987) and Ramana and Singh (1987)
9.	Seed weight	Gupta and Singh (1969), Singh and Malhotra (1970b), Giriraj (1973), Sandhu <u>et al.</u> (1979), Virmani <u>et al.</u> (1983), Misra and Sahu (1985), Bhadra <u>et al.</u> (1987), Tickoo <u>et al.</u> (1988) and Xianghuai He <u>et al.</u> (1988)	Bhargava <u>et al.</u> (1966), Chowdhury <u>et al.</u> (1982) and Ramana and Singh (1987)

Contd..

Contd..

S.No.	Character	Wider genetic variability	Narrow genetic variability
10.	Grain yield	Bhargava <u>et al.</u> (1966) Singh and Malhotra (1970b), Chowdhury <u>et al.</u> (1971), Giriraj (1973), Veeraswamy <u>et al.</u> (1973), Sandhu <u>et al.</u> (1979), Pandya <u>et al.</u> (1979) Singh and Sharma (1981) Virmani <u>et al.</u> (1983), Rosaiah <u>et al.</u> (1987), Siddaraju (1987), Ramana and Singh (1988) Bhadra <u>et al.</u> (1987), Sandhu <u>et al.</u> (1988), Tickoo <u>et al.</u> (1988),	—
11.	Seed protein	Gill <u>et al.</u> (1975), Hymowitz <u>et al.</u> (1975), Sandhu <u>et al.</u> (1979) and Bhadra <u>et al.</u> (1987)	Yohe and Poehlman (1972), Tsou and Hsu (1979), Rosaiah <u>et al.</u> (1987) and Sandhu <u>et al.</u> (1988)

Table 2.2: Available literature on heritability and genetic advance in mungbean

S.No.	Character	High h2 and high GA	High h2 and low GA	Low h2 and high GA	Low h2 and low GA
1.	Days to 50% flowering	Chowdhury <u>et al</u> (1971) Giriraj (1973)	Singh and Malhotra (1970b)	—	—
2.	Days to maturity	Empig <u>et al</u> (1970)	Medhi <u>et al</u> (1980) Singh and Pathak (1986) Ramana and Singh (1987)	—	Singh and Pathak (1986); Rosaiah <u>et al</u> (1987); Ramana and Singh (1987)
3.	Plant height	Bhargava <u>et al</u> (1966) Chowdhury <u>et al</u> (1971); Giriraj (1973); Veeraswamy <u>et al</u> (1973) Medhi <u>et al</u> (1980) Shah and Patel (1981); Siddaraju (1987), Ramana and Singh (1987) Tickoo <u>et al</u> (1988)	—	—	Singh and Pathak (1986); Rosaiah <u>et al</u> (1987)

Contd..

Contd..

S.No.	Character	High h2 and high GA	High h2 and low GA	Low h2 and high GA	Low h2 and low GA
4.	Number of branches per plant	Krishnaswamy <u>et al</u> (1973); Siddaraju (1987);	Pokle and Nomulwar (1975)	—	—
5.	Number of clusters per plant	Bhargava <u>et al</u> (1966) Chowdhury <u>et al</u> (1971) Veerawamy <u>et al</u> (1973) Medhi <u>et al</u> (1980) Shah and Patel (1981) Siddaraju (1987) Rosafah <u>et al</u> (1987) Ramana and Singh (1987)		Singh and Malhotra (1970b)	Tickoo <u>et al</u> (1988)
6.	Number of pods per plant	Bharagava <u>et al</u> (1966) Giriraj (1973) Paramasivan and Rajasekharan (1980) Shah and Patel (1981) Parida (1982); Chowdhury <u>et al</u> (1982); Parida and Singh (1984); Siddaraju (1987) Rosafah <u>et al</u> (1987) Ramana and Singh (1987)	Singh and Pathak (1986)	Gupta and Singh (1969); and Singha and Malhotra (1970b)	Tickoo <u>et al</u> (1988)

Contd..

Contd..

S.No.	Character	High h2 and high GA	High h2 and low GA	Low h2 and high GA	Low h2 and low GA
7.	Pod length	Chowdhury <u>et al</u> (1971) Ratnaswamy <u>et al</u> (1978)	Gupta and Singh (1969) Giriraj (1973) Veeraswamy <u>et al</u> (1973); Pokle and Nomulwar (1975); Chowdhury <u>et al</u> (1982)	Paramasivan and Rajasekharan (1980)	Bhargava <u>et al</u> (1966); Singh and Malhotra (1970b); Shah and Patel (1981); Rosaiah <u>et al</u> (1987)
8.	Seeds per pod	Joshi and Kabari (1973) Reddy and Krishnaiah (1977); Medhi <u>et al</u> (1980); Shah and Patel (1981); Tickoo <u>et al</u> (1988)	Giriraj (1973); Chowdhury <u>et al</u> (1982); Parida (1982)		Bhargava <u>et al</u> (1980); Singh and Malhotra (1970b); Singh and Pathak (1986); Siddaraju (1987); Rosaiah <u>et al</u> (1987); Ramana and Singh (1987)
9.	Seed weight	Bhargava <u>et al</u> (1966) Singh and Malhotra (1970b); Chowdhury <u>et al</u> (1971) Giriraj (1973) Pokle and Nomulwar (1975)	Gupta and Singh (1969) Chowdhury <u>et al</u> (1982) Ramana and Singh (1987)		Parida and Singh (1982)

Contd..

Contd..

S.No.	Character	High h2 and high GA	High h2 and low GA	Low h2 and high GA	Low h2 and low GA
10.	Grain yield	Giriraj (1973) Rosaiah <u>et al</u> (1987) Ramana and Singh (1987)	Bhargava <u>et al</u> (1966) Gupta and Singh (1969) Singh and Pathak (1986)	Singh and Mulhotra (1970b); Parida and Singh (1982)	Tickoo <u>et al</u> (1988)
11.	Seed protein	Chowdhury <u>et al</u> (1982) Rosaiah <u>et al</u> (1987)	—	—	—

2.4 GENETIC DIVERGENCE

Mungbean like other pulse crops was reported by many that it might have lost genetic variability for high yield potential during the process of its domestication, as a result of its continued cultivation on marginal lands and under neglected management conditions (Jain, 1981). Hence, he suggested that variability thus lost needs to be regenerated by organizing massive hybridization programme using genetically diverse parents. A cross involving genetically diverse parents is likely to produce rare and useful recombinations. Wider variability can also be expected in the segregating generations of such cross combinations (Rao et al., 1981).

Murty et al. (1965) in Brassica, Murty and Anand (1966) in Linseed, Arunachalam and Jawahar Ram (1967) in Sorghum, Singh and Bains (1968) in cotton, Gupta and Singh (1970) in mungbean, Jayaprakash et al. (1974) in cowpea and Shanmugam (1983) in urdbean have indicated that geographic diversity may not be associated with genetic diversity.

Multivariate D^2 analysis was found to be the best technique to classify the genotypes on the basis of genetic distance between the characters. Gupta and Singh (1970) studied genetic divergence using

Mahalanobis D^2 technique on 36 cultures of mungbean for yield and yield components. They classified these 36 strains into 10 clusters depending on similarities of their D^2 values. The parentage had definite effect on clustering. Pod length and seed weight contributed maximum towards the total divergence. Whereas Malhotra and Singh (1971) in urdbean and Tawar et al. (1988) in mungbean reported narrow range of variability for Pod length and seed weight.

Ramanujam et al. (1974) classified ten parents and 35 F₁ hybrids into eight clusters and suggested that there was considerable amount of a genetic diversity among the genotypes studied. They also reported that primary branches, days to flowering and to maturity, seed size and seed density contributed maximum towards genetic divergence. From the studies involving 60 genotypes of mungbean, Malhotra et al. (1974), grouped the material into fourteen clusters. They also indicated that geographic diversity did not seem to have a direct association with genetic diversity.

Clustering pattern and characters contribution varied with the environments studied in urdbean (Rao and Suryawanshi, 1988), Shanmugam and Sree Rangaswamy (1982) reported that seed yield per plant contributed most to the genetic diversity for their studies involving 45

genotypes of urdbean. In mungbean Shanmugam and Sree Rangaswamy (1982) classified 45 genotypes in 16 clusters and also indicated that geographic diversity was not related to genetic diversity.

Santhisree (1985) based on D^2 analysis grouped 45 genotypes of greengram into 9 clusters. No relation between geographic diversity and genetic diversity was observed. Pod length, number of seeds per pod, seed protein, plant height and seed yield contributed maximum to the diversity.

Tawar et al. (1988) studied genetic divergence using D^2 analysis in 34 diverse strains of mungbean and grouped them into five clusters. Maximum range of variability was observed for number of seeds per plant followed by number of clusters and pods per plant.

2.5 GENOTYPE - ENVIRONMENT INTERACTION

Phenotypic expression of any character is influenced not only by its genetic constitution but also the environment under which it is grown. These two factors are not independent and there is always some interplay between genotype and its environment. A specified genotype does not exhibit the same phenotypic characteristics under all environments and different genotypes respond differently to a specified

environment. This variation arising from the lack of correspondence between the genetic and non genetic effects is known as the genotype-environment (gxe) interaction. In other words, the failure of a genotype to give the same phenotypic performance when tested under different environments is the reflection of the genotype-environment interaction (Verma et al. 1987).

2.5.1 Environment and its kinds

Environment is the sum total of physical, chemical and biological factors. Comstock and Moll (1963) have classified the environment into two categories. (i) Micro-environment includes physical and chemical attributes of soil, climatic variables, solar radiation, insect pests and diseases (ii) Macro-environment is the environment associated with a general location and period of time and is a collection of micro environments. Allard and Bradshaw (1964) coined the terms predictable and unpredictable environment. The predictable environment includes the permanent features of the environment, such as climate, soil type and day length. It also includes what are called controllable variables (Perkins and Jinks, 1973) viz. the level of fertilizer applied, sowing dates and sowing density. The unpredictable or the uncontrollable environment includes weather fluctuations, such as differences

between seasons in terms of amount and distribution of rainfall, and the prevailing temperatures.

2.5.2 Significance of G X E interaction in Plant Breeding

The contribution of environmental effects in the phenotypic expression of a trait was first recognised by Johansson (1908) while formulating pure line theory. He advocated that selections made under environmental fluctuations were ineffective. Since then, the choice of environment under which selection has to be practiced became an important part in quantitative genetics. Genotype X environment interaction reduces the progress by selection. It also reduces the accuracy in predicting the phenotypic ranking of a series of genotypes over several environments (Comstock and Moll, 1963). The lack of genotype x environment interaction has a great significance to the plant breeder. In such a case, a variety breed and tested at one of the locations will give a similar performance at other locations and if, has a high mean performance, it may, be recommended throughout the area. If g x e interaction exists, then strains would have to be bred for each ecological niche (Verma et al., 1987).

2.5.3 Mechanisms Promoting Stability

Stability of a genotype refers to the ability of a genotype to avoid substantial fluctuations in a character(s) over a range of environments. There can be two ways by which a variety can achieve stability (Allard and Bradshaw, 1964) viz. individual buffering and population buffering. Individual buffering is the ability of an individual or a population to produce a certain narrow range of phenotypes under different environments. Adams and Shank (1959), Griffing and Langridge (1963) and Allard and Workman (1963) reported that individual buffering is a property of the heterozygotes. Population buffering refers to stability above and beyond that due to individual buffering due to interaction and compensation among the different genotypes within the population.

2.5.4 Measurement of Genotype x Environment interaction

Even though the genotype x environment interactions were known to be heritable (Jinks and Mather, 1955), and the importance of genotype x environment interactions were recognised (Allard, 1961), the conventional statistical technique available (Factorial design) did not pin point the genotypes, which were stable in productivity, owing to the change

in ranks at different locations and recently these were termed instabilities (Sprague, 1966). Important advances in biometrical genetics has been made in the last few years on elucidation and understanding of the genotype-environment interactions (Breese, 1972). A summary of the stability statistics available are presented in table 2.3.

2.5.5 Linear Regression Approach

The most widely used method to analyse phenotypic stability is to calculate regression of the particular character of a given genotype in different environments on the mean of all tested genotypes. Eberhart and Russell (1966) used environmental index (EI) instead of actual yield. This model provides three statistics namely mean performance ($\bar{X}$), linear regression (b_i) and deviations from linear regression ($S^2 d_i$). According to this model, a stable variety should have average linear response ($b_i = 1$), least deviations ($S^2 d_i = 0$) accompanied by desirable mean performance. The relationship among the stability parameters is presented below.

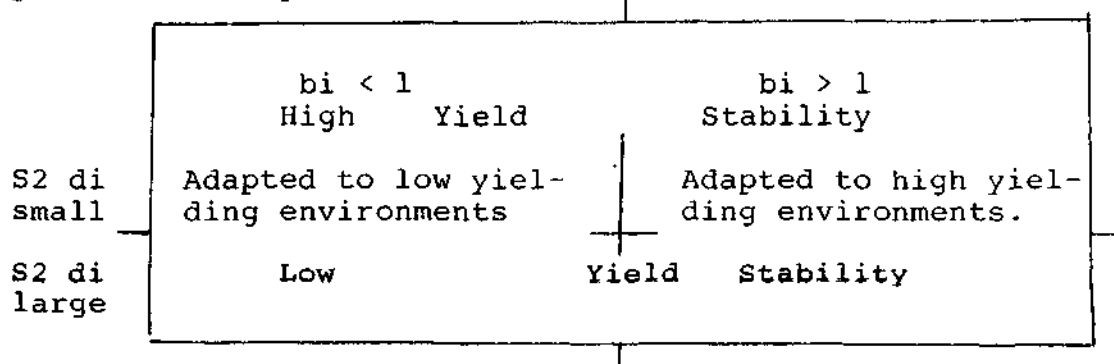


Table 2.3: Summary of univariate stability statistics (Leon, 1985)

Statistic	Symbol	Stability	Reference
<u>Parametric:</u>			
Environmental variance	S^2_{xi}	Static	Roemer (1917)
Stability factor	S.F.		Lewis (1954)
Ecovalence	W_i	Dynamic	Wricke (1962)
Regression coefficient	b_i	Static/ Dynamic	Finlay and Wilkinson (1963)
Deviation from mean squares	S^2_{di}	Dynamic	Eberhart and Russell (1966) Tai (1971) Perkins & Jinks 1968 & 1973
Genotypic stability	D_i^2		Hanson (1970)
Stability variance	^2_i	Dynamic	Shukla (1972)
Coefficient of determination	r_i^2	Dynamic	Pinthus (1973)
Coefficient of variation	C.V.	Dynamic	Francis and Kenenberg (1978)
Modified linear Regression Coefficient			Verma <u>et al.</u> (1978)
<u>Non parametric</u>			
Mean rank difference	S_i	Dynamic	Huhn (1979)
Variance of ranks	S_i^4	Dynamic	Huhn and Nassar (1987)

Though several stability models are available, the regression analysis of Eberhart and Russell (1960) has been widely used by many plant breeders to describe the production response of individual genotypes in multienvironment trials because of its simplicity and biological relevance.

2.5.6 Number and choice of Environments

In the measurement of stability of a genotype fixing of environments to which the genotypes or varieties exposed is important. These environments should have their own potentials to react with genotypes. Sprague and Federer (1951) concluded that increase in number of locations at the expense of number of replications was good for stability analysis. Perkins and Jinks (1973) felt that the quality of environments (Physical and biological factors) are responsible for the magnitude and properties of genotype x environmental interactions. Kallisikes and Larter (1970) indicated that environment should include all those factors under which the crop is grown.

2.5.7 Genotype - Environment interaction studies and stability of performance in Mungbean

Most of the studies on genotype - environment interaction of mungbean were confined to yield. Information on the relative importance of various plant

characters in determining adaptation is limited. Available literature on mungbean and urdbean are reviewed hereunder.

Joshi (1969) found that the varieties grown under different environments (Locations and years) responded differently for seed yield. He explained this differential response due to specific environmental conditions may not be accounted for by the years but mainly by the location groupings because variety (6) x year (3) x location (3) interaction component was nearly eight times as large as variety x year component but were close to variety x location component. Joshi (1972) further concluded that from his studies on six genotypes of mungbean over six environments that genotypes responded significantly to environments. The variety D2-15 yielded well under all the environments studied, while, D 45-6 though, had a higher yield potential but was specifically adapted to better environments.

Tomar et al. (1972) noticed significant variety x season interaction for seed yield in mungbean.

Ramanujam et al. (1973) studied 12 varieties of mungbean at several locations and observed that the varieties differed significantly for seed yield, but did not differ in their adaptation. In another set also

variety x environment (linear) component was not significant, indicating that the varieties did not differ in their adaptability.

Ramanujam (1975) further studied 35 genotypes of mungbean at nine environments and found that linear portion of $g \times e$ interaction was substantial for number of days to flower, plant height, pods/plant, seed size, seed protein content and seed yield per plant while non linear component was high for primary and secondary branches per plant and seeds per pod.

Chowdhury and Haque (1977) found significant differences between varieties for seed yield when 9 genotypes of mungbean were studied for four years during kharif season but none of the genotypes were ideally stable. Line No.22 however, had an average stability and high yield than the other genotypes.

Verma et al. (1978) applied segmented regression analysis using 36 advanced breeding lines and superior accessions from the International Mungbean Nursery (IMN) trials and classified them into three groups (i) suitable only for favourable environments (ii) high yield and stable under unfavourable environments (iii) better suitable to low yielding environments.

Raghuram Reddy (1980) studied 11 varieties of mungbean over two years at three locations for seed yield stability. They observed that $g \times e$ interactions of the first order were not significant but the second order interactions (genotype $\times$ location $\times$ year) were significant. Both linear and non linear portions of $g \times e$ interactions were significant for pods per plant while only non-linear component was significant for seed yield.

Imrie et al. (1981) studied $g \times e$ interaction using 21 genotypes of mungbean grown under 12 locations over two years. All main effects (genotypes, locations and years) and interactions were significant for seed yield. The high $g \times e$ interaction measured by variance analysis was also confirmed by the regression analysis of genotype performance on an environmental index.

Imrie and Butler (1982) observed that main effects (Lines, locations and years) and interactions were statistically significant among 30 genotypes of mungbean. Estimated variance due to environment exceeded that due to genotypes for all characters and made greater contribution to total estimated variance for plant height, days to flower and days to harvest. Genotype $\times$ environment interaction and residual components of variance of seed yield were particularly

high (37.2 and 4.4%) which ultimately reflected in low estimate of heritability for seed yield.

Ahn et al. (1985) used the Eberhart and Russel method to evaluate the stability index of mungbean lines in the ninth and tenth International Mungbean Nursery (IMN) trials, separately. The estimated stability indices were inconsistent between trials. A positive relationship was observed between yield potential and stability index which indicates that high yielding lines showed below average stability.

Pandey et al. (1985) studied $g \times e$ interactions for seed size, seed yield, seed protein and percentage of hard seeds in mungbean grown under summer, rainy and winter seasons. They observed that $g \times e$ interactions were significant for all the four characters.

Naresh Mehrotra and Chowdhury (1986) studied 10 genotypes of mungbean in nine rainfed environments differentiated by years, sowing dates and by considering yields of middle and border rows, observed that genotypes, environment (linear) and $g \times e$ interaction effects were significant. They indicated that genotypes having around unit regression ($b_i=1$) and low deviations from linear regression (S^2_{di}) coupled

with high seed yield are suitable for unstable rainfed environments.

Imrie and Shanmugasundaram (1987) observed that most of the variation in seed yield was environmental (70-80%) with 17-27% due to $g \times e$ interaction and less than 3% being variation among genotypes of mungbean studied under international mungbean nursery trials. High yielding environments were identified as those where water supply to plants was good and where climatic conditions favoured an extended crop duration and avoidance of severe disease epidemics. No plant character consistently characterised high yielding genotypes.

Ramana and Singh (1987) observed that all the 37 genotypes studied, showed differences in mean values in both the seasons (kharif and rabi) for plant height, clusters and pod per plant, seeds per pod, 100 seed weight and seed yield per plant indicating the profound effect of environment.

Ilyas Ahmad Malik et al. (1988) studied the performance of seven mutants along with parental types of mungbean at four different locations in three summer seasons. Stability for seed yield was estimated through regression analysis and found that some mutants were widely adapted while others performed better in

favourable environments whereas the parental lines tended to respond well under poor environments.

Singh et al. (1988) studied 40 genotypes of mungbean in four environments (Summer and kharif seasons under narrow and wide spacings) based on parametric approach (Regression co-efficient and deviations from linear regression). The linear regression coefficients were significant for 26 out of 40 genotypes used while deviation from regression was not significant for any of the genotypes. Two genotypes ML 370 and MUM 3 were identified as stable genotypes.

Shaikh et al. (1988) screened 60 winter type mutants and exotic and local collections of mungbean in multi-environment trial (seven locations in three years) and identified 3 lines based on seed yield and resistance to diseases. The lines differed considerably in the regression coefficient of their means on the respective trial means.

Yadav and Kumar (1985) studied 23 varieties of urdbean at two locations in different sowing dates and reported that locations as well as the sowing dates influenced the seed protein substantially and the location effect was more pronounced. Both linear and non linear components of $g \times e$ interactions were

present. Similar results were also obtained for plant height from the studies involving 31 genotypes of urdbean under three environments (Yadav and Tommer, 1985). 90 diverse and elite strains of urdbean grown at three loations indicated high stability for pods per plant and seeds per pod conferred stability for yield (Katiyar, 1988).

2.5.8 Association between the Stability Parameters

The desired genotype in any practical situation is one with high mean performance ($\bar{x}$), desired linear regression coefficient (b_i) and low deviations from linear regression (S^2_{di}). If these aspects are controlled by different genetic systems then the desirable genotype may be bred through standard breeding procedures. Finlay and Wilkinson (1963), Perkins and Jinks (1963 and 1968) and Fripp and Caten (1973) observed that the linear regression was positively correlated with mean performance. On the other hand, Eberhart and Russell (1966), Westerman (1971), Paroda and Hayes (1971), and Yadav and Kumar (1985) found that the mean performance, linear and non linear responses were independent from each other.

Available literature on pulse crops is reviewed on this subject. Gupta (1971) in chickpea indicated that stability appears to be specific for

individual characters within a population whereas, Dahiya and Jeswani (1974) showed that stability for yield was positively correlated with stability for pods per plant and 100 seed weight in Lathyrus. Ramanujam and Gupta (1974) recorded a strong association between the mean performance and ability to respond to environment with respect to yield and pods per plant but not for yield and protein content. While Ramanujam (1975) observed in mungbean, a positive correlation of performance of a variety (yield) with responsiveness (capacity to respond to better environment) in respect to number of pods per plant but not with seed size. No relationship between the measure of deviation from the response line of any character and mean performance or responsiveness to yield was noticed. Samolo et al. (1979) observed that the stability of important yield components like pods per plant and seeds per plant was associated with stability of yield in mutants of mungbean. Mehera and Ramanujam (1979) from the studies on the association between the adaptation parameters of yield and its components indicated that the main component of yield stability was due to stability of pods per plant in chickpea. Yadava and Kumar (1979) in blackgram reported that stability parameters were governed by independent genetic system for yield components and oil content. Sanghi and Kandalakar (1983) reported that the three parameters of stability

were positively correlated in case of pods per plant and seed weight in cowpea. Jain and Pandya (1988) observed positive and significance association of mean performance and linear responses for primary branches, pods per plant, seeds per pod, 100 seed weight and yield per plant in chickpea. These two aspects of adptation were negatively correlated in case of days to 50% flowering, secondary branches per plant and significant association with non linear response of secondary branches per plant, pods per plant, 100 seed weight and seed yield per plant. Negative but non significant association was observed for days to 50% flowering and seeds per pod. A positive and significant correlation was observed between linear and non linear regression coefficeint in case of 100 seed weight.

2.6 COMBINING ABILITY AND GENE ACTION

2.6.1 Combining ability

Combining ability analysis helps the breeder in selecting the parents to be used in a hybridization programme, to select an appropriate breeding method by providing necessary information on the nature of gene action governing a character and also in identifying cross combinations showing high specific combining ability.

Sprague and Tatum (1942) defined the terms general combining ability (gca) and specific combining ability (sca). GCA refers to the average performance of a parent in a series of hybrid combinations and is attributable to additive (fixable) gene action, while, SCA refers to the deviation in the performance of crosses in certain specific combinations (Worse or better) than what would be expected on the basis of the average performance the lines involved and is attributed primarily to dominant and epistatic gene effects (Non additive). The non-additive gene action is usually non fixable but often brings about phenotypes that are not attainable from additive gene action (Griffing, 1956).

The major approaches used in the genetic analysis have been the diallel cross and its variant--incomplete diallel or partial diallels. Some analyses have been made based on first degree statistics such as generation means (Ramanujam, 1987). Limited use has also been made of the line x tester approach proposed by Kempthorne (1957) or North carolina designs proposed by Comstock and Robinson (1948, 1952). Most of the earlier studies were based on limited number of genotypes, usually the adapted varieties selected for yield. The analyses generally indicated that the end characters such as seed yield or pods per plant or

seeds per plant were predominantly governed by non additive gene action. Yield components such as seed size, seeds per pod, Physiological characters such as days to flowering, or days to maturity and morphological characters such as plant height or branches showed predominance of additive effects or equal contribution by both additive and non additive gene effects (Ramanujam and Mehra, 1983).

2.6.2 Gene action

The review of literature on gene action governing the inheritance of a particular trait is summarised in Table 2.4. Only additive gene actions were reported so far for days to maturity. Whereas, additive or non-additive type of gene action were reported for days to 50% flowering, and for all other traits additive or non-additive or additive and non-additive types of gene actions have been reported. Published information on the nature of gene action of shoot nitrogen and shoot dry weight is not available.

2.7 HETEROSIS AND INBREEDING DEPRESSION

2.7.1 Heterosis

Heterosis is a complex biological phenomena manifested in the superiority of hybrids over the parental forms. The term heterosis was first coined by

Table 2.4: Review of literature on gene action for various characters in mungbean

S.No.	Character	Additive	Non additive	Additive and Non additive
1.	Days to 50% flowering	Singh and Singh (1974a 1974b) Tiwari and Ramanujam (1974); Yohe and Poehlman (1975); Ramanujam (1978); Godhani <u>et al</u> (1978) Raghu Ram Reddy (1980) Singh (1980) Nagaraja Rao and Mahboob Ali (1983) Patel (1983) Rao <u>et al</u> (1984); and Patel <u>et al</u> (1988)	Murthy <u>et al</u> (1976) Swindell and Poehlmen (1978); and Deshmukh and Manjare (1980)	
2.	Days to maturity	Murty <u>et al</u> (1976) Gupta <u>et al</u> (1978) Ramanujam (1978) Raghu Ram Reddy (1980); Patel (1983); Rao <u>et al</u> (1984) Patel <u>et al</u> (1988)	Deshmukh and Manjare (1980)	

Contd..

S.No.	Character	Additive	Non additive	Additive and Non additive
3.	Plant height	Yohe and Poehlman (1975) Gupta <u>et al</u> (1978)	Ahuja (1980) Lal <u>et al</u> (1982)	Swindell and Poehlman (1978)
		Deshmukh and Manjare (1980); Nagaraja Rao and Mahboob Ali (1983); Singh (1984); Malik and Singh (1986)	Reddy and Sreeramulu (1984); Ahuja and Chowdhury (1984); Patel <u>et al</u> (1988)	Malik and Singh (1986); Rao <u>et al</u> (1984)
4.	Branches per plant	Nagaraja Rao and Mahboob Ali (1983); Malik and Singh (1986)	Sen and Murthy (1960) Murthy <u>et al</u> (1976) Godhani <u>et al</u> (1978) Singh (1980); Patel <u>et al</u> (1988)	Singh and Singh (1972); Singh <u>et al</u> (1972)
5.	Number of clus- ters per plant	Singh (1974a) Raghu Rami Reddy (1980) Malik and Singh (1986)	Sen and Murthy (1960) Singh and Singh (1972) Singh and Singh (1974b) Murthy <u>et al</u> (1976) Godhani <u>et al</u> (1978) Natarajan <u>et al</u> (1989)	Deshmukh and Manjare (1980); Malhotra <u>et al</u> (1980)

Contd..

Contd..

S.No.	Character	Additive	Non additive	Additive and Non additive
6.	Number of pods per plant	Singh and Singh (1971a, 1974a) Raghu Ram Reddy (1980) Singh (1984) Malik and Singh (1986)	Singh (1972) Singh and Singh (1974b) Singh <u>et al</u> (1975) Gupta <u>et al</u> (1978) Deshmukh and Manjare (1980); Ahuja (1980); Singh (1980); Lal <u>et al</u> (1982); Nagaraja Rao and Mahboob Ali (1983) Patel <u>et al</u> (1988)	Malhotra <u>et al</u> (1980); Rao <u>et al</u> (1984)
7.	Pod length	Singh and Jain (1971b) Chowdhury et al (1971) Raghu Ram Reddy (1980) Singh (1980); Patel (1983); Patel <u>et al</u> (1988);	Pokle and Nomulwar (1975) Gupta <u>et al</u> (1978) Nagaraja Rao and Mahboob Ali (1983) Lal <u>et al</u> (1982)	Singh <u>et al</u> (1972) Singh and Singh (1974a); Murthy <u>et al</u> (1976); Godhani <u>et al</u> (1978); Luthra <u>et al</u> (1977); Malhotra <u>et al</u> (1983);

Contd..

Contd..

S.No.	Character	Additive	Non additive	Additive and Non additive
8.	Seeds per pod	Singh <u>et al</u> (1970)	Sen and Murthy (1960)	Singh and Singh (1971a)
		Singh and Singh (1974a)	Murthy (1976)	(1971a)
		Yohe and Poehlman (1975)	Godhani <u>et al</u> (1978)	Tiwari and Ramanujam (1974)
		Swindell and Poehlman (1978); Ramanujam (1978)	Gupta <u>et al</u> (1978)	Luthra <u>et al</u> (1977)
		Raghu Ram Reddy (1980)	Deshmukh and Manjare (1980); Singh (1980); Lal <u>et al</u> (1982); Nagaraja Rao and Mahboob Ali (1983); Patel (1983); Patel <u>et al</u> (1988)	Malhotra <u>et al</u> (1983)
9.	Seed weight	Singh and Jain (1971b)	Sen and Murthy (1960)	Singh and Singh (1974a and 1974b)
		Singh and Singh (1972)	Tiwari and Ramanujam (1974);	
		Ramanujam (1978); Gupta <u>et al</u> (1978); Deshmukh and Manjare (1980); Raghu Ram Reddy (1980); Singh (1984); Malik and Singh (1986) Patel (1983); Patel <u>et al</u> (1988)	Murthy <u>et al</u> (1976)	Imrie <u>et al</u> (1988)
			Godhani <u>et al</u> (1978)	
			Nagaraja Rao and Mahboob Ali (1983)	
			Malik and Singh (1983)	

Contd.. 50



Contd..

S.No.	Character	Additive	Non additive	Additive and Non additive
10.	Grain yield	Singh and Jain (1971a) Singh and Jain (1972) Yohe and Poehlman (1975) Tiwari and Ramanujam (1974); Ahuja (1979) Raghu Ram Reddy (1980) Singh (1984); Malik and Singh (1986);	Singh and Singh (1972) Singh and Singh (1974b) Tiwari and Ramanujam (1974); Singh <u>et al</u> (1975); Murthy <u>et al</u> (1976); Gupta <u>et al</u> (1978); Krishna Rao and Nagur (1979) Rao and Nagur (1979) Deshmukh and Manjare (1980); Singh (1980) Basaeeruddin and Nagur (1981)	Singh and Jain (1971); Singh and Singh (1974b) Luthra <u>et al</u> (1977); Rao <u>et al</u> (1984); Ahuja and Chowdhury (1984) Patel <u>et al</u> (1988) Tawar and Sudanshu Jain (1989)
11.	Seed protein	Tiwari and Ramanujam (1976); Raghu Ram Reddy (1980)	Wilson <u>et al</u> (1985)	Singh and Singh (1973b); Luthra <u>et al</u> (1977); Singh (1984); Sharma <u>et al</u> (1984)

Shull (1914) and is defined as the increased vigour of F_1 over parental mean (Muntzing, 1945; Pal and Singh, 1946) or better parent (Whaley, 1952). Williams and Gilbert (1969) emphasised that the heterosis over better parent helps the breeder in eliminating the less productive crosses at F_1 itself. Heterosis could be used as an indicative of the crosses which are likely to generate productive transgressive segregants (Singh and Jain, 1970). Heterosis manifestation for grain yield, is expressed in the form of increased grain yield, which in turn is dependent on the contribution of its components. Therefore, all the component characters of yield need to be studied together with regard to heterosis manifest in order to assess the worth of a cross (Grafius, 1956).

The heterotic effect in intervarietal crosses of grain legumes is generally due to dominance gene effects (Singh and Singh, 1971) but some times it is due to epistatic interaction (Sethi, 1975). In self pollinated crops, it is possible to exploit this kind of genetic manifestation only if there is potentially workable male sterility mechanism (Sagar and Candra, 1977). Heterosis over mid parent and better parent in mungeban is reviewed hereunder.

Heterosis in desirable direction (negative heterosis) for days to 50% flowering was reported by

Singh and Jain (1970) over mid parent and better parent while, Swindell and Poehlman (1976) and Ramanujam (1978) reported negative heterosis for this trait over mid parent only.

Misra et al. (1970), Singh and Jain (1979) and Ilyas Ahmad Malik et al. (1988) have reported significant heterosis for plant height over mid parent and better parent while Bhatnagar and Singh (1964), Swindell and Poehlman (1976) and Raghu Ram Reddy (1980) observed heterosis for plant height over mid parent only.

Heterosis for branches per plant was reported both over mid parent (Bhatnagar and Singh, 1964; Singh and Singh, 1972; Singh and Singh, 1974; Swindell and Poehlman, 1976; Malhotra et al., 1983 and Ilyas Ahmad Malik et al., 1988) and better parent (Misra et al., 1970).

Heterosis for cluster and pod number over mid parent was reported by Singh and Jain (1970), Singh and Singh (1972), Singh and Singh (1974), Gupta et al. (1978); Raghu Ram Reddy (1980) and Malhotra et al. (1983). While, over better parent heterosis was reported by Ilyas Ahmad Malik et al. (1988). Positive heterosis for the number of pods per plant was reported by Misra et al. (1970), Singh and Singh (1974a),

Swindell and Poehlman (1976), Ramanujam (1978) over mid parent. While over better parent by Bhatnagar and Singh (1964).

Positive heterosis for pod length was reported in mungbean by Bhatnagar and Singh (1964) over mid parent whereas, Singh and Jain (1970) reported over both mid and better parent. However, Singh and Singh (1972), Singh and Singh (1974), Sreekumar and Abraham (1978), Malhotra et al. (1983) and Ilyas Ahmad Malik et al. (1988) reported negative heterosis for pod length over mid and better parents.

Heterosis for the number of seeds per pod was positive over mid parent as reported by Singh and Singh (1972), Singh and Singh (1974), Swindell and Poehlman (1976), Ramanujam (1978) and Ilyas Ahmad Malik et al. (1988) whereas Bhatnagar and Singh (1964) and Singh and Jain (1970) recorded heterosis over better parent.

Misra et al. (1970) reported positive heterosis for seed weight over mid and better parent while Bhatnagar and Singh (1964) observed over mid parent only. While Singh and Jain (1970), Singh and Singh (1971), Singh and Singh (1972), Swindell and Poehlman (1976), Singh and Singh (1974), Sreekumar and Abraham (1978), and Ilyas Ahmad Malik et al. (1988)

have reported negative heterosis for seed weight over mid parent.

Tiwari and Ramanujam (1976) and Quah et al. (1983) reported positive heterosis for seed protein content in three out of 25 crosses. Negative heterosis or no heterosis was observed by Singh and Singh (1973) in mungbean for seed protein content.

Significant and positive heterosis for seed yield over mid parent was reported by Singh and Singh (1972), Singh (1974a), Singh and Singh (1974a), Gupta et al. (1978), Sreekumar and Abraham (1978), Raghu Ram Reddy (1980), Malhotra et al. (1980) and Quah et al. (1983). Whereas, Bhatnagar and Singh (1964), Singh (1974), Ramanujam (1975), Krishna Rao and Nagur (1979) reported heterosis over better parent of the order of 108 to 252, 48, 50 to 82 and 180 per cent, respectively. Singh and Jain (1979), Misra et al. (1970) Swindell and Poehlman (1976) Imrie et al. (1988) and Ilyas Ahmad Malik et al. (1988) reported positive heterosis over mid and better parents for seed yield.

2.7.2 Inbreeding Depression

Singh and Singh (1970) reported that the heterotic effects observed in F_1 s were maintained in F_2 generation in large number of crosses indicating that major portion of hybrid vigour in F_1 generation was due

to gene effects which are of fixable nature. Singh and Singh (1974) reported appreciable amount of inbreeding depression in F_2 . Yields dropped from 1.1 to 67.9 per cent of that of F_1 whereas yield reductions in F_3 was much more drastic ranging from 11.6 to 63.9 per cent of that of F_1 . Parida (1982) observed inbreeding depression for yield and yield components in all the wide and intervarietal crosses. In varietal crosses, the character seeds per pod expressed the lowest inbreeding depression indicating that this character is governed by additive gene action or complementary epistasis which are fixable in nature.

2.8 CORRELATIONS

Genetic improvement of yield is the primary concern of the plant breeder. Yield is a complex character and is highly influenced by the environment. On the contrary, the yield component traits are not only less complex and simply inherited but are influenced much less due to environmental deviations. Thus, selection based on the component characters has been considered to be more effective as compared to the selection of yield per se (Grafius, 1956). A knowledge on the association of yield components with yield is of paramount important while aiming at improvement in yield. Unfavourable associations between the desired

attributes under selection may result in genetic slippage (Dickerson, 1985) and limit genetic advance.

Phenotypic correlation is the correlation of phenotypic values and are subjected to changes in the environment. Phenotypic correlations measures the environmental deviations together with non-additive gene action while genotypic correlations is the correlation of breeding value (Additive + Additive x Additive gene action).

Several workers have studied the correlation coefficients in Mungbean. Contradictory associations have been reported for almost all the character pairs reported. This may be because of the different experimental material handled by them. Information on association analysis with a set of genotypes simultaneously over a number of environments and from segregating and non-segregating populations is scanty.

2.8.1 Association of component characters with yield

Positive and significant association between days to flowering and yield in mungbean was reported by Chandel et al. (1973), Joshi and Kabaria (1973), Malhotra et al. (1973), Giriraj and Vijayakumar (1974), Raghu Ram Reddy (1980) and Lill et al. (1988) whereas negative correlation of the same trait with yield was

recorded by Gupta and Singh (1969) and Xianghuai He et al. (1988).

Singh et al. (1968), Joshi and Kabaria (1973), Gupta et al. (1982) observed a positive association between days to maturity and yield whereas Singh and Malhotra (1970a), and Shah and Patel (1981) observed no correlation between these two traits. While Mungomery et al. (1972), Lawn (1979a), Gupta et al. (1982), Malik et al. (1982) and Misra and Sahu (1985) reported negative association for the same traits.

Significantly positive association of plant height with seed yield was reported by Giriraj and Vijayakumar (1974), Yohe and Poehlman (1975), Upadhya et al. (1980), Raghu Ram Reddy (1980), Boomikumaran and Rathinam (1981), Liu et al. (1984), Misra and Sahu (1985), Rosaiah (1985) and Sandhu et al. (1988). Negative correlation of plant height with yield was recorded by Bhaumik and Jha (1976) and Xianghuai He et al. (1988).

Malhotra et al. (1974a), Pokle and Patil (1975), Upadhya et al. (1980), Nagaraja Rao (1981), Shamsuzzaman et al. (1983) reported significant and positive correlation between the numebr of branches per plant and yield while singh and Malhotra (1970a), Tomar et al. (1972), Singh et al. (1975), Singh et al.

(1976), and Raut et al. (1988) observed non significant positive correlation.

Significant and positive correlation of number of clusters per plant with yield was noted by Malhotra et al. (1973 and 1974), Krishnaswamy et al. (1973) Raghu Ram Reddy (1980), Boomikumaran and Rathinam (1981), Nagaraja Rao (1981), Thandapani and Sakharam Rao (1984a), Ramana and Singh (1987) and Raut et al. (1987) while non significant positive correlation of the same trait with seed yield was observed by Singh and Singh (1970a, 1970b and 1973), Sandhu et al. (1979), Parida and Singh (1984), Rosaiah et al. (1987), Misra and Sahu (1985) and Sandhu et al. (1988).

Number of pods per plant with yield was found to have significantly positive correlation in most of the studies Singh et al. (1968), Malhotra (1968), Gupta and Singh (1969), Singh and Malhotra (1970b), Chandel et al. (1973), Joshi and Kabaria (1973), Krishnaswamy et al. (1973), Singh and Singh (1973), Malhotra et al. (1973, 1974), Giriraj and Vijayakumar (1975), Bhaumik and Jha (1976), Rathnaswamy et al. (1978), Raghu Ram Reddy (1980), Nagaraja Rao (1981), Singh and sharma (1981), Chowdhury et al. (1982), Parida and Singh (1982), Gupta et al. (1982), Shamsuzzaman et al. (1983), Kumari and George (1985), Liu et al. (1985), Misra and Sahu (1985), Rosaiah (1985), Ramana and Singh

(1987) Sandhu et al. (1988) and Xianghuai He et al. (1988) whereas Singh and Singh (1970), Tomar et al. (1973), Shakoor et al. (1979), and Parida and Singh (1984) recorded positive but non significant association.

Positive and significant association of pod length with seed yield was reported by Singh et al., 1968; Gupta and Singh, 1969; Singh and Malhotra (1970a); Singh and Malhotra (1970b); Joshi and Kaharia, 1973; Giriraj and Vijayakumar, 1974; Singh et al., 1980; Chowdhury et al., 1982; Sandhu et al., 1988; Xianghuai He et al., 1988. While positive but non significant association of the same trait with yield was also reported in mungbean (Tomar et al., 1973; Sandhu et al., 1979; Shakoor et al., 1979 and Raghu Ram Reddy, 1980).

Number of seeds per pod showed significantly positive correlation with seed yield by Singh et al. (1968), Singh and Malhotra (1970b), Malhotra et al. (1973), Joshi and Kabaria (1973), Singh and Singh (1973), Giriraj and Vijayakumar (1974), Pokle and Patil (1975), Bhumik and Jha (1976), Sandhu et al. (1979), Parida (1982), Chowdhury et al. (1983), Parida and Singh (1984), Ramana and Singh (1987), Sandhu et al. (1988), Raut et al. (1988) and Xianghuai He et al. (1988) whereas positive but non significant association

of seeds per pod with seed yield was reported by Singh and Singh (1970), Tomar et al. (1973), Shakoor et al. (1979) and Raghu Ram Reddy (1980).

Positive and significant correlation of seed weight with yield was reported by Singh et al. 1968; Malhotra, 1968; Gupta and Singh, 1969; Bhaumik and Jha, 1976; Parida, 1982; Chowdhury et al., 1982; Kumari and George, 1985; Rosaiah, 1985; Sandhu et al., 1988; Raut et al., 1988 and Xianghuai He et al., 1988 while positive but non significant association of the same trait with yield was reported by Singh and Singh (1970), Singh and Malhotra (1970a), Tomar et al. (1973), Singh et al. (1976) and Sandhu et al. (1979). Negative association of seed weight with yield was reported by Chandel et al. (1973), Giriraj and Vijayakumar (1974), Rathnaswamy et al. (1979), Raghu Ram Reddy (1980) and Nagaraja Rao (1981) in mungbean.

Positive association of total dry matter content of the plant with seed yield was reported by Pawar and Bhatia (1980), Santhisree (1985), Arwooth Lampang et al. (1988) and Natarajan and Palaniswamy (1988).

Raghu Ram Reddy (1980), Thandapani and Rao (1984), Rosaiah (1985), Bhadra et al. (1987) and Sandhu et al. (1988) reported that the seed protein and seed

yield were not related. However, positive association of seed protein with seed yield was reported in Mungbean under high nutrient conditions by Satijo et al. (1980).

2.8.2 Association among the yield component traits

Singh and Bahatnagar (1965) Singh and Malhotra 1970a), Malhotra et al. (1974), Gupta et al. (1982) reported positive correlation of days to flowering with days to maturity. Positive and significant correlation of days to flowering with plant height Singh and Malhotra (1970a), Raghu Ram Reddy (1980), Ramana and Singh (1987), Branches per plant (Malhotra et al., 1974 and Nagaraja Rao, 1981) Clusters per plant and pods per plant (Malhotra et al., 1974 and Raghu Ram Reddy, 1980) Seeds per pod (Singh and Malhotra, 1970a; Malhotra et al., 1974 and Ramana and Singh, 1987) were reported while negative correlation between days to flowering and clusters per plant Sandhu et al. (1978), pod length (Gupta and Singh, 1969; Singh and Malhotra, 1970a; Malhotra et al., 1974 and Sandhu et al., 1978). Seeds per pod (Sandhu et al., 1978), Seed weight (Gupta and Singh, 1979); Singh and Malhotra, 1970; Malhotra et al., 1974; Sandhu et al., 1978; Raghu Ram Reddy, 1980 and Nagaraja Rao, 1981) and with seed protein Malhotra et al. (1974) was reported in mungbean.

Significant and positive correlation of days to maturity with plant height and branches per plant (Malhotra et al., 1974), clusters per plant and pods per plant (Singh and Malhotra, 1970a; Malhotra et al., 1974) and negative correlation of days to maturity with seed weight (Singh and Malhotra, 1970a and Malhotra et al., 1974) and with seeds per pod (Sandhu et al., 1979) were reported in mungbean.

Positive association of branches per plant with clusters per plant, pods per plant, seeds per pod was reported by Tomar et al., 1972; Malhotra, 1974; Bhaumik and Jha, 1976; and Singh and Sharma, 1981, whereas negative correlation between the number of branches per plant with the pod length Singh et al., 1968; Malhotra et al., 1974; Sandhu et al., 1979 and Singh et al., 1981; seed weight (Malhotra et al., 1974; Sandhu et al., 1979; Singh et al., 1980 and Siddaraju, 1987) was observed in mungbean.

Positive correlation of plant height with number of clusters, pods per plant and pod length was reported in mungbean by Saraswathy et al., 1981; Sandhu et al., 1979; Raghu Ram Reddy, 1980; Satyan et al., 1981; Singh and Sharma, 1981 and Xianghuai He et al., 1988 while negative association of plant height with seed weight was reported by Raghu Ram Reddy (1980) and Nagaraja Rao (1981).

Significantly positive correlation between clusters per plant and pods per plant (Singh and Malhotra, 1970a; Malhotra et al., 1970; Singh et al., 1975; Sandhu et al., 1979; Raghu Ram Reddy, 1980 and Nagaraja Rao, 1981) seeds per pod (Singh and Malhotra, 1970a) were reported. Negative correlation of clusters per plant with seeds per pod (Singh et al., 1980), seed weight (Singh and Malhotra, 1970a; Raghu Ram Reddy, 1980 and Singh et al., 1980) and with pod length (Singh et al., 1970 and 1981) were also reported.

Singh and Singh (1970), Malhotra et al. (1974) and Rathinam et al. (1981) observed positive correlation of number of pods per plant with pod length and seeds per pod while negative correlation between pods per plant and seeds per pod (Singh et al., 1980); Seed weight (Malhotra et al., 1974; Raghu Ram Reddy, 1980; Nagaraja Rao, 1981 and Siddaraju, 1987; Pod length (Singh et al., 1968; Pokle and Patil, 1975 and Sandhu et al., 1979, 1988) was also observed.

Positive association of pod length with seeds per pod was reported by Malhotra et al., 1974; Bhaumik and Jha, 1976; Singh et al., 1981 and Nagaraja Rao, 1981; Parida and Singh, 1984; Ramana and Singh, 1987 and Sandhu et al., 1988; whereas positive but non significant association of pod length with seeds per pod was reported by Singh and Malhotra (1970), Giriraj

and Vijayakumar (1974), Raghu Ram Reddy (1980) and Boomikumaran and Rathinam (1981). Similar associations with seed weight was reported by Malhotra et al. (1974), Boomikumaran and Rathinam (1981) and Sandhu et al. (1988). Malhotra et al. (1968) reported that pod length had no association with any of the yield component trait.

Negative association of seeds per pod with seed weight was recorded by Singh and Malhotra (1970), Malhotra et al. (1974) and Raghu Ram Reddy (1980) while Shakoor et al. (1978) reported negative association of seeds per pod with seed protein.

Positive association of seed weight with seed protein was reported by Malhotra et al. (1974), Shakoor et al. (1979). While negative association was observed by Ong et al. (1978) whereas Bhadra et al. (1987) reported no association between seed weight and Seed protein content.

Sandhu et al. (1978) observed negative association of seed protein with clusters per plant, pods per plant, pod length and seeds per pod in mungbean.

2.9 PATH COEFFICIENT ANALYSIS

Path coefficient analysis devised by Wright (1921) is a standardised partial regression coefficient

which helps in partitioning of the correlation coefficient in to direct and indirect effects of independent variable on dependent variable. Dewey and Lu (1959) demonstrated the utility of path coefficient analysis in plant selection. Path analysis helps to elucidate the intrinsic nature of the observed associations and imparts a degree of confidence in the selection schemes adopted for a given situation (Dewey and Lu, 1959).

The available literature on direct and indirect effects of yield components on seed yield are presented hereunder.

Positive direct effect of pods per plant (Singh et al., 1970; Singh and Malhotra, 1970a; Chandel et al., 1973; Malhotra et al., 1974; Pokle and Patil, 1975; Reddy and Krishnaiah, 1977; Sandhu et al., 1980; Saraswathy et al., 1979; Shakoor et al., 1979; Sandhu et al., 1980; Upadhy and Singh, 1981; Malik et al., 1982; Gupta et al., 1982; Cheema et al., 1984; Khalid et al., 1984; Thulasidas and Rao, 1984; Kumari and George, 1985; Misra and Sahu, 1985; Santhisree, 1985; Khan, 1987; Raju, 1987 and Raut et al., 1988) Clusters per plant (Reddy and Krishnaiah, 1977; Saraswathy et al., 1979; Boomikumaran and Parthasarathy, 1981; Gupta et al., 1982; Vidhyadhar et al., 1981 and Rant et al., 1988) pod length (Shakoor et al., 1979; Saraswathy et

al., 1979; Khalid et al., 1984 and Thulasidas, 1984) seeds per pod (Singh et al., 1970; Singh and Malhotra, 1970a; Pokle and Patil, 1975; Reddy and Krishnaiah, 1977; Rathnaswamy et al., 1978; Saraswathy et al., 1979; Sandhu et al., 1980; Gupta et al., 1982; Malik et al., 1982; Vidhyadhar et al., 1984; Cheema et al., 1984, Khan, 1987 and Raut et al., 1988) seed weight (Singh et al., 1970; Singh and Malhotra, 1970; Chandel et al., 1973; Singh and Singh, 1973, Rathnaswamy et al., 1978; Saraswathy et al., 1979; Sandhu et al., 1980; Malik et al., 1982; Vidhyadhar et al., 1984; Thulasidas, 1984; Khalid et al., 1984; Kumari and George, 1985; Raju, 1987 and Raut et al., 1988) number of branches per plant (Pokle and Patil, 1975; Khalid et al., 1984 and Khan, 1987) days to flowering (Khan, 1987) days to maturity (Upadhaya and Singh, 1981 and Khan, 1987) total biomass on seed yield (Pokle and Patil, 1975; Khalid et al., 1984; Santhisree, 1985 and Khan, 1987) on seed yield was reported in mungbean.

Seeds per pod (Chandel et al., 1973; Malhotra et al., 1974 and Thulasidas and Rao, 1984) Seed weight (Malhotra et al., 1974 and Thulasidas and Rao, 1984) plant height (Boomikumaran and Parthasarathy, 1981), clusters per plant (Singh and Singh, 1973) and days flowering (Chandel et al., 1973) influenced seed yield indirectly through pods per plant.

MATERIALS & METHODS

CHAPTER III

MATERIAL AND METHODS

3.1 MATERIAL

The experimental material used in the present study comprised for released and pre-release mungbean cultures developed through selection, hybridization (single, double and multiple crosses) and mutation breeding under the All India Co-ordinated Pulses improvement Project (AICPIP), main centre, Regional Agricultural Research Station, Lam Guntur. The details of the cultures used in conducting studies on (i) Genotype - Environment interaction (ii) genetic divergence (iii) combining ability through a Line x Tester design during 1987-'88 to 1988-'89 in kharif, rabi (uplands) at Regional Agricultural Research Station and rabi (Rice fallows) at Munipalle are given in Table 3.1. Meteorological data pertaining to the experimental period are presented in Appendix-I.

3.2 FIELD PLOT TECHNIQUE

Experiment No.1 :

3.2.1 Studies on Genetic variability and genetic divergence

Forty Nine genotypes derived from various breeding programmes (hybridization through single

Table 3.1: CHARACTERISTICS OF THE GENOTYPES USED IN THE STUDY

S.NO.	CULTURE	PEDIGREE	SOURCE	CHIEF CHARACTERISTICS
1.	Pusa 105	Tainan-1/ML-6 x EGMG-16/ML3	Delhi	Pod bearing confined to the top of the plant, synchronous in maturity, seeds medium bold, shining green in colour. Tolerant to leaf spot diseases.
2.	ML 267	ML-1/L.No.987	Punjab	Leaflets, pods, seeds are small in size. All the clusters are not visible from the top, resistant to YMV, Seeds are shining green in colour.
3.	K 851	H 453-3/T 44	U.P.	Medium tall, dark green glossy foliage, pods long, seeds bold and shining green in colour.
4.	D12/333	Amrit/pusa baisakhi	Bihar	Short and compact in habit, Early and tolerant to drought. Seeds reddish green in colour.
5.	PDM 54	Sel.from Kundwa (Bahraich)	U.P.	Early and synchronous in maturity. Tolerant to moisture stress and heat. Moderately resistant to YMV.
6.	MH 309	PS16/ML37	Haryana	Early and Synchronous in maturity. Tolerant to heat and drought. Resistant to YMV. Seeds reddish green in colour.

Contd..

Contd..

S.NO.	CULTURE	PEDIGREE	SOURCE	CHIEF CHARACTERISTICS
7.	PS 16	Sel.from P596 Iran germplasm	Delhi	Wider adaptability beak of the pod small, seeds medium bold shining and light green.
8.	LGG 127 (Konda- veedu)	Sel.from PBM	A.P.	Early, pods glabrous, purple pigmentation along the suture of the pod. Dull green seed.
9.	LGG 402	Mutant from LGG 127.	A.P.	Medium in plant hight, Early in maturity longer pods. Seeds shining green.
10.	LGG 403	Mutant from LGG 127	A.P.	Bearing in compact clusters on the top of the canopy. Though susceptible to diseases it tolerates and gives good yields.
11.	LGG 404	Mutant from LGG 127	A.P.	Medium in plant height, long pods and more seeds/pod.
12.	LGG 405	Mutant from Pant mung-2	A.P.	Broad and dark green leaflets, seeds bold and shining green.
13.	LGG 407	Mutant from Pant mung-2	A.P.	Tall, medium duration, Dark green foliage, seeds medium bold, shining green seed, Resistant to YMV, root rot and angular black spot diseases.
14.	LGG 408	Mutant from Pant mung-2	A.P.	Late in maturity, medium in plant height, seeds medium bold and shining green.

Contd..

Contd..

S.NO.	CULTURE	PEDIGREE	SOURCE	CHIEF CHARACTERISTICS
15.	LGG 409	Mutant from Pant mung-2	A.P.	Tall and late in maturity seeds medium bold shining green.
16.	LGG 410	Mutant from Pant mung-2	A.P.	Tall, dark green foliage, bearing confident to the top seeds bold attractive shining green Resistant to YMV.
17.	LGG 414	Mutant from Pant mung-2	A.P.	Early in maturity, medium in height, seeds small and shining green.
18.	LGG 417	ML 33/UPM79- -3-4	A.P.	Tall bearing mainly on long terminal branched clusters, seeds small in size and shining green.
19.	LGG 418	ML 33/UPM 79- 3-4	A.P.	Tall in height, bearing confined to the top of plant, seeds shining green in colour.
20.	LGG 419	ML 33/UPM 79- 3-4	A.P.	Medium in height seed size small shining green in colour.
21.	LGG 421	UPM 79-34/ ML 267	A.P.	Tall, seed size small, shining green colour and high yielder.
22.	LGG 422	UPM 79-3-4/ ML 267	A.P.	Bearing confined to the top of the plant, seeds small, and shining green.
23.	LGG 423	UPM 79-3-4/ ML 267	A.P.	Tall, bearing confined to the top seed size small and shining green in colour.

Contd..

Contd..

S.NO.	CULTURE	PEDIGREE	SOURCE	CHIEF CHARACTERISTICS
24.	LGG 424	Pusa 105/ Patchaesalu	A.P.	Medium tall, Broad and darkgreen leaflets, bold and shining green seed.
25.	LGG 426	LGG 487-3/ ML 267	A.P.	Determinate in habit, early and synchronous in maturity. Dull green seed.
26.	LGG 429	UPM 79-3-4/ ML 267	A.P.	Tall, Medium bold shining green seed.
27.	LGG 431	ML 267/UPM 79- 3-4	A.P.	Tall, light green foliage, medium dull green seed.
28.	LGG 434	(Pusa 105/ Patchapesalu)x (LGG 487-3/ML267) x(Tara/M 986) x (ML 26-10-3/LGG 127)	A.P.	Tall, early in matu- rity. Seeds bold and shining green.
29.	LGG 435	(Pusa 105/Pat- pesulu) x (LGG 487-3/ ML 267) x (Tara/M986) x (ML26-10-3/ LGG 127)	A.P.	Tall and late in maturity, long pods and more seeds per pod.
30.	LGG 436	(Pusa 105/Patch- pesulu) x LGG 487-3/ML267) x(Tara/M 896) x (ML 26-10-3/ LGG 127)	A.P.	Late, Tall, seeds medium bold shining green.
31.	LGG 438	Mutant from LGG 127	A.P.	Tall, Bearing confined to the top, shining green seed.

Contd..

Contd..

S.NO.	CULTURE	PEDIGREE	SOURCE	CHIEF CHARACTERISTICS
32.	LGG 437	(Pusa 105/ Patchapesalu) x (LGG 487-3/ML267) x (Tara/M986) x (ML 26-10-3/ LGG 127)	A.P.	Late in maturity, long pods. Medium in height more seeds/pod.
33.	LGG 439	ML 33/UPM 79- 3-4	A.P.	Tall, seeds shining green seed.
34.	LGG 441	(Pusa 105/ Patchapesalu) x (LGG 487-3 x ML 267).	A.P.	Bearing confined to the top, pods long, seeds medium dull green seed.
35.	LGG 442	(Pusa 105/ Patchapesalu) x (LGG 487-3 x ML 267)	A.P.	Bearing confined to the top, Dark green foliage, long pods dull green seed.
36.	LGG 443	(UPM 79-3-4 ML 267) x Pusa 111/ Pusa 105)	A.P.	Medium in plant height, seeds medium bold and shining, tolerant to YMV.
37.	LGG 445	LGG 127/ML267	A.P.	Determinate in habit, long pods, Leaflets small and seed size small and dull green in colour.
38.	LGG 446	Mutant from LGG 127	A.P.	Determinate in habit, Leaflets broad and light green, Bearing confined to the top of the plant, medium size dull green seeds.
39.	LGG 447	Mutant from LGG 127	A.P.	Bearing confined to the top of the plant, seed size small and dull green in colour.

Contd..

Contd..

S.NO.	CULTURE	PEDIGREE	SOURCE	CHIEF CHARACTERISTICS
40.	LGG 449	(UPM 79-3-4/ ML 267) x (Pusa 111/ Pusa 105)	A.P.	Tolerant to YMV, seed size small and shining green.
41.	LGG 450	Mutant from Pantmung-2.	A.P.	Semi erect in habit shining green seed resistant to Pre- harvest sprouting, ABLS and YMV.
42.	LGG 453	Mutant from Pantmung-2	A.P.	Multifoliate leaf, seeds medium in size and shining green in colour.
43.	LGG 454	LGG 487-3/ ML 267	A.P.	Bearing confined to the top of the plant, long pods and dull green seed.
44.	LGG 487-3	Germplasm selection	A.P.	Long pods, more number of seeds per seed.
45.	Patcha- pesalu	Local collection	A.P.	Tall, seeds dull green in colour.
46.	DC1xDC2- 4SB-SB	(UPM 79-3-4/ ML 267) x Pusa 111/ Pusa 105) x (Pusa 105/ ML 267) x LGG 127/ ML 267)	A.P.	Tall in habit, bearing confined to the top of the plant shining green seed Tolerant to YMV.
47.	DC1xDC3- 5SB-SB	(UPM 79-3-4/ ML 267) x (Pusa 111/ Pusa 105)	A.P.	Medium Tall, profuse flowering shining green seed, tolerant to YMV.

Contd..

Contd..

S.NO.	CULTURE	PEDIGREE	SOURCE	CHIEF CHARACTERISTICS
48.	DC1xDC3- 6SB-SB	(UPM 79-3-4 x ML 267) X Pusa 111 x Pusa 105) x (Pusa 111/ ML 267) x (ML 267/Pusa 105)	A.P.	Synchronous in maturity, bearing at the top, Tolerant to YMV and CLS.
49.	DC1xDC2- ISB-SB	(UPM 79-3-4/ ML 267) x Pusa 111/ Pusa 105) x (Pusa 105/ML267) x LGG 127/ML 267.	A.P.	Medium in plant height synchronous in maturity, tolerant to YMV and CLS.
50.	ML 33	ML 1 x ML 23	Punjab	More number of branches per plant. Medium tall Resistant to YMV.
51.	UPM 79-3-4	Hyb. 45/L-80	U.P.	Shining green seed. Medium duration Resistant to YMV.
52.	M 986	Local selec- tion	U.P.	Profuse branching from basal nodes Bold seed.
53.	Tara	Selection from germ plasm	U.P.	Spreading and Radial branching.
54.	Pusa 111	76-16 x V 3476	Delhi	Dark green foliage. Synchronous in maturity, Photo and thermo-insensitivity Resistant to YMV, and CLS.
55.	Pusa 103	S-8 x CJ-4	Delhi	Medium bold seed Lodging resistant synchronous in maturity, Resistance to MYMV, CLS, root rot and.

Contd..

Contd..

S.NO.	CULTURE	PEDIGREE	SOURCE	CHIEF CHARACTERISTICS
56.	ML 26-10-3 (Pantmung-2)	ML 26 Mutant from	Punjab	Shining green seed, moderately resistant to YMV.
57.	MUG 125	ML 37/ Mash G-31	Punjab	High yield glabrous
58.	PDM 84-145	20/19 x CO-3	U.P.	Early, medium bold seed and shining green in colour.
59.	PDM 84-155	SPM 63-1/T 44	U.P.	Early, seeds medium bold and shining green in colour.
60.	ML 131	ML I/ML 23	Punjab	Tall, shining green seed, Resistant to YMV.
61.	UPM 83-10	ML 5/LM 214	U.P.	Tall, shining green seed, Resistant to YMV.
62.	UPM 79-4-12	LM 294-1/L 80	U.P.	Dull green seed Resistant to YMV.

YMV = Yellow mosaic virus
 CLS = Cercospora leafspot
 MYMV = Mungbean Yellow mosaic virus
 PBM = Pusa baisakhi mung
 LGG = Lam greengram

crosses, or multiple crosses and mutation breeding), were studied under three major situations in which mungbean is cultivated in Andhra Pradesh i.e. kharif, rabi (uplands) and rabi Rice fallows during 1987-88 and 1988-89 at the Regional Agricultural Research Station, Lam and at the Satellite Research Centre, Munipalle. The material was planted in a simple lattice design with two replications. Ten random plants were used for recording the data on 1) Days to 50% flowering, 2) Days to maturity, 3) Plant height (cm), 4) Number of branches per plant, 5) Number of clusters per plant, 6) Number of pods per plant, 7) Pod length (cm), 8) Number of seeds per pod, 9) 1000 seed weight (g), 10) Dry weight of shoot (g) at maturity, 11) Nitrogen content of shoot at 35 DAS (%), 12) Seed protein (%) and 13) seed yield per plant (g). The details of the field plot technique followed are given in Table 3.2.

Table 3.2: Details of the experiment on genetic variability and genetic divergence.

Number of geno- types studied	Number of environments studied	Date of sowing	Design adopted	No. of repli- cations	Plot size
<u>THREE</u>					
49*	E1: Rabi (uplands)	24-10-87	Simple	2	5.0x2.4 m
	E2: Rabi (Rice fallows)	29-11-87	Lattice		
	E3: Kharif	11-7-88			

* List of genotypes used for genetic variability and genetic divergence studies

1. LGG 402	11. LGG 419	21. LGG 436	31. LGG 449
2. LGG 403	12. LGG 421	22. LGG 437	32. LGG 450
3. LGG 404	13. LGG 422	23. LGG 438	33. LGG 453
4. LGG 405	14. LGG 423	24. LGG 439	34. LGG 487-3
5. LGG 408	15. LGG 424	25. LGG 441	35. Patchapesalu
6. LGG 409	16. LGG 426	26. LGG 442	36. DCIxDC2-4SB-SB
7. LGG 410	17. LGG 429	27. LGG 443	37. ML 267
8. LGG 414	18. LGG 431	28. LGG 445	38. Pusa 105
9. LGG 417	19. LGG 434	29. LGG 446	39. DCIxDC3-5SB-SB-49
10. LGG 418	20. LGG 435	30. LGG 447	40. DCIxDC3-65SB-SB
41. DCI x DC2-ISB-SB	46. Pusa 111		
42. ML 33	47. Pusa 103		
43. UPM 79-3-4	48. LGG 127		
44. M 986	49. ML 26-10-3		
45. Tara			

Experiment No.2:

3.2.2 Genotype - Environment interaction studies

Twenty diverse genotypes mostly released or pre release cultures under All India Co-ordinated Varietal Trials were studied in a randomized block design with three replications in three seasons over two years during 1987-88 to 1988-89. Each plot consisted of four rows of five metres length adopting a spacing of 30 cm.

between rows and 10 cm within the row. Data were recorded on 10 randomly selected competitive plants from each replication on Days to 50% flowering, Days to maturity, plant height (cm), Number of branches per plant, Number of clusters per plant, Number of pods per plant, Pod length (cm), Number of seeds per pod, 1000 seed weight (g), Dry weight of shoot (g) at maturity, Nitrogen content of shoot at 35 DAS (%), Seed protein (%), seed yield per plant (g) and seed yield per plot (g). The number of genotypes, test environments and replications used in the experiment are given in Table 3.3.

Experiment No.3:

3.2.3 Combining ability studies

Through Line x Tester Programme, Four lines viz., Pusa 105, ML 267, K 851 and D 12/333 and five testers viz., PDM 54, MH 309, LGG 410, LGG 450 and UPM 79-4-12 were sown in paired rows during August - September 1987 with three staggered sowings at 15 days interval. A row spacing of 60 cm was kept to facilitate easy handling while effecting crosses. Hybridization was carried out by simultaneous emasculation and pollination using clipping off technique. Half of the crossed seeds of each cross combination was grown during rabi 1987-88 under rice fallows to advance material to F_2 . The experimental material comprising' twenty single

Table 3.3: Details of environments and genotypes used in genotype-environment interaction studies.

S.No.	Genotype	Environment	Date of sowing	Season	Design and Number of replications	Plot Size
1.	MUG 125	6	1-8-87	Kharif	3	5.0 x 1.2 m
2.	LGG 403					
3.	LGG 407					
4.	LGG 410					
5.	LGG 426					
6.	PDM 84-145					
7.	PDM 84-155	Environment-II	6-10-87	Rabi uplands	RBD	5.0 x 1.2 m
8.	PDM 84-155	Environment-III	29-11-87	Rabi rice fallows	RBD	5.0 x 1.2 m
9.	D12/333	Environment-IV	11-7-88	Kharif	RBD	5.0 x 1.2 m
10.	MH 309	Environment-V	30-11-88	Rabi uplands	RBD	5.0 x 1.2 m
11.	ML 131					
12.	LGG 127					
13.	PS 16					
14.	UPM 83-10					
15.	PDM 54					
16.	Pusa 105	Environment-VI	27-11-88	Rabi rice fallows	RBD	5.0 x 1.2 m
17.	LGG 450					
18.	K 851					
19.	ML 26-10-3					
20.	ML 267					
21.	UPM 79-4-12					

crosses at F_1 and F_2 generations along with parents were studied in a randomized block design with 3 replications during kharif 1988-89, the main season in which the mungbean is cultivated in Andhra Pradesh. The details of the experimental design are as follows :

Table 3.4: Details of the experiment on combining ability studies.

Number of genotypes studied	Date of sowing	Number of repli- cations	Design adop- ted	Plot Size (M ²)
9 Parents,) 20 F_1 hybrids) and) 20 F_2 popula-) tions)	12-7-88	3	RBD	Parents - 5.8x1.8 m F_1 hy- brids - 5.0x0.6 m F_2 hy- brids - 5.0x3.0 m (500 plants).

3.2.3.1 Details of cross combinations studied at F_1 and F_2 generations

1. Pusa 105 x PDM 54	11. K 851 x PDM 54
2. Pusa 105 x MH 309	12. K 851 x MH 309
3. Pusa 105 x LGG 410	13. K 851 x LGG 410
4. Pusa 105 x LGG 450	14. K 851 x LGG 450
5. Pusa 105 x UPM 79-4-12,	15. K 851 x UPM 79-4-12
6. ML 267 x PDM 54	16. D12/333 x PDM 54
7. ML 267 x MH 309	17. D12/333 x MH 309
8. ML 267 x LGG 410	18. D12/333 x LGG 410
9. ML 267 x LGG 450	19. D12/333 x LGG 450
10. ML 267 x UPM 79-4-12,	20. D12/333 x UPM 79-4-12

Lines	Testers
1. Pusa 105	5. PDM 54
2. ML 267	6. MH 309
3. K 851	7. LGG 410
4. D 12/333	8. LGG 450
	9. UPM 79-4-12.

The experimental material was successfully raised following the recommended package of practices as suggested in the ZREAC (1987 & 88) proceedings of the Krishna - Godavari Zone.

3.3 DATA RECORDED

Data were recorded on 10 randomly selected plants from each replication in all the experiments except in F_2 wherein the data were recorded on 25 sample plants. The details of the data are described below :

3.3.1 Days to 50% flowering

Number of days taken from sowing to flowering by half of the population or plants in each replication were counted and recorded as days to 50% flowering.

3.3.2 Days to maturity

This character was recorded as the number of days taken from the date of sowing to 85 per cent pod

maturity in each plant and the mean value of the sample plants is taken as the number of days to maturity.

3.3.3 Plant height (cm)

Length of main stem from ground level to the tip of the main raceme was measured in centimeters at maturity. The mean value of sample plants was recorded as the plant height in centimeters.

3.3.4 Number of branches per plant

Number of branches were counted on the randomly selected plants at maturity in each replication and the mean value was taken as the number of branches per plant.

3.3.5 Number of clusters per plant

Number of pod bearing clusters were counted on each plant at the time of harvest and the mean of sample plants was recorded as the number of clusters per plant.

3.3.6 Number of pods per plant

Number of well filled pods from all clusters on each plant were counted and the mean value of the random sample plants was recorded as the number of pods per plant.

3.3.7 Pod length (cm)

Five randomly selected pods from each sample plant were used for measuring pod length. Length of pods was measured in centimeters from the base of the pod to the tip excluding the beak. The average of all the pods taken from the sample plants was expressed as the pod length in centimeters.

3.3.8 Number of seeds per pod

Five random pods from each plant were chosen to count the number of seeds per pod. The average number of seeds from all pods counted from the sample plants was expressed as the number of seeds per pod.

3.3.9 1000 seed weight (g)

One thousand well developed seeds from each sample plant were counted and their weight was recorded in grams. The average value of the sample plants was expressed as seed weight for 1000 seeds.

3.3.10 Dry weight of the shoot at maturity (g)

Sample plants were collected at harvestable maturity i.e., five days before the harvest date and dried in an oven at 72°C until constant dry weight was recorded. Average value of sample plants was taken as the dry weight of shoot per plant in grams.

3.3.11 Seed protein (%)

Nitrogen content of the seeds of sample plants was estimated following micro-kjeldahl 'N' estimation method and the crude protein content was calculated using the formula.

Per cent protein = per cent nitrogen x 6.25.
The average seed protein content of random sample plants was taken as the seed protein content in percentage.

3.3.12 Nitrogen content of shoot at 35 DAS (%)

Nitrogen content of the individual plant was analysed by microkjeldahl method from the shoot samples collected at 35 DAS. Mean value of the sample plants was given as the percent nitrogen content of the shoot material.

3.3.12.1 Estimation of nitrogen content

Nitrogen content was estimated using micro-kjeldahl 'N' method given by AOAC (1970). 200 milligrams of finely powdered plant or seed sample was digested in micro kjeldahl flask by adding 3 ml of concentrated sulphuric acid in the presence of 1:4 ratio of K_2SO_4 and $CuSO_4$ mixture for about 30 minutes till the solution became colourless. The digest was diluted with distilled water and transferred to

distillation flask by washing and then the sample was neutralised with 40% of NaOH. The liberated ammonia was collected in four per cent boric acid containing mixed indicator (Methyl red and phenolphthalln in 1:2 ratio). The distillate was titrated against the standard H_2SO_4 . A blank titre value was obtained by conducting one blank experiment.

1 ml of 0.1N H_2SO_4 was taken as equivalent to 0.0014 g. of Nitrogen.

$$\text{Nitrogen per cent} = \frac{(\text{Titre value} - \text{blank titre value}) \times 0.0014 \times 100}{\text{Weight of sample}}$$

3.3.13 Grain yield per plant (g)

All the seed harvested from each of the sample plant was dried and the weight was recorded in grams up to one decimal. The average of the sample plants was expressed as seed yield per plant in grams.

3.3.14 Grain yield per plot (g)

This character was recorded by weighing the total seed produced from each replication and the mean value of three replications was expressed as seed yield per plot in grams.

3.4 STATISTICAL TECHNIQUE

Experiment No.1:

3.4.1 Genetic variability and divergene studies

General form of analysis of variance in simple lattice design is given below:

Table 3.5: Analysis of variance and mean sum of squares in a simple Lattice design.

Source of variation	Degrees of freedom	Sum of squares	Mean Sum of squares
Replications	$r-1$	SSQR	$\frac{SSQR}{r-1}$
Treatments (Adjusted)	k^2-1	SSQT (adjusted)	$\frac{SSQT}{k^2-1}$ (adjusted)
Block within replication adjusted for treatment effect	$r(K-1)$	SSQB (adjusted)	$\frac{SSQB}{r(K-1)}$ (adjusted)
Intra block error	$(k-1) \times (rk-k-1)$	SSQB	$\frac{SSQE}{(K-1)(rk-k-1)}$
Total	rk^2-1		

Standard errors:

- (a) Standard error for difference between two means occuring in the same block

$$SE (s) = \sqrt{\frac{2Ee}{r} [1+(r-1) U]}$$

SE(s) = Standard error for intra block varieties

Ee = Intra block mean sum of squares

$$U = \text{Weightage factor} = \frac{Eb - Ee}{K(r-1)Eb}$$

(b) Standard error for comparing treatment means that occur in different blocks SE(D)

$$= \frac{2 Ee}{r} [i + rU]$$

(c) Average standard error SE(M)

$$= \sqrt{\frac{2Ee}{r} \left(i + \frac{rku}{(K+1)} \right)} \quad \begin{array}{l} K = \text{No. of varieties} \\ \text{in each block} \end{array}$$

3.4.1.1 Estimation of genetic parameters

(a) Genotypic M.S. due to varieties - Error mean S.S.
variance = $\frac{\text{M.S. due to varieties} - \text{Error mean S.S.}}{\text{No. of replications}}$
(σ^2_g)

(b) Phenotypic variance(σ^2_p) = $\sigma^2_g + \sigma^2_e$

(c) Genotypic coefficient of variation (GCV) = $\frac{\sigma_g}{x} \times 100$

(d) Phenotypic coefficient of variation (PCV) = $\frac{\sigma_p}{x} \times 100$

(e) Heritability [$h^2(b)$] = $\frac{\sigma^2_g}{\sigma^2_p} \times 100$

(f) Genetic advance (GA) = $k \times \sigma_p \times h^2(b)$

$$(e) \text{ Genetic advance as per cent of mean} = \frac{GA}{\bar{x}} \times 100$$

Where σ_p = Phenotypic standard deviation
 σ_g = Genotypic standard deviation
 $\bar{x}$ = General mean
 $h^2(b)$ = Heritability in broad sense.
 k = Selection differential which takes care of mean phenotypic value of all material studied, mean phenotypic value of lines selected for further study, phenotypic standard deviation of original lines and proportion of lines selected K value at 5% selection intensity is 2.05.

GCV and PCV were calculated using the formula suggested by Burton (1952), Heritability in broad sense according to Allard (1960) while genetic advance was calculated following the formulae suggested by Lush (1940) and Johnson et al. (1955).

3.4.1.2 Genetic diversity with D^2 statistic

A measure of group distance based on multiple characters was given by Mahalanobis (1936). D^2 technique with the help of which, genetic diversity between genotypes can be estimated. The D^2 value

between 'Ist and 'Jth genotypes for 'P' characters was calculated as

$$D^2_{ij} = p \sum_{t=1} (\bar{Y}_{it} - \bar{Y}_{jt})$$

Where $\bar{Y}_{it}$ = un correlated mean value of ith genotype for (t) character.

$\bar{Y}_{jt}$ = un correlated mean value of Jth genotype for (t) character and $D^2_{ij} = D^2$ between ith and Jth genotype.

The steps involved are:

(a). Test of significance:

Variances were calculated from all the 13 characters investigated and test of significance was done. Analysis of covariance for the character pairs was estimated on the basis of mean values (Panse and Sukhatme, 1967). From the estimates, a dispersion table was prepared. After testing the differences between genotypes for each of the characters, a simultaneous test of significance of differences between the mean values of a number of correlated variables was done (Rao, 1952) by using 'V' statistic, which inturn, utilizes wilk's criterion (Wilks' 1932). The sum of squares and sum of products of error and error variety variance-covariance matrix were used for this purpose. The estimates of Λ (Wilk's criterion) were done using the following relation.

$$-\lambda, \frac{W}{S} \text{ where } -\lambda, \text{ wilk's criterion}$$

W = Determinant of error matrix

S = Determinant of error + variety
matrix

$$V \text{ stat} = -m \log \lambda = -\frac{(n-P+Q+1)}{2} \log e$$

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

p = Number of variables or characters

q = Number of genotypes - 1

n = Degrees of freedom of error + varieties

$$\log e \lambda = 2.3407 \log 10$$

v (stat) is distributed as χ^2 with PQ

(b). Transformation of correlated variables

In the present model, computation of D^2 values was reduced to simple enumeration of differences in mean values of various characters of the two genotypes i.e. Edi2, therefore, transformation of correlated variables in to standardised uncorrelated ones was done before working out the D^2 values. Transformation was done using pivotal condensation method.

(c). Computation of D^2 values

For a given combination of 'i' and 'j' genotype the mean deviation: $\bar{Y}_{it} - \bar{Y}_{jt}$ for $t = 1, 2, \dots, P$

variables are computed and the D^2 values were calculated as sum of squares of the deviation i.e.

$$\sum_{t=1}^P (\bar{Y}_{it} - \bar{Y}_{jt})^2$$

(d). Testing the significance of D^2 values

The D^2 values obtained for a pair of genotypes was taken as the calculated value of Y^2 and tested against tabulated Y^2 at 'P' degrees of freedom where 'P' is the number of variables or characters considered.

(e). Grouping of genotypes in to various clusters:

Grouping of the genotypes in to different clusters was done by using Tocher's method as described by Rao (1952). The criterion used in clustering by this method was that any two genotypes belonging to the same cluster should atleast on an average show a smaller D^2 value among themselves than those belonging to two different clusters.

The first step in grouping the genotypes into different clusters was to arrange the genotypes in to order was their relative distance from each others. For this purpose, D^2 values of all the possible combinations in each genotype was arranged in increasing order of this magnitude in a tabular form as described by Singh and Chowdhury (1977). To start with, the two genotypes having the smallest distance from each other are

considered first to which third population having the smallest average D^2 value from the first two genotypes were added. Then comes the nearest fourth genotype and so it goes on. At certain stage when it was felt that after adding a particular variety, there was a disrupt increase in the average D^2 value, then that variety was not considered for inclusion in that cluster. Thus, the process was continued till all the genotypes are included in one or the other cluster.

(i) Average intra cluster distance:

For the measure of intra-cluster distances, the formula used was $\sum D_i^2/n$ where $\sum D_i^2$ was the sum of distances between all possible combinations (n) of the genotypes included in a cluster.

(ii) Average inter-cluster distance:

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

Experiment No.2:

3.4.2 Genotype x Environment Interaction Studies

3.4.2.1 Analysis of variance: The analysis of variance for each character was carried out as per the method suggested by Panse and Sukhatme (1978). The significance was tested by referring to 'F' table value to Fisher and Yates (1963). Per plant values for all the characters under each experiment were used for statistical analyses except in case of grain yield wherein per plot grain yield was analysed and general form of analysis variance is given in Table 3.6.

Table 3.6: General form of environment wise analysis of variance and expected mean squares in randomized block design in Experiment No. 2.

Source of variation	Degree of freedom	Mean observed	Squares expected
Replications	2	Mr	$\sigma^2_e + \sigma^2_r$
Genotypes	19	Mg	$\sigma^2_e + \sigma^2_g$
Error	38	Me	σ^2_e
Total	59		

- r = number of replications
- g = number of genotypes
- Mg = Genotype mean squares
- Mr = replication mean squares
- Me = Error mean squares
- σ^2_e = Error variance
- σ^2_g = variance due to genotypes
- σ^2_r = variance due to replications.

The form of analysis of variance of multi-environmental data is given in Table 3.7.

Table 3.7: Analysis of variance of multi-environmental data and means sum of squares according to Eberhart and Russell model (1966).

Source	Degress of freedom	mean sum of squares	F test
Genotypes (G)	t-1	MS2	MS2/MS4
Env. + Gx Env.	t(S-1)		
Env. (linear)	1		
G x Env (linear)	t-1	MS3	MS3/MS4
Pooled deviations	t (S-2)	MS4	MS4/MS5
Pooled error	St (r-1)(t-1)	MS5 = Me'	

Stability parameters for the characters studied were estimated following the model given by Eberhart and Russel (1966).

$$Y_{ij} = m + BiI_j + S_{ij} \quad (i = 1, 2, \dots, t) \\ (j = 1, 2, \dots, s)$$

t = varieties

s = Environments

Y_{ij} = Mean performance of 'I'th variety in the 'J'th environment

$\bar{m}$ = Mean of all the varieties over all the experiments

B_i = The regression coefficient of the 'I'th variety on the environmental index which measures the response of the variety to varying environments.

I_j = The environmental index which is defined as the deviation of the mean of all the varieties at a given location from the over all means.

$$= \frac{\sum_i V_{ij}}{t} - \frac{\sum_i \sum_i Y_{ij}}{ts} \text{ with } \sum_i I_j = 0$$

and S_{ij} = The deviation from regression of the 'I'th variety at the 'J'th environment.

3.4.2.2 Stability parameters

a) **Regression coefficient(b_i)** Regression of the performance of each variety under different environments on the environmental means over all genotypes. This is estimated as follows.

$$b_i = \frac{\sum_j Y_{ij} I_j}{\sum_j I_j^2}$$

where $\sum_j Y_{ij} I_j$ is the sum of products and $\sum_j I_j^2$ is the sum of squares

(b) Mean square deviation ($S^2 d^{-2}$) from linear regression

$$= \frac{\sum_{j=1}^s s_{ij}^2}{(s-2)} - \frac{s^2}{r} e$$

$$\text{where } \sum_{j=1}^s s_{ij}^2 = \sum_{j=1}^s Y_{ij}^2 - \frac{Y_i^2}{t} - \frac{(\sum_{j=1}^s Y_{ij} I_j)^2}{\sum_{j=1}^s I_j^2}$$

and $S^2 e$ = the estimate of pooled error

I Computation of environmental Index (I_j)

$$I_j = \frac{\sum_{i=1}^s Y_{ij}}{t} - \frac{\sum_{j=1}^s \sum_{i=1}^s Y_{ij}}{ts}$$

$$= \frac{\text{Total of all the varieties at Jth location}}{\text{No. of varieties}} - \frac{\text{Grand total}}{\text{Total No. of observations}}$$

$$\text{check } \sum_{j=1}^s I_j = 0$$

II Computation of regression coefficient (b) for each variety

$$b_i = \frac{\sum_{j=1}^s Y_{ij} I_j}{\sum_{j=1}^s I_j^2}$$

$\sum_{j=1}^s Y_{ij} I_j$ = Product of environmental Index and with corresponding means of that variety at each location.

$\sum_j I_j^2 =$ Sum of environmental Index squares from all locations.

These values are obtained in the following manner

$$(\bar{X}) (I_j) = \left(\sum_j V_{ij} I_j \right) = (S)$$

$(\bar{X})$ = Matrix of means

(I_j) = Vector for environmental Index

(S) = Vector for sum of products ie., $\sum V_{ij} I_j$

III Computation of $s^{-2} d$: In regression analysis it is possible to partition the variance of the dependent variable (y) into two parts, the one which explains the linearity between dependent and independent variables (variance due to regression) and the other which explains the variance due to deviations from linearity.

Symbolically $\sigma^2 y = \sigma^2 \text{ regression} + \sigma^2 \text{ deviation from the regression.}$

Obviously by subtracting the variance due to regression from $\sigma^2 y$, one can get the variance due to deviations from regression which in turn can be used for estimating $s^{-2} d$ values. The variance of means over different environments with regard to individual varieties may be obtained in the following way.

$$\sigma^2 V_i = \sum_j Y_{ij}^2 - (Y_i^2/t)$$

Deviations from their regressions

$$\begin{array}{c}
 \text{Varieties } \sigma^2_{vi} \quad b_i \quad \sum_j Y_{ij} \quad I_j \quad b_i \quad \sum_j Y_{ij} \quad I_j \\
 \hline
 \sum_j S_{ij}^2 = \sigma^2_{vi} - b_i \sum_j Y_{ij} I_j \\
 \hline
 \end{array}$$

Variance due to deviations from regression

$$\left(\sum_j S_{ij}^2 \right)^2 \text{ for a variety }$$

$$\sum_j S_{ij}^2 = \frac{\left[\sum_j Y_{ij}^2 - \frac{(\sum_j Y_{ij} I_j)^2}{\sum_j I_j^2} \right]}{t}$$

Where $\sum_j Y_{ij}^2 - (Y^2_{i..} / t) =$ The variance due to dependent variable.

$$\frac{(\sum_j Y_{ij} I_j)^2}{\sum_j I_j^2} = \text{The variance due to regression}$$

$$\begin{aligned}
 \text{Because } \frac{(\sum_j Y_{ij} I_j)^2}{\sum_j I_j^2} &= \frac{(\sum_j Y_{ij} I_j)}{\sum_j I_j^2} \cdot \frac{(\sum_j Y_{ij} I_j)}{\sum_j I_j^2} \\
 &= b_i \sum_j j_{ij} I_i
 \end{aligned}$$

$$\text{Check for pooled deviation} = \sum_j \sigma^2_{vi} - (b_i \sum_j Y_{ij} I_j)$$

stability parameter $s^{-2}d$ for each variety is computed like this.

$$s^{-2} d_i = \frac{\sum_j s_{ij}^2}{(S-2)} - \frac{s^2 e}{r}$$

$s^2 e$ = Mean square for pooled error

t = No. of genotypes r = No. of replications

S = No. of environments Me = Pooled $\sigma^2 e/r$

S.S. due to environment + (Variety x environment)

$$= \sum_i \sum_j Y_{ij}^2 - (\sum_i Y_i^2/t)$$

S.S.(Env.+(variety + Env.) = S.S.Env.+(SS.VarietyxEnv)

$$\text{Where S.S. Env.} = \frac{(1/t) (\sum_j Y_{.j} I_j^2)}{\sum_j I_j^2}$$

$$\text{S.S. Env. (linear)} = t \times \sum_j I_j^2$$

$$\text{S.S. variety x Env. (linear)} = \frac{\sum_j (\sum_i Y_{ij} I_j^2)^2}{\sum_j I_j^2}$$

- S.S. Env. (Linear)

$$\frac{(\sum_j Y_{.j} I_j^2)}{\sum_j I_j^2} = b_i \sum_j Y_{ij} I_j$$

Pooled deviation is the sum of S.S due to deviation for individual varieties.

'F' test:

- (a) To test the significance of the differences among the variety means i.e., $H_0 = \mu_1 = \mu_2 = \mu_3 \dots \mu_t$

$$F = \frac{MS_2}{MS_4} \quad \begin{array}{l} MS_2 = \text{Variety mean S.S} \\ MS_4 = \text{pooled deviation} \end{array}$$

- (b) To test the varieties that do not differ for their regression on environmental index

$$H_0 = b_1 = b_2 = \dots b_t$$

$$F = \frac{MS_3}{MS_4} \quad \begin{array}{l} MS_3 = \text{Mean S.S. due to variety x} \\ \text{Env. (linear)} \end{array}$$

- (c) Individual deviations from linear regression is tested as follows:

$$F = \frac{\sum_j s_{ij}^2}{S-2} \quad / \text{ pooled error}$$

Mean and Standard error of 'b'

$$\text{Mean of } b = \bar{b} = \sum_i b_i / V$$

$$S.E.(b) = \sqrt{\frac{\text{M.S. due to pooled deviation}}{\sum_j I_j^2}}$$

Population mean (μ) and standard error are calculated as follows:

$$\text{Population mean (U)} = \frac{\text{Grand total}}{\text{No. of observations}}$$

$$\text{S.E. (mean)} = \sqrt{\frac{\text{M.S. due to pooled deviation}}{\text{No. of environments} - 1}}$$

Experiment NO.3:

3.4.3 Combining Ability Studies

Combining ability analysis in a Line x Tester design was carried out following Kempthorne (1957). The mathematical model for combining ability analysis is given below.

$$Y_{ijk} = \mu + g_i + g_j + S_{ij} + r_k + e_{ijk}$$

Where

Y_{ijk} = Any measurable characters of the cross ixj

g_i = gca effect of the female parent

g_j = gca effect of the male parent

S_{ij} = Sca effect of the cross ij

r_k = Kth replication effect

e_{ijk} = Environmental effect particular to
(ijk) to individual

μ = Population mean effect

Table 3.8: Analysis of variance with parents and crosses in RBD.

Source of variation	Degree of freedom	Mean sum of squares	F test	
Replications	r-1	RMS	M1	M1/M6
Treatments	t-1	Tr.Ms	M2	M2/M6
Parents (P)	p-1	PMS	M3	M3/M6
Crosses (C)	(C-1)	CMS	M4	M4/M6
PVsC	1	P.VMs	M5	M5/M6
Error	(r-1)(t-1)	EMS	M6	

Table 3.9: Anova for line x tester analysis

Source of variation	Degrees of Freedom	Mean Sum of Squares	
		Observed	Expected
Lines	(L-1)	$M1 \sigma^2_e + r \text{Cov}(\text{FS}) - 2\text{Cov}(\text{HS}) + \text{Lr Cov}(\text{HS})$	
Testers	(T-4)	$M2 \sigma^2_e + r \text{Cov}(\text{FS}) - 2\text{Cov}(\text{HS}) - \text{Tr Cov}(\text{HS})$	
Line x Tester	(L-1)(T-1)	$M3 \sigma^2_e + r \text{Cov}(\text{FS}) - 2 \text{Cov}(\text{HS})$	
Error	(r-1)(LT-1)	$M4 \sigma^2_e$	

3.4.3.1 Estimation of heterosis

Heterosis is expressed as per cent of mean of parents and also as per cent of superior parent known as heterobeltiosis:

$$\text{Heterosis (H)} = \frac{\bar{F}_1 - \overline{M.P.}}{\overline{M.P.}} \times 100$$

$$\text{Heterobeltiosis (H2)} = \frac{\bar{F}_1 - \overline{B.P.}}{\overline{B.P.}} \times 100$$

Where

$\bar{F}_1$ = Mean of F_1

$\overline{M.P.}$ = Mid parental value

$\overline{B.P.}$ = Better parental value

To test the significance of heterosis, the following formula suggested by Arunachalam (1980) (Personal communication) was utilised.

$$t = \frac{\bar{F}_1 - \overline{B.P.}}{\sqrt{\frac{2.E MS(F_1)}{r}}}$$

Where

r = No. of replications

EMS = Error mean sum of squares

Significance of 't' tested by referring to 't' table values.

3.4.3.2 Estimation of inbreeding depression

$$\text{Inbreeding depression} = \frac{\bar{F}_1 - \bar{F}_2}{\bar{F}_1} \times 100$$

Where,

$$F_1 = F_1 \text{ mean}$$

$$F_2 = F_2 \text{ mean}$$

3.4.3.3 Estimation of Combining Ability Effects

The individual effects are estimated as follows:

$$\text{i) gca effect of line} \quad g_l = \frac{x_{l..}}{tr} - \frac{x_{...}}{ltr}$$

$$\text{ii) gca effect of tester} \quad g_t = \frac{x_{.t}}{lr} - \frac{x_{...}}{ltr}$$

$$\text{iii) sca effect of crosses} = \frac{x_{lt}}{r} - \frac{x_{l..}}{tr} - \frac{x_{.t}}{lr} + \frac{x_{...}}{ltr}$$

Where

- x_l = Total of female parent over all males and replications
- x_t = Total of male parent over all females and replications
- $x_{...}$ = Total of all cross combinations over all replications
- x_{lt} = lt combination total over all replications.
- t = Number of tester
- l = Number of lines
- r = Number of replications.

3.4.3.4 Estimation of standard errors for combining ability effects

The standard errors pertaining to gca effects of lines and testers and sca effects of different cross combinations were calculated as shown below :

$$\text{S.E. } g(l) \text{ lines} = \sqrt{\frac{\text{Error variance}}{rt}}$$

$$\text{S.E. } g(t) \text{ tester} = \sqrt{\frac{\text{Error variance}}{rl}}$$

$$\text{S.E. } g(lxt) = \sqrt{\frac{\text{Error variance}}{r}}$$

$$\text{S.E. } (gl-gt) \text{ line} = \sqrt{\frac{2 \text{ Error variance}}{rt}}$$

$$\text{S.E. } (gl-gt) \text{ tester} = \sqrt{\frac{2 \text{ Error variance}}{rl}}$$

$$\text{S.E. } (slt-skl) = \sqrt{\frac{2 \text{ Error variance}}{r}}$$

3.4.3.5 Genetic components

Estimation of variances due to combining ability over estimated using the following formulae.

$$\text{Cov. H.S. (line)} = \frac{Ml - Ml \times t}{rt}$$

$$\text{Cov. H.S. (tester)} = \frac{Mt - Ml \times t}{rl}$$

$$\text{Cov.H.S.(average)} = \frac{1}{r(2lt-1-t))} \frac{(1-l)(Ml)+(t-l)(Mt)}{1+t-2} - Mlt$$

$$\text{Cov. (FS)} = \frac{(Ml-Me) + (Mt-Me) + (Mlxt-Me) +}{3r}$$

$$\frac{6r \text{ Cov HS} - r (1+t) \text{ Cov. (HS)}}{3r}$$

$$\sigma^2_{gca} = \text{Cov. HS} = \frac{(HF)^2}{(4)} = \sigma^2_A$$

$$\sigma^2_{sca} = \frac{Ml \times t - Me}{r}$$

3.4.3.6 Heritability in narrow sense (h^2 n.s)

$$h^2 \text{ (n.s)} = \frac{2\sigma^2_{gca}}{2\sigma^2_{gca} + \sigma^2_{sca} + \sigma^2_e} \times 100$$

3.4.3.7 Average degree of dominance

$$\text{Degree of dominance} = \sqrt{\frac{\sigma^2_{sca}}{2\sigma^2_{gca} + \sigma^2_{sca}}}$$

3.4.5 Simple correlation coefficients

Simple phenotypic correlation coefficients between different variables were calculated by using covariance technique (Falconer, 1964).

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

Where

$r(x_i, x_j)$ = Correlation between i th and j th characters

$\text{Cov.}(x_i, x_j)$ = Covariance between i th and j th characters

$v(x_i)$ and $v(x_j)$ = Variance for the i th and j th characters.

Significance of correlations was tested by referring 'r' table values (Fisher and Yates, 1963) at $P=2$ degrees of freedom.

3.4.6 Path analysis

The path coefficients were obtained by solving the following simultaneous equations as suggested by Dewey and Lu (1959).

$$r_{ly} = p_{ly} + p_{2y} r_{l2} + p_{3y} r_{l3} \dots \dots \dots PKY r_{lK}$$

Where

r_{ly} = is simple correlation coefficient between x_1 and y the dependent character.

p_{ly} = Direct effect of x_1 on y the dependent character

$p_{2y} r_{l2}$ = indirect effect of x_1 on y through x_2

$p_{3y} r_{l3}$ = indirect effect of x_1 on y through x_3

r_{l2} = correlation coefficient between x_1 and x_2

r_{l3} = correlation coefficient between x_1 and x_3

$PKY r_{lK}$ = indirect effect of x_1 on y through K variables.

In the same way equations for r_{2y} , r_{3y} , r_{4y} upto r_{12y} were written and path coefficients viz., direct and indirect effects were calculated by solving the simultaneous equations. Besides the direct and indirect effects, the residual effect was computed by using the formula.

$$R = 1 - (P_1 r_{1y} + P_2 r_{2y} + P_3 r_{3y} + \dots)_{\Sigma}$$

Where R = Residual effect

P_1 = Direct effect of x_1 on y

r_{1y} = correlation coefficient of x_1 and y

All the statistical computations were carried out through the courtesy of the computer centre of Directorate of Rice Research, Hyderabad.

RESULTS

CHAPTER IV

RESULTS

Experiment No.1

4.1 STUDIES ON GENETIC VARIABILITY AND GENETIC DIVERGENCE

4.1.1 Genetic variability

The range, mean, standard error of mean, phenotypic coefficient of variation, genotypic coefficient of variations and heritability in broad sense, genetic advance expressed as percentage of mean were calculated for each of the character from a study involving 49 genotypes of mungbean grown over three environments i.e., kharif (E1), rabi uplands (E2) and rabi rice fallows (E3). The details of the results are presented in the Tables 4.1 to 4.3 and are described below character wise.

4.1.1.1 Days to 50% flowering

The number of days taken to 50% flowering were more under rabi rice fallows (46.03), whereas it was less in rabi uplands (35.78) and kharif (35.55). The range of variation for this trait was high in kharif (30.00-40.00) but low in rabi uplands (31.47-39.51). The coefficients of variation were in general low for this trait. However, the magnitude of the phenotypic and

e 4.1: Mean, variability, heritability and genetic advance for yield and its components of mungbean in kharif 1988 (E1)

S. No.	Character	Mean	S.E.m	Range		PCV	GCV	h ²	G.A. in percent over mean
				Maximum	Minimum				
	Days to 50% flowering	35.55	0.559	44.00	30.00	11.60	11.38	96.32	23.01
	Days to maturity	65.82	0.368	74.00	60.50	5.91	5.86	98.21	11.96
	Plant height (cm)	82.28	0.671	95.30	63.60	8.85	8.77	98.30	17.91
	Number of branches per plant	1.68	0.078	2.50	0.89	23.08	22.12	91.85	43.67
1	Number of clusters per plant	4.82	0.117	6.29	3.60	11.33	10.79	90.84	21.19
2	Number of pods per plant	27.38	1.454	36.00	19.00	15.34	13.38	76.04	24.03
3	Pod length (cm)	7.17	0.036	7.90	6.60	4.14	4.08	97.05	8.27
4	Seeds per pod	11.25	0.087	12.70	9.50	8.38	8.31	98.30	16.98
5	1000 seed weight (g)	33.57	0.317	38.50	30.25	6.68	6.54	95.99	13.20
6	Shoot dry weight (g)	22.55	0.374	31.05	15.75	18.39	18.24	98.37	37.27
7	Seed protein (%)	26.07	0.222	28.30	21.58	5.25	5.05	92.79	10.03
8	Shoot nitrogen (%)	2.46	5.332	2.90	1.94	8.84	8.31	88.37	16.09
9	Grain yield (g)	9.11	0.108	12.43	6.27	18.02	17.94	99.13	36.81

CV: Phenotypic coefficient of variation

CV: Genotypic coefficient of variation

h² : Heritability in broadsense

A : Genetic advance

Table 4.2: Mean, variability, heritability and genetic advance for yield and its components of Rabi uplands, 1987-88 (E2)

S. No.	Character	Mean	S.E.m	Range		PCV	GCV	h ²	G.A. in percent over mean
				Maximum	Minimum				
1	Days to 50% flowering	35.78	0.334	39.51	31.47	5.88	5.73	94.96	11.49
2	Days to maturity	65.61	0.407	69.58	61.01	3.15	3.03	92.24	5.98
3	Plant height (cm)	51.04	0.655	69.65	39.5	13.41	13.28	98.17	27.12
4	Number of branches per plant	1.79	0.064	2.7	1.09	17.91	17.17	91.93	34.08
5	Number of clusters per plant	4.34	0.100	5.93	3.01	16.46	16.13	96.03	32.49
6	Number of pods per plant	23.95	0.524	31.02	17.47	16.76	14.14	71.18	24.59
7	Pod length (cm)	6.88	0.044	8.85	5.95	5.28	5.21	97.16	10.61
8	Seeds per pod	10.19	0.088	11.00	8.90	4.52	4.35	92.74	8.63
9	1000 seed weight (g)	33.56	0.466	40.00	29.75	7.32	7.05	92.80	13.97
10	Shoot dry weight (g)	18.16	0.289	23.54	11.05	18.20	18.06	98.47	36.89
11	Seed protein (%)	26.13	0.183	27.86	22.56	4.44	4.33	95.04	8.69
12	Shoot nitrogen (%)	2.49	0.041	2.85	2.00	7.67	7.31	90.68	14.46
13	Grain yield (g)	7.46	0.098	9.47	5.23	17.53	17.43	98.88	35.66

PCV: Phenotypic coefficient of variation
GCV: Genotypic coefficient of variation
h²: Heritability in broadsense
G.A.: Genetic advance

Table 4.3: Mean, variability, heritability and genetic advance for yield and its components of Rabi Rice Fallows, 1987-88 (E3)

No.	Character	Mean	S.E.m	Range		PCV	GCV	h ²	G.A. in percent over mean
				Maxi-mum	Mini-mum				
1	Days to 50% flowering	46.03	0.544	52.00	43.00	4.99	4.70	88.79	9.72
2	Days to maturity	76.08	0.367	82.00	73.00	2.78	2.69	93.97	5.38
3	Plant height (cm)	39.29	0.644	48.50	29.90	10.78	10.53	95.37	21.18
4	Number of branches per plant	1.47	0.094	2.21	0.90	24.93	23.23	86.85	44.22
5	Number of clusters per plant	3.80	0.069	5.53	3.00	14.69	14.47	97.07	29.23
6	Number of pods per plant	17.59	0.914	27.00	12.50	20.31	18.94	86.93	36.33
7	Pod length (cm)	6.86	0.029	7.45	6.15	5.31	5.27	98.68	10.79
8	Seeds per pod	10.96	0.358	12.90	9.60	8.63	7.35	71.31	15.88
9	1000 seed weight (g)	32.90	0.344	39.49	29.47	7.58	7.48	96.19	15.08
10	Shoot dry weight (g)	13.54	0.287	20.26	8.43	18.43	18.18	97.35	36.93
11	Seed protein (%)	25.56	0.273	27.25	21.25	5.20	4.98	91.57	9.82
12	Shoot nitrogen (%)	2.42	0.074	2.85	1.85	10.42	9.48	82.70	17.77
13	Grain yield (g)	5.54	0.994	8.05	3.58	63.11	57.79	83.85	109.00

CV: Phenotypic coefficient of variation

CV: Genotypic coefficient of variation

h²: Heritability in broadsense

A: Genetic advance

genotypic coefficients of variation were high in kharif when compared to rabi uplands or rice fallows. High heritability (96.32%) estimates along with high genetic advance over mean (23.01) was recorded for this trait in kharif. High heritability coupled with low genetic advance over mean was recorded both in rabi uplands and rabi rice fallows.

4.1.1.2 Days to maturity

The number of days taken to mature were more in rabi rice fallows (76.08) while it was lower in kharif (65.82) and rabi uplands (65.62). The range of variation for days taken to maturity was high in kharif (60.50 - 74.00) whereas in rabi uplands (61.01-69.58) and rabi rice fallows (73.00-82.00) it was low. Phenotypic and genotypic coefficient of variation were in general low for this trait, however when these estimates were compared over environments they were high in kharif season. High heritability estimates (98.21%) along with moderate genotypic advance over mean (11.96) were recorded in kharif whereas high heritability coupled with low genetic advance over mean were recorded in rabi uplands (92.24% and 5.98) and rabi rice fallows (93.97% and 5.38).

4.1.1.3 Plant height (cm):

The mean plant height was high in kharif (82.28 cm) while it was low under rabi rice fallows (39.29 cm). The range of variation was also high in kharif (63.6-95.3 cm) compared to rabi uplands (39.50-69.5 cm) or rabi rice fallows (29.90-48.50 cm). PCV and GCV were low in kharif (8.85 and 8.77) and moderate in rabi uplands (13.41 and 13.28) and rabi rice fallows, (10.78 and 10.53). High heritability (98.30%) coupled with moderate estimates of genetic advance over mean (17.91) was recorded for this trait in kharif. Whereas, in rabi uplands and rabi rice fallows high heritability (98.17 and 95.37) coupled with high genetic advance (27.12 and 21.18) was recorded.

4.1.1.4 Number of branches per plant

Mean number of branches per plant and the range of variation were high in rabi uplands (1.79 and 1.09 - 2.70) followed by kharif (1.68 and 0.89-2.50). Phenotypic and genotypic coefficients of variation were high in rabi rice fallows (24.93 and 23.23) followed by kharif (23.08 and 22.12) and rabi uplands (17.91 and 17.17) for this trait. High heritability coupled with high genetic advance over mean was recorded in all the environments (Table 4.1 to 4.3).

4.1.1.5 Number of clusters per plant:

Mean number of clusters per plant and the range of variation were high in kharif (4.82 and 3.6-6.29) and rabi uplands (4.34 and 3.01-5.93), while they were low in rabi rice fallows (3.90 and 3.00-5.53). The PCV and GCV were moderate under all the environments. Heritability estimates for this trait were high in all the environments. High heritability coupled with high genetic advance over mean was recorded in rabi uplands (96.03% and 32.49) followed by rabi rice fallows (97.07% and 29.23) and kharif (90.84% and 21.19).

4.1.1.6 Number of pods per plant

Mean number of pods per plant (27.38) and the range of variation (19.00-36.00) were high in kharif compared to rabi uplands and rabi rice fallows (Table 4.1 to 4.3). PCV and GCV were moderate in all the environments with 20.31 and 18.94 in rabi rice fallows 16.76 and 14.14 in rabi uplands and 15.34 and 13.38 in kharif, respectively. High heritability coupled with high genetic advance was noticed in all the environments.

4.1.1.7 Pod length (cm)

Mean pod length was more in kharif (7.17 cm) followed by rabi uplands (6.88 cm) and rabi rice fallows

(6.86 cm). The range of variation for pod length was high in rabi uplands (5.95-8.85 cm) and low in kharif (6.6-7.9 cm) and rabi rice fallows (6.15-7.45 cm). Phenotypic and genotypic coefficients of variation were low for this trait in all the environments. High heritability coupled with low genetic advance was recorded under all the environments (Table 4.1 to 4.3).

4.1.1.8 Number of seeds per pod

Mean number of seeds per pod were more in kharif (11.25) followed by rabi rice fallows (10.96). The range of variation was also high in kharif (9.5-12.7), rabi uplands (8.90-11.00) and rabi rice fallows (9.6-12.9). Both PCV and GCV were low for this trait under all the environments. High heritability along with low genetic advance over mean was recorded under all the environments (Table 4.1 to 4.3).

4.1.1.9 1000 seed weight (g)

Mean 1000 seed weight was high in kharif (33.57 g) followed by rabi uplands (33.56 g). The range of variation for 1000 seed weight was high in rabi uplands (29.75-40.00 g) and rabi rice fallows (29.47-39.49 g) compared to kharif (30.25-38.50 g). PCV and GCV were low in all the environments. High heritability estimates coupled with low genetic advance over mean was recorded for this trait in all the environments.

4.1.1.10 Shoot dry weight (g)

Mean shoot dry weight and the range of variation was high in kharif (22.55 g and 15.75-31.05 g) compared to rabi uplands (18.17 g and 11.05-23.54 g) and rabi rice fallows (13.54 g and 8.43-20.26 g). Estimates of phenotypic coefficients of variation, heritability in broadsense and genetic advance over mean were high in all the environments for this trait (Table 4.1 to 4.3).

4.1.1.11 Seed protein content (%)

Mean seed protein content was high in rabi uplands (26.13%) followed by kharif (26.07%). The range of variation was high for this trait in kharif (21.58-28.30%) followed by rabi rice fallows (21.25-27.25%). Phenotypic and genotypic coefficients of variation were low in all the environments. High heritability coupled with low genetic advance over mean was recorded for this trait in all the environments (Table 4.1 to 4.3).

4.1.1.12 Shoot nitrogen content (%)

Mean shoot nitrogen content was high in rabi uplands (2.49%) followed by kharif (2.46%). The range of variation for this trait was high in rabi rice fallows (1.85-2.85%) whereas it was low in kharif (1.94-2.90%). Estimates of both phenotypic and genotypic coefficients of variation were low in all the

environments. High heritability coupled with moderate estimates of genetic advance over mean was recorded for this character in all the environments (Tables 4.1 to 4.3).

4.1.1.13 Grain yield per plant (g)

Mean grain yield per plant was high (Tables 4.1 to 4.3) in kharif (9.11g) followed by rabi uplands (7.41g) and rabi rice fallows (5.54 g). Range of variation for this trait was also high in kharif (6.27-12.43g) followed by rabi rice fallows (3.58-8.06g). Estimates of PCV and GCV were high under rice fallows (63.11 and 57.79) followed by kharif (18.02 and 17.94) and rabi uplands (17.53 and 17.43). High heritability (96.73, 96.68 and 83.85%) coupled with high genetic advance (36.81, 35.66 and 109.00%) over mean was recorded in all the three environments.

4.1.2 Genetic divergence

Forty nine genotypes of Mungbean comprising of released, pre release cultures and advanced breeding lines developed through hybridization (single, double and multiple crosses) and mutation breeding were studied under three seasons : kharif (E1), Rabi uplands (E2), and Rabi rice fallows (E3) using D^2 to study i) the relationship between geographic and genetic diversity, ii) the influence of environment and genotype x

environment interactions on clustering pattern of genotypes, iii) to identify genetically diverse genotypes and iv) to suggest a suitable breeding methodology for improvement of Mungbean based on genetic divergence studies using D^2 statistic. Results obtained are presented hereunder.

4.1.2.1 Test with Wilk's criterion

Analaysis of variance revealed significant differences among the genotypes for all the characters studied viz. days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, 1000 seed weight (g), shoot dry weight (g), seed protein (%), shoot nitrogen at flowering (%) and grain yield per plant (g) under all the environments.

Wilk's 'v' criterion was used to test the differences between the genotypes based on the pooled effect of all the characters. The significance of 'v' statistic was tested by χ^2 at 624 degrees of freedom. The 'v' statistic was highly significant indicating that the genotype differed significantly when all the characters were considered simultaneously.

4.1.2.2 Mahalanobis's D^2 values

To estimate the D^2 values, correlated means of characters were transformed into standardized uncorrelated characters using pivotal condensation method. The statistical differences (D^2) between pairs of genotypes was obtained as the sums of squares of the differences between the pairs of corresponding uncorrelated values of any two genotypes considered at a time. Thus, the possible 1176 combinations and the corresponding D^2 values were obtained.

The D^2 values ranged from 42.77 (Between LGG 417 and LGG 418) to 7784.55 (Between LGG 421 and LGG 434) under E1; from 66.09 (Between LGG 418 and LGG 422) to 9933.02 (LGG 402 and LGG 424) under E2 while it ranged from 64.05 (Between LGG 402 and LGG 127) to 5697.91 (Between LGG 446 and Pusa 111) in E3.

4.1.2.3 Grouping of genotypes into various clusters

The 49 genotypes were grouped into different clusters using Tocher's method with the criterion that the intra cluster average D^2 values should be less than the inter cluster D^2 values. Distribution of genotypes in various clusters is shown in Tables 4.4 to 4.6 under the three environments studied.

Table 4.4: Clustering pattern of 49 genotypes in Mungbean on the basis of genetic divergence in E1 (Kharif, 1988).

Cluster Number	Number of genotypes	Genotypes included
I	8	LGG 417, LGG 418, LGG 419, LGG 435, LGG 422, DC 1 x DC 3-5 SB-SB, DC 1 x DC 3-6 SB-SB and Tara.
II	21	LGG 402, LGG 403, LGG 404, LGG 405, LGG 408, LGG 409, LGG 410, LGG 414, LGG 431, LGG 436, LGG 445, LGG 446, LGG 447, LGG 449, LGG 450, Patchapesalu, Pusa 105, ML 33, UPM 79-3-4, M 986, Pusa 111.
III	3	LGG 421, LGG 442 and LGG 487-3.
IV	3	LGG 453, Pusa 103, and LGG 423.
V	2	ML 267 and LGG 127
VI	2	LGG 449 and LGG 441
VII	3	LGG 424, LGG 437 and LGG 438.
VIII	1	LGG 426
IX	1	LGG 429
X	1	LGG 434
XI	1	LGG 443
XII	1	DC 1 x DC 2 - 4SB-SB
XIII	1	DC 1 x DC 2 - 1SB-SB
XIV	1	ML 26-10-3

Table 4.5: Clustering pattern of 49 genotypes in Mungbean on the basis of genetic divergence in E2 (Rabi uplands, 1987-88)

Cluster Number	Number of genotypes	Genotypes included
I	3	LGG 417, LGG 418 and LGG 422.
II	12	LGG 402, LGG 404, LGG 408, LGG 426, LGG 431, LGG 434, LGG 439, LGG 443, LGG 445, LGG 446, DC 1 x DC 3-5 SB-SB, and UPM 79-3-4.
III	16	LGG 410, LGG 414, LGG 419, LGG 421, LGG 424, LGG 429, LGG 435, LGG 436, LGG 437, LGG 442, LGG 447, LGG 453, DC 1 x DC 3-6 SB-SB, ML 33, M 986 and Pusa 111
IV	4	LGG 423, LGG 438, LGG 487-3 and DC 1 x DC 2 - 4SB-SB.
V	5	LGG 403, Patchapesalu, ML 267 Pusa 105 and ML 26-10-3.
VI	2	LGG 449 and DC1 x DC 2 - 1SB-SB
VII	2	LGG 405 and Tara
VIII	2	LGG 409 and LGG 127
IX	1	LGG 441
X	1	LGG 450
XI	1	Pusa 103

Table 4.6: Clustering pattern of 49 genotypes in Mungbean on the basis of genetic divergence in E3 (Rabi rice fallows, 1987-88)

Cluster Number	Number of genotypes	Genotypes included
I	31	LGG 402, LGG 403, LGG 404, LGG 405, LGG 408, LGG 409, LGG 410, LGG 419, LGG 421, LGG 426, LGG 429, LGG 431, LGG 434, LGG 435, LGG 436, LGG 437, LGG 438, LGG 439, LGG 445, LGG 447, LGG 453, Patchapesalu, DC 1 x DC 2-4 SB-SB, ML 267, Pusa 105, ML 33, UPM 79-3-4, M 986, Tara, LGG 127 and ML 26-10-3.
II	11	LGG 414, LGG 417, LGG 418, LGG 422, LGG 423, LGG 442, LGG 443, LGG 487-3, DC 1 x DC 3-5 SB-SB, DC 1 x DC 3-6 SB-SB and DC 1 x DC 2-1 SB-SB.
III	2	LGG 405 and LGG 424.
IV	1	LGG 441
V	1	LGG 446
VI	1	LGG 449
VII	1	Pusa 111
VIII	1	Pusa 103

The number of clusters formed were high under E1 - kharif (14) followed E2 - Rabi uplands (11), whereas under E3 - Rabi rice fallows only eight clusters were formed. Cluster I comprised maximum number of genotypes under E1 (21), whereas under E2 cluster III contained maximum number of genotypes (16). Maximum number of genotypes (31) were included in cluster (III) under E3. The number of clusters containing single genotypes were 7 in E1, 3 in E2 and 5 in E3.

4.1.2.4 Average intra and inter cluster D^2 values

The average intra and inter cluster distances are presented in tables 4.7 to 4.9 for E1, E2 and E3, respectively. Highest intercluster distance of 6986.03 (Between cluster VIII and IX) was recorded in E1 followed by E2 with 5748.08 (Between cluster I and VIII) while in E3 it was 5697.91 (Between cluster V and VII). The closest distance was noticed between clusters IX and XII (707.25) under E1; between clusters X and XI (626.00) under E2 and between cluster II and V (638.96) under E3. The intra cluster distance ranged from zero to 542.03 (cluster I) under E1; zero to 475.3 (cluster VIII) under E2 and zero to 429.53 in E3 (cluster II).

File 4.7: Average intra and inter cluster D2 values among 14 clusters of mungbean under kharif, 1988 (E1)

Cluster number	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	542.03	2073.97	2389.68	750.73	3022.79	1282.21	1041.82	3744.58	2210.41	1424.89	3789.02	2003.86	1094.53	1804.09
II		539.72	1727.63	1526.34	881.82	1988.29	3289.16	1176.48	947.17	3845.68	1797.42	1857.83	964.88	804.20
III			280.81	3154.54	2837.26	2621.37	3217.37	1365.89	834.19	6683.93	2231.78	1516.73	1049.05	2527.40
IV				490.69	2030.18	1178.76	1814.48	3387.72	2425.60	1181.62	2826.84	2522.97	1233.55	923.99
V					394.33	3294.28	4951.81	1074.15	1622.86	3270.83	2322.07	1954.23	1606.07	1070.21
VI						399.51	1271.56	3706.45	2298.01	1569.25	2393.33	3011.68	1569.25	2255.28
VII							466.98	4946.74	2344.34	2253.83	4904.44	2456.11	1387.08	3517.87
VIII								0.00	1046.10	6985.03	1878.92	1619.19	1668.07	2494.49
IX									0.00	5133.88	2116.41	707.25	942.39	2161.29
X										0.00	5024.59	5416.26	2926.69	2585.02
XI											0.00	4190.43	1473.88	1589.55
XII												0.00	1491.48	2977.33
XIII													0.00	1486.01
XIV														0.00

Table 4.8: Average intra and inter cluster D2 values among 11 clusters of mungbean under Rabi uplands, 1987-1988 (E2)

Cluster number	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	65.56	2247.16	1483.19	1391.24	1390.42	628.03	2436.55	5748.08	2164.52	2904.95	2480.84
II		357.17	1165.13	920.57	724.76	2018.44	839.25	1246.24	2298.25	980.40	799.21
III			407.08	769.48	1991.88	814.32	1688.78	3368.23	1142.93	767.58	942.77
IV				435.57	1664.58	1020.55	1110.01	2503.66	1861.18	1026.66	1036.03
V					390.32	3008.21	1426.92	1949.40	3367.60	1516.91	1526.98
VI						237.42	1973.20	3935.32	1942.12	1024.60	1167.20
VII							382.17	1261.39	2800.68	1542.29	862.55
VIII								475.53	5170.50	1540.66	2175.56
IX									0.00	1749.64	1756.12
X										0.00	626.00
XI											0.00

Table 4.9: Average intra and inter cluster D2 values among 8 clusters of mungbean under Rabi Rice Fallows, 1987-88 (E3)

Cluster number	I	II	III	IV	V	VI	VII	VIII
I	381.68	771.30	660.84	665.80	1402.28	895.14	2144.99	732.66
II		429.53	695.18	1071.72	638.96	722.44	3108.21	1501.96
III			422.54	765.87	1215.47	232.92	3044.04	928.62
IV				0.00	2437.99	1506.23	1403.61	1419.81
V					0.00	951.13	5697.91	2076.95
VI						0.00	3986.79	1685.05
VII							0.00	2904.68
VIII								0.00

4.1.2.5 Clustering pattern in relation to parentage and geographic diversity

The constellation of genotypes into different clusters are furnished in Tables 4.4 to 4.6. Distribution of genotypes in to different clusters was at random both in E1 and E2. The derivatives from single and multiple crosses were included in the same clusters under E2 (cluster I, II, IV and VI), E1 (cluster I, XII and XIII) and E3 (cluster I and II). However, some of the derivatives of multiple crosses $DC_1 \times DC_2 - 4$ SB-SB, LGG 444, LGG 434, $DC_1 \times DC_2 - 1$ SB-SB maintained their identity by forming a separate cluster in E1; while under E2 LGG 441 and LGG 449 derived from multiple crosses formed separate clusters.

No relationship between geographic origin and genetic diversity was observed as the genotypes developed from different geographic regions were included in the same cluster under E1 (cluster II and cluster III), E2 (cluster I, II, IV, V, VII and VIII) and E3 (cluster I).

4.1.2.6 Cluster means for various characters

Mean performance of different clusters for various characters are presented in Tables 4.10 to 4.12 for E1, E2 and E3, respectively. Considerable differences between clusters was observed for most of

Table 4.10: Cluster means for various characters of mungbean in E1 (kharif 1988)

Character ----- cluster	Days to 50% flo- wering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
I	40.00	69.87	82.28	1.73	4.79	28.12	7.12	11.68	32.59	24.06	26.63	2.48	9.55
II	32.81	63.40	81.91	1.56	4.81	25.83	7.10	10.64	33.36	20.73	26.24	2.37	8.35
III	33.00	63.17	92.24	1.63	5.38	33.67	7.85	12.27	36.00	29.82	25.93	2.73	11.97
IV	39.67	69.17	78.27	1.60	4.86	26.83	7.17	10.90	32.83	20.33	23.43	2.39	8.26
V	30.75	61.00	66.36	2.05	5.15	22.85	6.97	10.75	33.00	18.75	24.67	2.40	7.59
VI	36.00	66.00	82.92	1.44	4.64	28.25	7.40	10.75	34.37	20.10	26.86	2.35	8.71
VII	42.33	72.33	91.05	2.13	4.77	33.00	7.27	12.04	35.67	29.42	24.95	2.79	11.75
VIII	30.00	61.50	66.88	1.98	4.95	26.00	7.60	12.50	33.75	21.63	28.30	2.65	8.88
IX	32.00	62.00	81.79	1.29	4.52	32.00	7.00	10.60	32.00	28.15	26.58	2.75	11.27
X	44.00	74.00	81.64	1.84	4.44	24.50	7.15	9.60	35.25	18.80	27.46	2.44	7.45
XI	32.50	62.50	94.26	2.09	4.82	24.00	7.80	9.80	32.01	17.45	27.40	2.24	6.95
XII	34.00	64.00	67.76	2.11	4.67	29.00	6.95	12.40	32.49	30.50	24.19	2.76	12.25
XIII	37.00	67.00	89.71	1.82	4.18	24.50	7.60	12.20	32.99	22.60	27.73	2.25	9.23
XIV	34.00	64.50	85.83	1.81	4.97	23.00	6.60	10.80	32.50	16.75	24.16	2.21	6.70

Table 4.11: Cluster means for various characters of mungbean in E2 (Rabi uplands 1987-88)

Character ----- cluster	Days to 50% flo- wering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
I	44.67	73.00	72.00	1.47	4.33	26.62	6.72	10.30	32.17	20.44	26.54	2.62	8.22
II	35.45	64.99	46.95	1.82	3.83	21.61	6.88	10.10	32.55	15.85	26.84	2.41	6.42
III	35.62	65.84	52.26	1.91	4.23	26.69	6.97	10.35	34.12	20.84	26.24	2.63	8.45
IV	38.62	68.27	57.00	1.83	4.67	27.46	6.75	10.09	33.03	18.46	25.02	2.62	8.09
V	32.69	62.69	45.79	1.92	5.18	20.74	6.53	9.53	26.40	15.28	25.75	2.33	6.25
VI	37.49	66.76	64.65	1.45	3.69	22.55	6.75	10.22	31.75	20.32	26.54	2.55	8.72
VII	39.75	69.25	57.00	1.45	3.71	19.06	6.87	10.27	37.62	15.23	24.64	2.19	6.27
VIII	34.20	64.25	39.75	1.20	4.37	17.44	6.78	9.85	31.50	10.76	26.24	2.10	4.90
IX	37.02	66.56	57.56	1.88	4.83	30.05	8.85	10.80	46.00	22.14	27.05	2.65	9.02
X	32.03	62.01	48.25	2.09	5.50	25.00	6.90	10.30	36.25	19.23	24.77	2.54	8.10
XI	38.00	68.00	42.00	1.48	4.16	23.46	7.10	11.00	36.00	20.72	22.50	2.40	8.43

Table 4.12: Cluster means for various characters of mungbean in E3 (Rabi Rice Fallows, 1987-88)

Character ----- cluster	Days to 50% flo- wering	Days to maturity (cm)	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
I	45.84	75.94	38.17	1.48	3.70	16.61	6.82	10.66	32.78	12.75	25.46	2.39	5.05
II	46.77	77.73	41.66	1.55	4.31	20.41	7.10	11.91	31.78	15.78	26.10	2.48	6.75
III	47.75	77.25	40.20	1.82	4.42	19.20	6.55	10.90	38.62	15.82	24.22	2.57	6.30
IV	45.50	75.00	37.90	1.65	4.10	18.00	7.80	10.20	39.50	13.05	26.80	2.40	5.20
V	45.50	75.50	37.80	0.80	4.10	20.00	6.20	12.50	30.00	17.45	27.15	2.80	7.00
VI	45.00	74.50	48.50	0.90	3.60	17.00	6.50	10.70	29.75	18.50	26.00	2.20	6.37
VII	44.00	74.00	41.20	1.20	3.90	16.00	9.70	10.30	34.50	13.75	21.00	2.40	5.50
VIII	45.50	75.50	38.00	0.90	3.70	13.00	5.90	10.10	35.50	10.65	21.25	2.35	4.22

the characters studied. The different clusters were characterised by the differences in the means for the characters studied.

Cluster V (ML 267 and LGG 127) possessed low mean value for days to 50% flowering and days to maturity, cluster III (LGG 487-3, LGG 421 and LGG 442) possessed higher values for plant height, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, 1000 seed weight, shoot nitrogen content and grain yield; cluster VII (LGG 424, LGG 437 and LGG 438) recorded more branches per plant, higher number of pods per plant, more number of seeds per pod, higher 1000 seed weight, higher shoot dry weight, more shoot nitrogen and higher grain yield per plant, cluster IX (LGG 429) recorded higher mean values for number of pods per plant, shoot dry weight, shoot nitrogen and grain yield per plant along with earliness for flowering and maturity; cluster XII ($DC_1 \times DC_2 - 1$ SB-SB) possessed more number of branches per plant, pods per plant, number of seeds per pod, shoot dry weight, shoot nitrogen and grain yield per plant (Table 4.10).

Cluster IX (LGG 441) is characterised by more number of branches per plant, number of clusters per plant, pods per plant, pod length, number of seeds per pod, 1000 seed weight, shoot dry weight, seed protein, shoot nitrogen and grain yield per plant. While cluster

VI (LGG 449 and $DC_1 \times DC_2 - 1SB-SB$) with higher plant height, more number of pods per plant, higher shoot dry weight, seed protein, shoot nitrogen and grain yield per plant; cluster III (LGG 410, LGG 414, LGG 419, LGG 421, LGG 429, LGG 450, LGG 436, LGG 437, LGG 442, LGG 443, LGG 445, LGG 447, UPM 79-3-4 and $DC_1 \times DC_3 - 5SB-SB$) with more number of pods per plant, seeds per pod, higher shoot dry weight, seed protein, shoot nitrogen and grain yield per plant; cluster I (LGG 417, LGG 418 and LGG 422) with more number of pods per plant; seeds per pod, higher shoot dry weight, seed protein, shoot nitrogen and grain yield per plant; cluster IV (LGG 423, LGG 438, LGG 487-3 and $DC_1 \times DC_2 - 4SB-SB$) with more number of pods per plant, seed protein, shoot nitrogen and grain yield per plant (Table 4.11).

Cluster V (LGG 446) is characterised by high mean values for the number of clusters per plant, pods per plant, number of seeds per pod, shoot dry weight, seed protein, shoot nitrogen and grain yield per plant; cluster II (LGG 414, LGG 417, LGG 418, LGG 422, LGG 423, LGG 442, LGG 443, LGG 487-3, $DC_1 \times DC_3 - 5SB$, $DC_1 \times DC_3 - 6SB-SB$ and $DC_1 \times DC_2 - 1SB-SB$) recorded more number of clusters per plant, pods per plant, number of seeds per pod, and grain yield per plant, cluster III (LGG 405 and LGG 424) with more number of branches per plant, clusters per plant, pods per plant, 1000 seed weight and

grain yield per plant, and cluster VI (LGG 449) with more number of pods per plant and grain yield (Table 4.12).

Experiment No.2

4.2 GENOTYPE X ENVIRONMENT INTERACTION STUDIES

To understand the nature and magnitude of genotype x environment interactions on the character expression, an experiment involving '20' diverse genotypes of mungbean were studied under six environments over three seasons each in two different years (E1:kharif, 1987; E2:rabi uplands 1987-88; E3: rabi rice fallows 1987-88; E4: kharif 1988; E5 rabi uplands 1988-89; and E6: rabi rice fallows 1988-89).

Analysis of variance revealed significant differences among the genotypes under all the environments for all the characters studied viz., days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, pod length (cm), seeds per pod, 1000 seed weight (g), shoot dry weight (g), seed protein (%), shoot nitrogen (%) at flowering and grain yield (g). Stability parameters were worked out for grain yield on plot mean basis whereas correlations and path coefficients were calculated as per plant yield. The mean performance of

genotypes under six environments are presented in Appendix XII to XXV. The results obtained are described under sub-heads.

1. Mean performance of genotypes in different environments
 2. Genotype x environment interactions
 3. Linear and non-linear components of genotype x environment interaction
 4. Relation between mean performance and environmental index
 5. Stability analysis:- Stability parameters of individual characters
 6. Association among stability parameters
 7. Correlation coefficients and path analysis in different environments
- 4.2.1 Mean performance of genotypes in different environments

The mean performance of genotypes for various traits under different environments is presented in Appendix XII to XXV and is described character-wise hereunder.

The mean value for days to 50 per cent flowering ranged from 31.33 (E2) to 44.53 days (E3). The genotypes LGG 426, D12/333, MH 309, K 851, LGG 127 and PDM 54 were found to be early to flower over the environments, while, LGG 407, LGG 410, ML 26-10-3 and UPM 79-4-12 and PS 16 were late to flower and is given in Appendix XII.

In general, the genotypes took more time to mature under E3 (74.58 days) followed by E6 (69.68 days) i.e., under rice fallows, while they matured quickly in E2 (61.57 days). Five genotypes viz., D12/333, MH 309, K 851, PDM 54 and ML 267 were found to be early to mature, whereas, LGG 407, LGG 410 and PS 16 were late to mature under all environments and is presented in Appendix XIII.

Plant height ranged from 30.61 cm (E6) to 76.60 cm (E4) as shown in Appendix XIV. The plant height was low under E3 and E6 (Rabi rice fallows) while they grew tall in kharif seasons (E1 and E4). Among the genotypes LGG 407, LGG 410, ML 131, and PS 16 were found to be taller in E1, E2, E4 and E5 while, pusa 105 and LGG 450 were taller in E3 and E6.

The number of branches per plant were more in E2 (1.95) and E4 (1.95). The genotype D12/333 had more branches per plant while K 851, UPM 83-10, LGG 127 and

UPM 79-4-12 recorded less number of branches under all the environments and is furnished in Appendix XV.

The number of clusters per plant were more in kharif i.e., E4 (5.23) followed by E1 (5.05) and E2 (5.01) and were low under E3 (3.35) and E6 (3.13) (rice fallows) (Appendix XVI). The genotypes LGG 410, LGG 450, ML 267 and Pusa 105 recorded more number of clusters per plant over the environments studied.

The number of pods per plant ranged from 12.15 (E6) to 24.11 (E4). The genotypes LGG 407 and LGG 410 recorded more number of pods per plant in E1, E2, E4 and E5 while pusa 105 and LGG 450 recorded more number of pods in E3 and E6 (rice fallows) whereas the genotypes DL2/333, MH 309, K 851, LGG 127, PS 16, UPM 83-10 and ML 26-10-3 have recorded less number of pods per plant under majority of the environments (Appendix XVII).

Pod length ranged from 6.63 cm (E5) to 7.28 cm (E2). Among the genotypes MUG 125 had the lowest pod length in all the environments whereas K 851, LGG 426, PDM 84-145, PDM 84-155, and PS 16 have longer pods. This trait, in general, appears to be not much influenced by the environments (Appendix XVIII).

The number of seeds per pod were more in kharif season (E4 and E1) than under rabi rice fallows (E3 and E6) (Appendix XIX). Among the genotypes studied

K 851, LGG 426, LGG 127, PS 16, ML 131, PDM 84-145 and PDM 84-155 had more number of seeds per pod, while D12/333 recorded less number of seeds per pod over all the environments.

1000 seed weight ranged from 33.29 (E3) to 34.57 g (E5). Among the genotypes K 851, Pusa 105, PDM 54, PDM 84-145, LGG 407, LGG 410 and LGG 450 have recorded higher 1000 seed weight whereas, D12/333 recorded lowest seed weight over the environments. This trait is not much influenced by the environments (Appendix XX).

Maximum shoot dry weight at harvest was recorded in E4 (kharif, 1988) followed by E5 whereas the shoot dry weight was low in E3 and E6. Among the genotypes studied LGG 407 and LGG 410 recorded more shoot dry weight in E1, E2, E4, E5 and Pusa 105 and LGG 450 in E3 and E6. The genotype D12/333 recorded low shoot dry weight under all the environments (Appendix XXI).

The average seed protein content ranged from 23.96 per cent (E6) to 25.4 per cent (E5). Two genotypes LGG 403 and LGG 426 have recorded higher seed protein while MH 309 recorded lower seed protein in most of the environments (Appendix XXII).

Mean shoot nitrogen at flowering was high in E5 (2.38%) followed by E2 (2.36%) while it was low in E3 (2.26%) and E6 (2.18%). Four genotypes viz., LGG 407, LGG 410, LGG 426 and LGG 450 have recorded higher shoot nitrogen over the environments studied and the details are given in Appendix XXIII.

Mean grain yield was high in E4 (1309 kg/ha) followed by E5 (1196 kg/ha) and was low under rice fallows E3 (737 kg/ha) and E6 (690 kg/ha). The genotypes LGG 407, LGG 410, PDM 54, ML 267 and PDM 84-145 have recorded higher yields under E1, E2, E4 and E5 while the genotypes pusa 105 and LGG 450 recorded higher seed yields in E3 and E6 (Appendix XXV).

4.2.2 Genotype x environment interactions

Pooled analysis over six environments following Eberhart and Russell (1966) Model revealed significant differences due to genotypes for all the characters studied (Table 4.13) indicating the wider genetic diversity among the genotypes studied. Mean squares due to environments (linear) were significant indicating that the environments tested are different and more than 80% of the variation appears to be due to environment alone. Mean squares due to environments + (Genotype x environments) were also significant for all the characters indicating variable response of genotypes to changing environments.

e 4.13: Mean sum of squares in pooled analysis for 13 characters of mungbean in Genotype x environment interaction studies

Source of variation	Degrees of freedom	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield g per plot
Genotypes	19	10.596**	16.556**	118.636**	0.189**	0.877**	47.494**	1.173**	35.563**	46.056**	7.055**	0.292**	64672.840**
Genotype x environment	100	26.337**	25.291**	360.311**	0.164**	0.963**	23.916**	0.419**	0.413**	17.715**	0.504**	0.015**	25461.100**
Environment (near)	1	2582.345**	2424.438**	33962.883**	12.365**	84.105**	2198.119**	9.106**	18.325**	1633.172**	25.999**	0.532**	2263534.090**
Genotype x environment (near)	19	0.384#	0.541#	83.921**	0.075**	0.207**	5.034**	0.049**	0.402**	4.681**	0.359**	0.016**	5753.680**
Pooled variation	80	0.550**	1.179**	5.922**	0.032**	0.103**	1.223*	0.039**	0.174**	0.618**	0.219*	0.009**	2165.700**
Pooled error	240	0.076	0.133	0.359	0.005	0.009	0.898	0.001	0.023	0.294	0.142	0.002	397.450

Significant at 5% level of probability

Significant at 1% level of probability

Significant only when tested against pooled error

Genotype x environment (Linear) interaction was significant against pooled deviation for all the characters except for days to 50 per cent flowering and days to maturity indicating that the differences among the regression coefficients pertaining to various genotypes on environmental index are real. Mean squares due to genotype x environment (linear) interactions were significant for days to 50 per cent flowering and days to maturity when tested against pooled error. The pooled deviations were significant for all the characters when tested against pooled error indicating the importance of the non-linear component of G X E interaction.

4.2.3 Linear and non linear components of genotype x environment interaction

The linear and non linear portions of genotype x environment interaction for various characters are presented in Table 4.14. More than 80 per cent of variation was contributed by linear component for plant height, number of pods per plant and shoot dry weight while for number of branches per plant, number of clusters per plant, seeds per pod, 1000 seed weight (g), shoot nitrogen (%), seed protein (%) and grain yield, 60% of the variation was contributed linear component. The non-linear component was predominant for days to 50 per cent flowering and days to maturity.

Table 4.14: Relative contribution of linear and non linear portion of G-E interactions for 13 characters of mungbean

S.No.	Character	Linear (%)	Non linear (%)
1	Days to 50% flowering	41.11	58.89
2	Days to maturity	31.45	68.55
3	Plant height (cm)	93.41	6.59
4	Number of branches per plant	70.09	29.91
5	Number of clusters per plant	66.77	33.23
6	Number of pods per plant	80.45	19.55
7	Pod length (cm)	55.68	44.32
8	Seeds per pod	71.43	28.57
9	1000 seed weight (g)	67.68	32.32
10	Shoot dry weight (g)	88.34	11.66
11	Seed protein (%)	62.11	37.89
12	Shoot nitrogen (%)	64.00	36.00
13	Grain yield (g)	72.65	27.35

4.2.4 Relation between mean performance and environmental index

Environmental indices were calculated for all the characters in different environments and are presented in Table 4.15. Linear relation existed between mean performance and environmental index for all the characters studied. Plant height, number of branches per plant, number of clusters per plant, seeds per pod, shoot dry weight, shoot nitrogen and grain yield were found to be superior in E4 whereas days to 50 per cent flowering, days to maturity and pod length were desirable in E2 and for pods per plant, 1000 seed weight and seed protein, E5 was found to be the best environment.

Environment 3 was not found to be better for days to 50 per cent flowering, days to maturity, seeds per pod, and 1000 seed weight and similarly E5 for pod length. The expression of plant height, number of branches per plant, number of pods per plant, number of clusters per plant, shoot dry weight, shoot nitrogen, seed protein and grain yield was low in E6.

4.2.5 Stability analysis -Stability parameters for individual characters

Three stability parameters viz., mean ($\bar{X}$), linear regression coefficient (b_i) and deviations from

Table 4.15: Environmental index (E 1) for 13 characters of mungbean in
Genotype x environment interaction studies

S.No.	Character	Environments					
		E1	E2	E3	E4	E5	E6
1	Days to 50% flowering	-3.69	-3.89	9.31	-3.39	0.15	1.48
2	Days to maturity	-3.35	-5.28	7.73	-3.45	1.53	2.83
3	Plant height (cm)	17.41	-5.46	10.86	28.24	-10.60	-17.75
4	Number of branches per plant	0.19	0.34	-0.36	0.34	-0.06	-0.47
5	Number of clusters per plant	0.72	0.68	-0.98	0.90	-0.1	-1.2
6	Number of pods per plant	-0.22	2.26	-4.55	5.54	3.33	-6.42
7	Pod length (cm)	0.23	0.33	-0.19	0.24	-0.33	-0.29
8	Seeds per pod	0.41	0.07	-0.51	0.57	-0.03	-0.48
9	1000 seed weight (g)	0.03	-0.04	-0.58	0.15	0.7	-0.27
10	Shoot dry weight (g)	0.08	1.31	4.43	5.49	2.49	-4.89
11	Seed protein (%)	0.13	0.4	-0.1	-0.07	0.55	-0.89
12	Shoot nitrogen (%)	-0.01	0.07	-0.03	0.09	0.02	-0.11
13	Grain yield (g)	0.24	69.17	-161.16	182.0	144.34	-189.66

linear regression (S^2_{di}) were analysed for all the characters studied and are presented in Tables 4.16 to 4.28. The range of variation for mean performance, linear regression coefficient and deviations from regression for the characters studied are described below in detail.

4.2.5.1 Days to 50 per cent flowering

The number of days to 50 per cent flowering ranged from 33.17 (D12/333) to 37.33 (LGG 407) with a general mean of 35.22 days over six environments. Seven genotypes D12/333 (33.17), MH 309 (33.28), K 851 (33.56), PDM 54 (33.67), ML 267 (34.17), LGG 426 (34.11) and LGG 127 (34.44) were significantly early to flower. Linear regression coefficients ranged from 0.8630 (LGG 403) to 1.0702 (LGG 407). Deviations from linear regressions ranged from -0.0221 (K 851) to 2.0849 (LGG 403) and were significant among the genotypes except in MUG 125, PDM 84-155, D12/333, Pusa 105 and K 851. D12/333 and K 851 recorded low mean (desirable direction) with regression coefficient around unity and non significant deviations (Table 4.16).

Pusa 105 had high mean (35.56) with regression coefficient around unity ($b_i=1.0012$) and insignificant deviations from regression (0.1026). Four genotypes viz., MH 309, LGG 127, ML 267, and PDM 54 having low

Table 4.16: Stability parameters of mungbean genotypes for days to 50% flowering

S.No.	Variety	X	bi	s ² di
1	MUG 125	35.22	0.9331	0.0244
2	LGG 403	35.78	0.8680	0.0849**
3	LGG 407	37.33	1.0702	0.7900**
4	LGG 410	37.28	1.0461	0.6784**
5	LGG 426	34.11	0.9302	1.9553**
6	PDM 84-145	35.39	0.9931	0.2791**
7	PDM 84-155	35.78	0.9715	-0.0068
8	D12/333	33.17	1.0254	-0.0059
9	MH 309	33.28	1.0419	0.1846*
10	ML 131	35.28	0.9543	0.3295**
11	LGG 127	34.44	0.9931	0.1232*
12	PS 16	37.06	0.9698	0.2011*
13	UPM 83-10	35.00	0.9477	0.3775**
14	LGG 450	34.94	1.0355	1.1675*
15	PDM 54	33.67	1.0695	0.2819**
16	Pusa 105	35.56	1.0012	0.1026
17	K 851	33.56	1.0244	-0.0221
18	ML 26-10-3	37.05	1.0464	0.9943**
19	ML 267	34.17	0.9984	0.2931**
20	UPM 79-4-12	36.28	1.0400	1.423**
	General mean	35.22	0.9999	
	S.E (m)	0.33	0.0653	

* Significant at 5% level of probability

** Significant at 1% level of probability

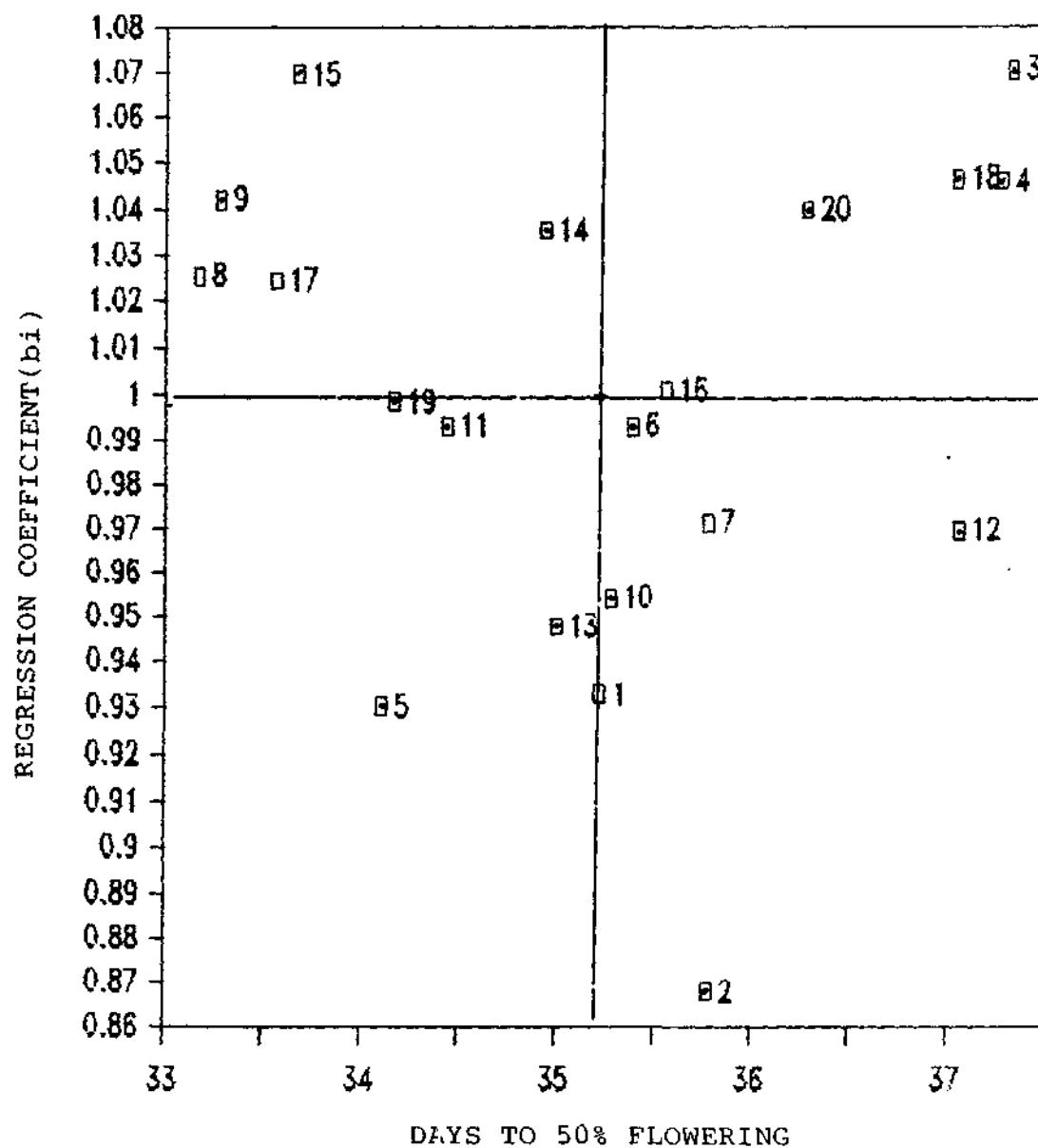


Fig.4 : PARAMETERS OF STABILITY PLOTTED AGAINST THE MEAN PERFORMANCE OF INDIVIDUAL GENOTYPE

DOT IN THE SQUARE BOX INDICATES THE SIGNIFICANT DEVIATIONS FROM REGRESSION.

SERIAL NUMBERS 1 TO 20 INDICATES GENOTYPES.

mean value recorded significant ' S^2_{di} ' with regression coefficient around unity whereas, LGG 407, LGG 410, ML 26-10-3 and UPM 79-4-12 with high mean and unit regression coefficient showed significant deviations. Two genotypes, PDM 84-145 and LGG 450 had mean value around general mean with average response ($b_i=1$) and non significant deviations from regressions. LGG 403, LGG 426, ML 131, PS 16 and UPM 83-10 had ' b_i ' values less than unity with significant deviations, whereas, MUG 125 and PDM 84-155 had linear regressions less than 1.00 and non significant ' S^2_{di} ' (Fig. 4).

4.5.1.2 Days to maturity

Stability parameters for days to maturity are presented in Table 4.17 and Fig. 5. Mean number of days taken to mature ranged from 64.00 (D12/333) to 69.83 (LGG 410) among genotypes over six environments with a general mean of 66.85 days. Four genotypes D12/333 (64.00) MH 309 (64.78), K 851 (64.11) and PDM 54 (64.72) were significantly early to mature. Linear regression coefficients ranged from 0.8496 (LGG 403) to 1.1165 (ML 26-10-3) while deviations from linear regression slope ranged from 0.1261 (PS 16) to 3.5427 (PDM 84-155) among the genotypes. The genotype D12/333 was the earliest to mature with a linear regression coefficient around unity ($b_i=1.0021$) and significant deviations from regression (0.9364) whereas, LGG 407

Table 4.17: Stability parameters of mungbean genotypes for days to maturity

S.No.	Variety	X	bi	S^2_{di}
1	MUG 125	66.83	0.9467	0.5796**
2	LGG 403	67.78	0.8496	1.0841**
3	LGG 407	69.61	0.9921	0.3964**
4	LGG 410	69.83	1.0009	0.3242*
5	LGG 426	66.00	0.9237	1.1740**
6	PDM 84-145	67.11	1.0145	0.2678*
7	PDM 84-155	66.83	1.0743	3.5427**
8	D12/333	64.00	1.0021	0.9364**
9	MH 309	64.78	0.9339	2.4752**
10	ML 131	67.17	1.0073	0.5479**
11	LGG 127	66.94	0.9182	1.9512**
12	PS 16	69.00	0.9863	0.1261
13	UPM 83-10	66.28	0.9726	0.4443**
14	LGG 450	66.39	1.0169	0.8267**
15	PDM 54	64.72	1.0148	0.8000**
16	Pusa 105	67.56	1.0627	1.7898**
17	K 851	64.11	1.0234	0.8329**
18	ML 26-10-3	68.39	1.1165	0.3900**
19	ML 267	65.94	0.9995	0.4515**
20	UPM 79-4-12	67.78	1.0741	1.9941**
	General mean	66.85	1.0000	
	S.E (m)	0.49	0.0986	

* Significant at 5% level of probability

** Significant at 1% level of probability

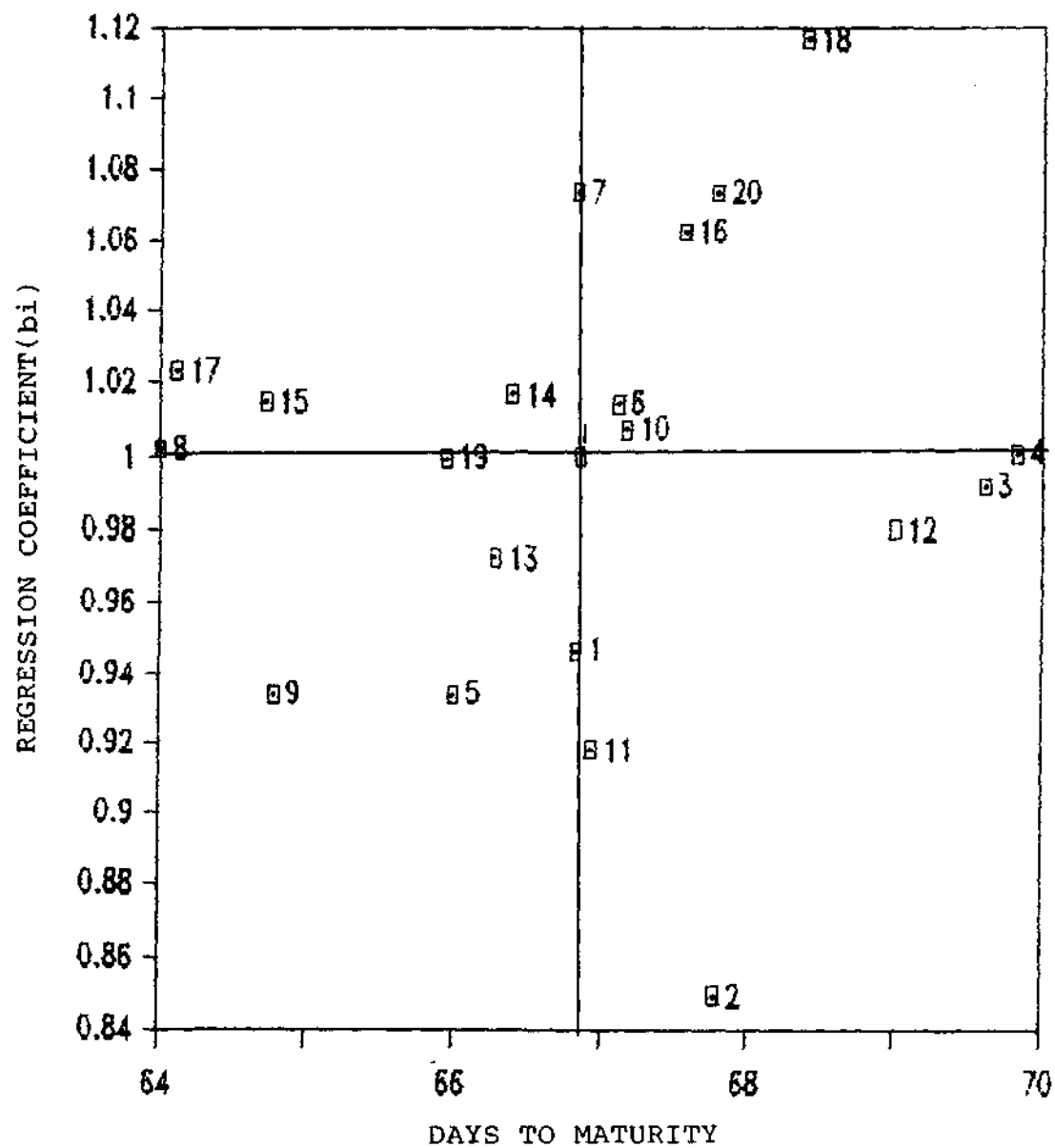


Fig. 5: PARAMETERS OF STABILITY PLOTTED AGAINST THE MEAN PERFORMANCE OF INDIVIDUAL GENOTYPE

DOT IN THE SQUARE BOX INDICATES THE SIGNIFICANT DEVIATIONS FROM REGRESSION.

SERIAL NUMBER 1 TO 20 INDICATES GENOTYPES.

(69.83) was late to mature with a regression coefficient of one (1.0009) and significant s^2_{di} value (0.3242). Linear and non linear portions of interactions were significant in all the genotypes except in case of PS 16. The genotype PS 16 had high mean, regression coefficient around one ($b_i=0.9663$) and non significant ' s^2_{di} ' (0.1261), K 851, ML 267, PDM 54 recorded low mean (desirable directions) and regression coefficient around unity with significant deviations from regression slopes. Whereas, PDM 84-155, UPM 83-10, LGG 450 with high mean and ' b_i ' values around unity recorded significant, ' s^2_{di} ' values. D12/333 MH 309 with low mean and linear regression less than 1.00 had significant deviations from linear regression. Among other genotypes LGG 407, PDM 84-145, UPM 74-4-12, ML 26-10-3, Pusa 105 and LGG 410 had high mean value, regression coefficient greater than unity and significant deviations from regression. MUG 125, LGG, 426 and LGG 127 recorded mean value around general mean with significant deviations and linear regression values less than 1.0. Two genotypes LGG 403 and ML 131 with high mean recorded ' b_i ' values less than one and significant deviations.

4.2.5.3 Plant height (cm)

Stability parameters for plant height are presented in Table 4.18 and Fig. 6. Mean plant height among the genotypes ranged from 34.50 (D12/333) to 54.36 cm (PS 16). Eight genotypes have recorded higher plant height (cm) viz., LGG 407 (51.21), LGG 410 (51.94), ML 131, (51.93), PS 16 (54.36), Pusa 105 (54.09), ML 26-10-3 (52.97), LGG 450 (51.33) and UPM 79-4-12 (50.28) over general mean. Linear regression coefficients ranged from 0.5403 (D12/333) to 1.2938 (ML 26-10-3) and deviations from regressions from 0.2347 (LGG 426) to 14.7851 (PS 16). Linear regression coefficients were significant for all the genotypes while deviations from regression coefficient (S^2_{di}) were significant for all except for LGG 426 and UPM 79-4-12. The genotype LGG 426 with low mean (46.24) and non significant deviations (0.2347) recorded regression coefficient less than unity ($b_i=0.7711$). Whereas UPM 79-4-12 recorded high mean (50.28) and non significant deviations (0.4204) had regression coefficient around unity ($b_i=1.0954$). The genotypes, LGG 407, LGG 410, Pusa 105, LGG 450 and ML 26-10-3 with high mean value had linear regressions around unity and significant deviations. K 851 and UPM 83-10 with low mean values recorded 'bi' values greater than one and significant deviations. Whereas, PDM 54 with low mean, unit regression coefficient showed

Table 4.18: Stability parameters of mungbean genotypes for plant height (cm)

S.No.	Variety	X	bi	s^2_{di}
1	MUG 125	47.20	0.9202	2.0302**
2	LGG 403	49.22	0.8825	1.7398**
3	LGG 407	51.21	1.1286	2.2514**
4	LGG 410	51.94	1.2238	4.4295**
5	LGG 426	46.24	0.7711	0.2347
6	PDM 84-145	45.75	0.6777	12.4921**
7	PDM 84-155	44.87	0.8649	4.6066**
8	D12/333	34.50	0.5403	5.3585**
9	MH 309	48.55	1.1978	12.3831**
10	ML 131	51.93	0.9093	5.9579**
11	LGG 127	46.50	0.8183	3.9634**
12	PS 16	54.36	1.2599	14.7851**
13	UPM 83-10	48.01	1.1369	1.8938**
14	LGG 450	51.33	1.1818	4.6299**
15	PDM 54	47.28	0.9928	3.2906**
16	Pusa 105	54.09	1.2181	10.0362**
17	K 851	45.93	1.1864	14.6189**
18	ML 26-10-3	52.97	1.2938	2.5239**
19	ML 267	44.97	0.7054	3.5988**
20	UPM 79-4-12	50.28	1.0954	0.4204**
	General mean	48.36	1.0000	
	S.E (m)	1.088	0.0594	

** Significant at 1% level of probability

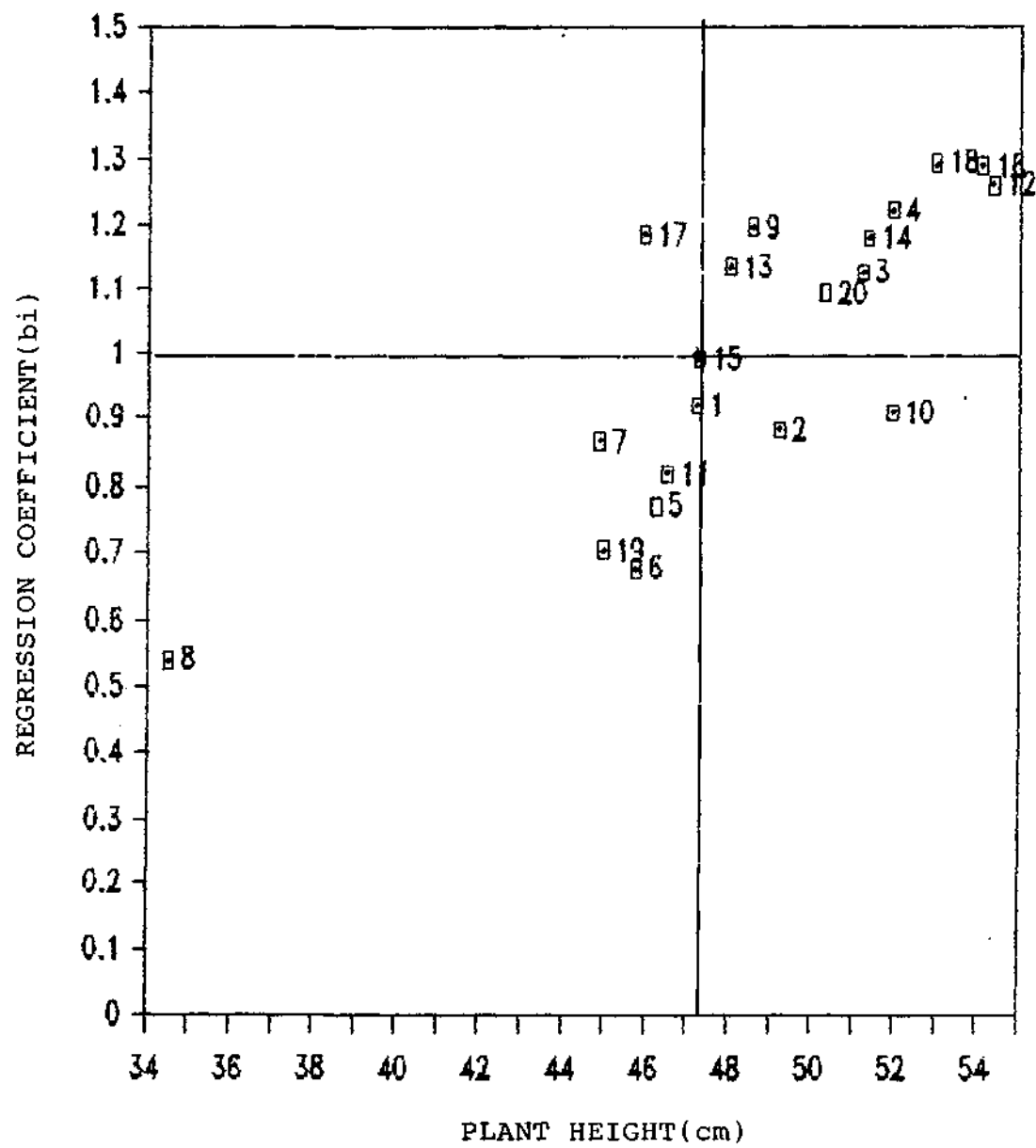


Fig. 5 : PARAMETERS OF STABILITY PLOTTED AGAINST THE MEAN PERFORMANCE OF INDIVIDUAL GENOTYPE

DOT IN THE SQUARE BOX INDICATES THE SIGNIFICANT DEVIATIONS FROM REGRESSION.

SERIAL NUMBERS 1 TO 20 INDICATES GENOTYPES.

significant deviations. Significant deviations from linear regression and regression coefficients less than one were recorded for LGG 426, ML 131, LGG 403, PDM 84-145, PDM 84-155, DL2/333, LGG 127 and ML 267 and MH 309.

4.2.5.4 Number of branches per plant

Stability parameters for number of branches per plant are presented in Table 4.19 and in Fig. 7. Mean number of branches per plant among genotypes ranged from 1.23 (K 851) to 1.92 (DL2/333). Eight genotypes, ~~PDM 84-145~~(1.86), PDM 84-155 (1.84), ~~DL2/333~~ (1.92), Pusa 105 (1.78), LGG 450 (1.77), ML 267 (1.73), MUG 125 (1.68), LGG 426 (1.67) and PS 16 (1.66) have recorded more number of branches per plant over general mean (1.61). Linear regression coefficients ranged from 0.4797 (K 851) and deviations from regression slope ranged from 0.0065 (PS 16) to 0.1099 (PDM 84-145). Among the superior genotypes for this trait, PDM 84-145, PDM 84-155 and Pusa 105 recorded linear regression coefficients around unity but with significant deviations from regressions, while LGG 450 recorded regression coefficients greater than unity ($b_i=1.4809$) and significant deviations. The genotypes, DL2/333, MUG 125, LGG 426 and ML 267 had higher mean value and regression coefficient greater than unity with ' S^2_{di} ' significant. The genotype PS 16 recorded higher mean with regression coefficient around unity(1.074)

Table 4.19: Stability parameters of mungbean genotypes for number of branches per plant

S.No.	Variety	X	bi	s ² _{di}
1	MUG 125	1.68	1.9058	0.0301**
2	LGG 403	1.55	0.9224	0.0378**
3	LGG 407	1.54	0.8022	0.0142**
4	LGG 410	1.57	0.8975	0.0263**
5	LGG 426	1.67	0.5282	0.0510**
6	PDM 84-145	1.86	1.1048	0.1099**
7	PDM 84-155	1.84	1.1510	0.0161**
8	D12/333	1.92	1.4251	0.0343**
9	MH 309	1.47	0.8141	0.0192**
10	ML 131	1.52	1.1485	0.0076**
11	LGG 127	1.37	0.6508	0.0357**
12	PS 16	1.66	1.0241	0.0065
13	UPM 83-10	1.47	1.0654	0.0175**
14	LGG 450	1.77	0.6766	0.0081**
15	PDM 54	1.4	0.5870	0.0195**
16	Pusa 105	1.78	1.1212	0.0266**
17	K 851	1.23	0.4797	0.0122**
18	ML 26-10-3	1.54	1.0966	0.0323**
19	ML 267	1.73	1.4809	0.0094**
20	UPM 79-4-12	1.57	1.0684	0.0291**
	General mean	1.61	1.0000	
	S.E (m)	0.08	0.2276	

** Significant at 1% level of probability

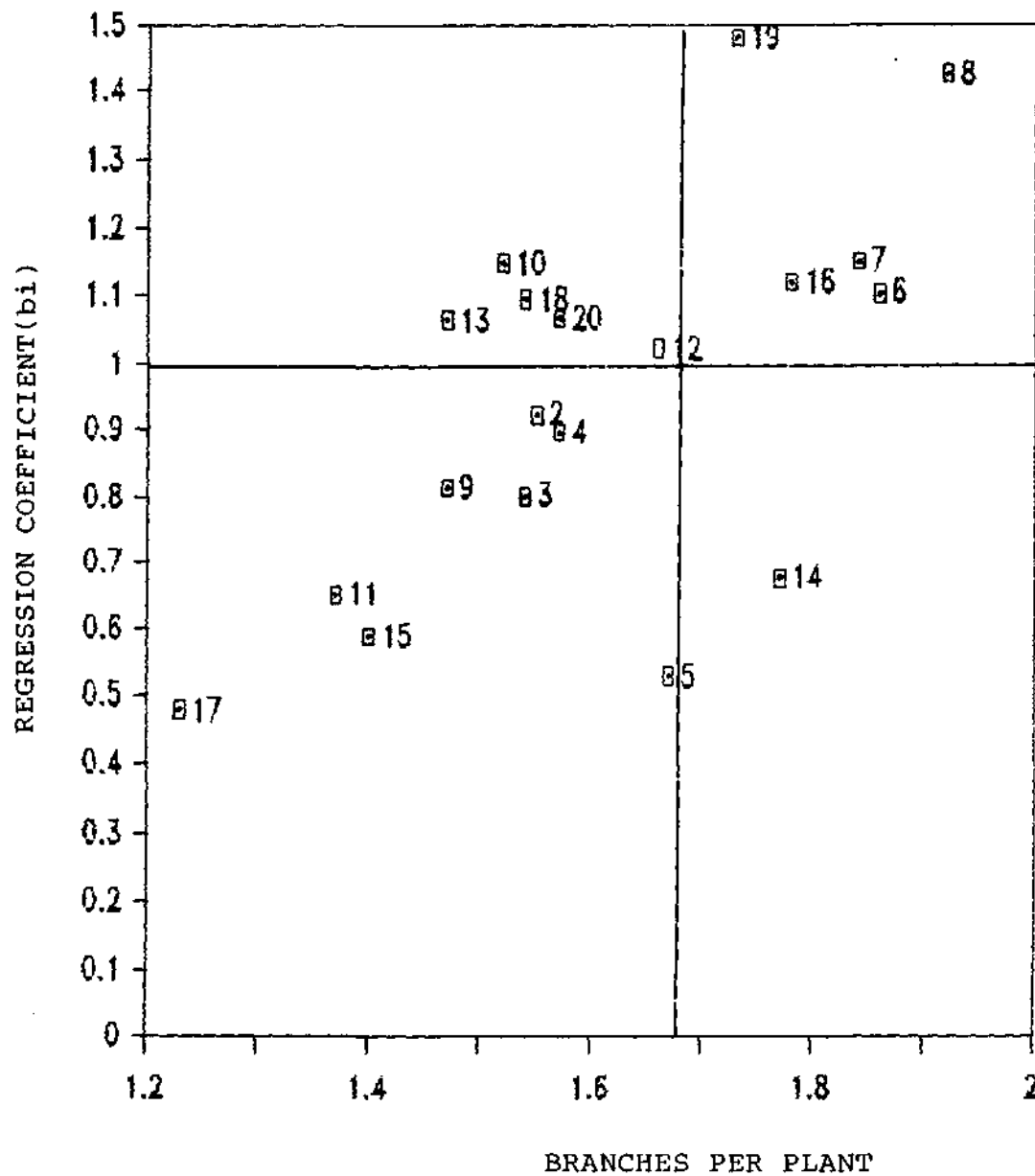


Fig.7 :PARAMETERS OF STABILITY PLOTTED AGAINST THE MEAN PERFORMANCE OF INDIVIDUAL GENOTYPE

DOT IN THE SQUARE BOX INDICATES THE SIGNIFICANT DEVIATIONS FROM REGRESSION.

SERIAL NUMBERS 1 TO 20 INDICATES GENOTYPES.

and non significant deviations from regression slopes (0.0065). LGG 405, LGG 407, LGG 410, UPM 79-4-12, MH 309, LGG 127, PDM 54, and K 851 have recorded low mean value, significant deviations from regression slope with linear regressions less than unity. Two genotypes viz., ML 131, and ML 26-10-3 with low mean values had regression coefficients around unity and significant deviations from linear regression. The genotypes UPM 83-10 with low mean recorded significant ' s^2_{di} ' values and ' b_i ' values greater than unity.

4.2.5.5 Number of clusters per plant

Stability parameters for the number of clusters per plant are presented in Table 4.20 and Fig. 8. Mean number of clusters per plant ranged from 3.76 (K 851) to 5.07 (LGG 450) with a general mean of 4.33 over six environments. Genotypes LGG 450 (5.07), MUG 125 (4.85), Pusa 105 (4.81), LGG 403 (4.72), LGG 407 (4.73), LGG 410 (4.51) and ML 267 (4.50) recorded more number of clusters per plant than general mean. Linear regression coefficients ranged from 0.7228 (LGG 127), to 1.6204 (MUG 125) while the deviations from linear regressions from -0.0024 (Pusa 105) to 0.3361 (D12/333). The genotype, LGG 450 with high mean and regression coefficient almost unity ($b_i=1.0316$) had significant deviations from regression coefficient (0.0591). The genotype LGG 407, LGG 410 and Pusa 105 recorded more

Table 4.20: Stability parameters of mungbean genotypes for number of clusters per plant

S.No.	Variety	X	bi	S^2_{di}
1	MUG 125	4.85	1.6204	-0.0018
2	LGG 403	4.72	0.9521	0.0595**
3	LGG 407	4.73	0.7887	0.0197
4	LGG 410	4.51	0.8760	0.0463
5	LGG 426	4.32	0.8831	0.0178
6	PDM 84-145	4.47	0.8952	0.1316**
7	PDM 84-155	4.13	1.1150	0.2486**
8	D12/333	3.77	0.9003	0.3361**
9	MH 309	4.31	0.9424	0.1954**
10	ML 131	4.38	0.9705	0.1262**
11	LGG 127	3.77	0.7228	0.0098
12	PS 16	3.93	0.7726	0.1014**
13	UPM 83-10	4.28	1.4005	0.2057**
14	LGG 450	5.07	1.0316	0.0591**
15	PDM 54	4.23	0.9643	0.1129**
16	Pusa 105	4.81	0.8936	0.0024
17	K 851	3.76	1.3115	0.1542**
18	ML 26-10-3	3.96	1.0881	0.0146
19	ML 267	4.51	1.0200	0.0498
20	UPM 79-4-12	4.17	0.8451	0.0019
	General mean	4.33	0.9999	
	S.E (m)	0.14	1.1567	

** Significant at 1% level of probability

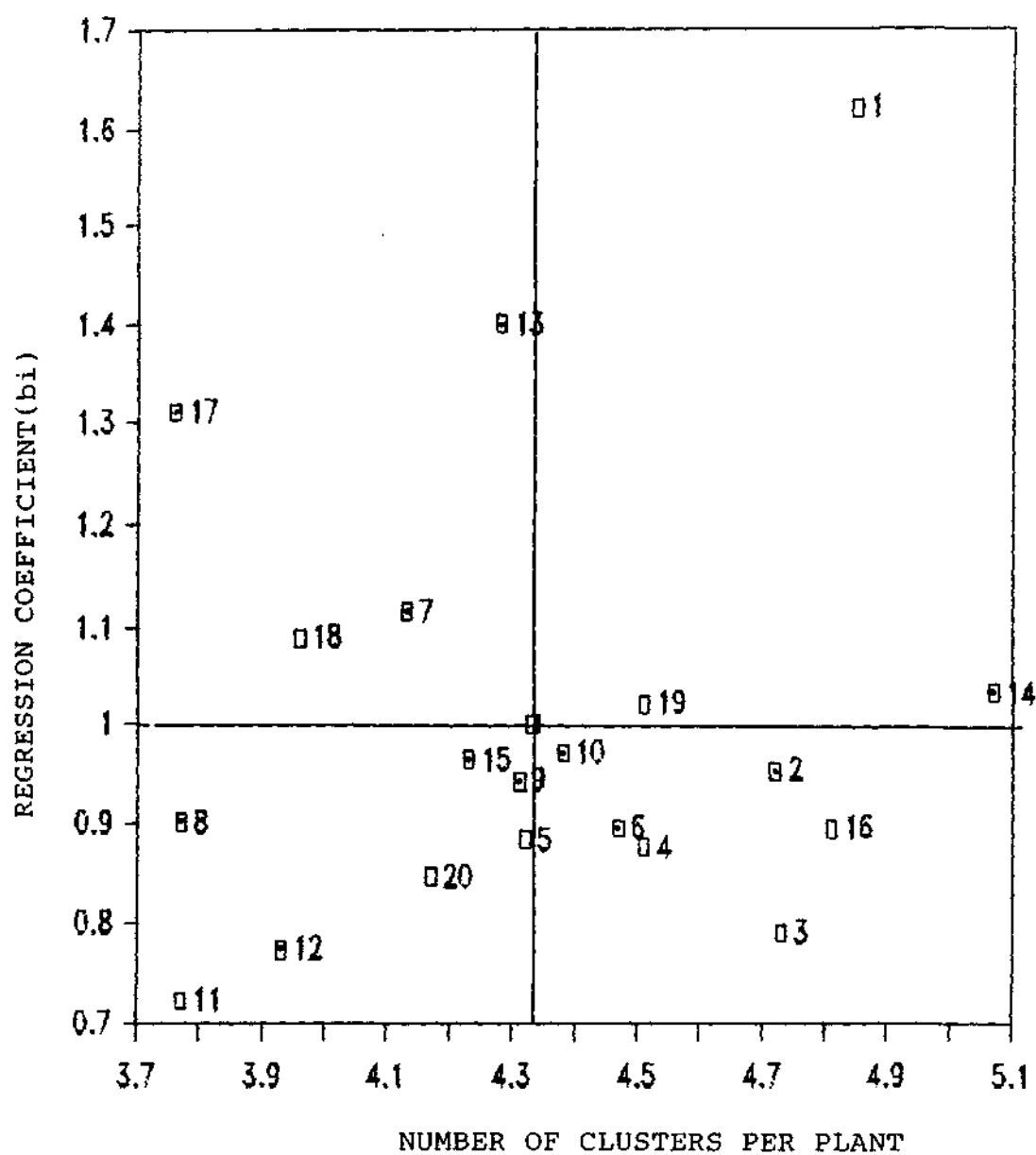


Fig.8 : PARAMETERS OF STABILITY PLOTTED AGAINST THE MEAN PERFORMANCE OF INDIVIDUAL GENOTYPE

DOT IN THE SQUARE BOX INDICATES THE SIGNIFICANT DEVIATIONS FROM REGRESSION.

SERIAL NUMBERS 1 TO 20 INDICATES GENOTYPES.

number of clusters along with non-significant deviations from regression slope and 'bi' values less than unity. While, MUG 125 with high mean, linear regression greater than one ($b_i=1.6204$), recorded non significant deviations from regression coefficient. LGG 403 with high mean, regression coefficient less than one recorded significant ' S^2_{di} ' values. ML 267 with high mean and linear regression coefficient around unity recorded non significant deviations from regressions. K 851, PDM 84-155, and UPM 79-4-12 had fewer number of clusters per plant and regression coefficient greater than unity along with significant deviations from regression slope. The genotype, LGG 127 recorded low mean value, regression coefficients less than one with non significant deviations. ML 26-10-3, UPM 79-4-12 and ML 131 with low mean, regression coefficient around one and LGG 426 with low mean and regression coefficients less than one, showed non-significant deviations.

4.2.5.6 Number of pods per plant

Stability parameters for this trait are presented in Table 4.21 and Fig. 9. Mean number of pods per plant over six environments ranged from 14.94 (D12/333) to 24.28 (LGG 410) with a general mean value of 18.57. Eight genotypes viz., LGG 410 (24.28), ML 131 (19.67), Pusa 105 (20.89), LGG 403 (19.94), LGG 407 (23.88), LGG 450 (22.56), PDM 84-145 (19.72) and ML 267

Table 4.21: Stability parameters of mungbean genotypes for number of pods per plant

S.No.	Variety	$\bar{x}$	b_i	s^2_{di}
1	MUG 125	18.61	1.0230	-0.8139
2	LGG 403	19.94	1.0330	3.0642**
3	LGG 407	23.88	1.2411	-0.07
4	LGG 410	24.28	1.3519	-0.8139
5	LGG 426	18.83	1.1563	-0.0354
6	PDM 84-145	19.72	1.0201	-0.2441
7	PDM 84-155	16.67	1.1269	-0.6221
8	D12/333	14.94	0.5790	4.4137**
9	MH 309	17.94	0.9750	-0.6588
10	ML 131	19.67	1.2578	-0.2003
11	LGG 127	15.22	0.6238	1.7262**
12	PS 16	15.44	0.8143	-0.5262
13	UPM 83-10	16.83	1.0361	2.8690**
14	LGG 450	22.56	0.7973	0.0059
15	PDM 54	18.61	1.1213	-0.4794
16	Pusa 105	20.89	0.6844	-0.0097
17	K 851	15.39	0.9633	-0.4283
18	ML 26-10-3	15.78	0.9716	-0.5206
19	ML 267	19.61	1.2565	-0.1992
20	UPM 79-4-12	16.67	0.9697	0.0421
	General mean	18.57	1.0000	
	S.E (m)	0.49	0.1059	

* Significant at 5% level of probability

** Significant at 1% level of probability

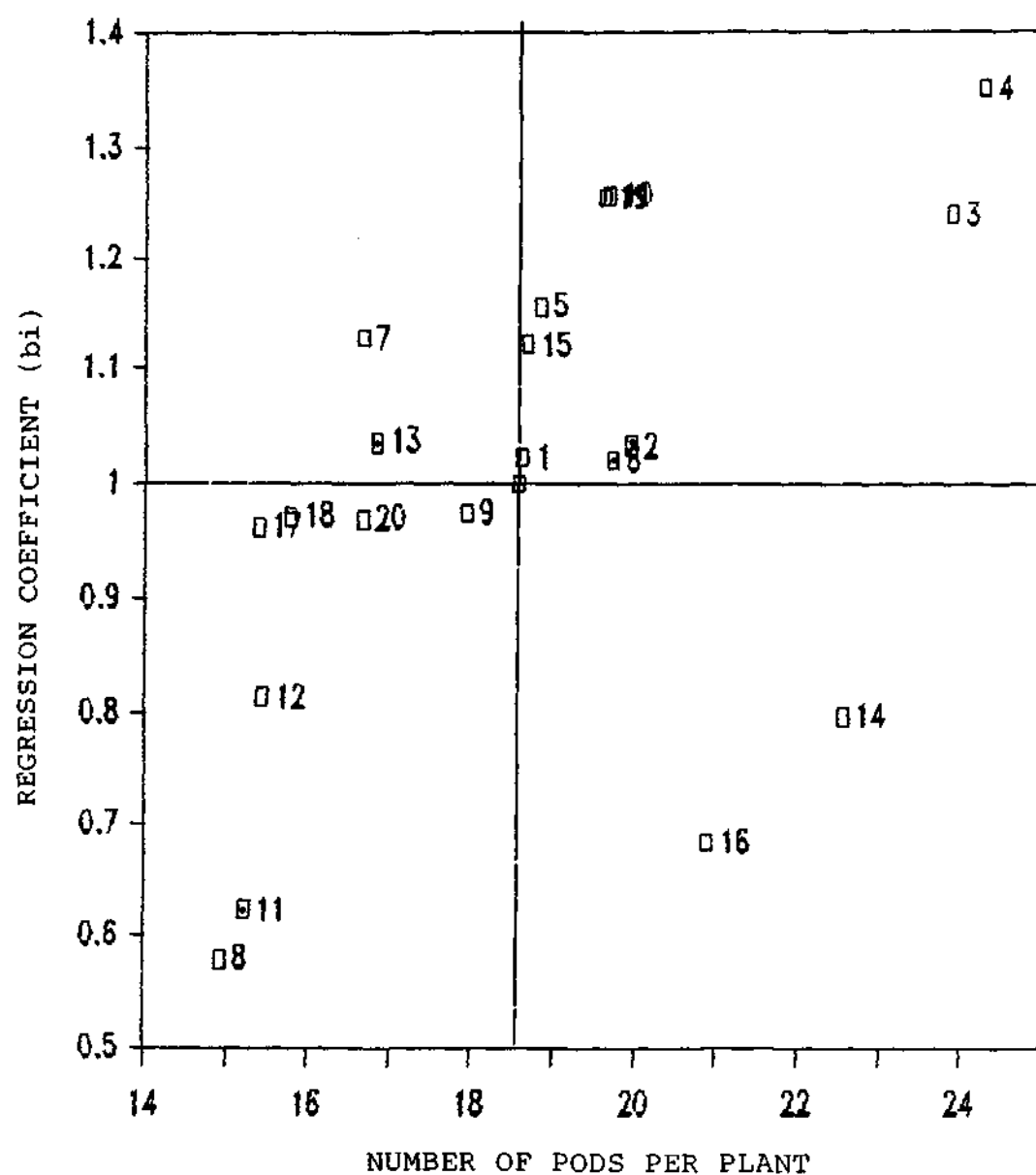


Fig.9 : PARAMETERS OF STABILITY PLOTTED AGAINST THE MEAN PERFORMANCE OF INDIVIDUAL GENOTYPE

DOT IN THE SQUARE BOX INDICATES THE SIGNIFICANT DEVIATIONS FROM REGRESSION.

SERIAL NUMBER 1 TO 20 INDICATES GENOTYPES.

(19.61) have recorded more number of pods per plant over general mean. Linear regression coefficients ranged from 0.5790 (D12/333) to 1.3519 (LGG 410) and deviations from regressions slope ranged from -0.8139 (MUG 125) to 4.4137 (D12/333). Linear regression coefficients were significant among the genotypes. The deviations from linear regression slopes were significant only for LGG 403, D12/333, LGG 127 and UPM 83-10 of the nine genotypes which recorded significantly more number of pods per plant. ML -131, PDM 54, ML 267, LGG 410 and LGG 407 had regression coefficient greater than unity ($b_i > 1$) and deviations from linear regressions non significant. While, LGG 450 and Pusa 105 had high mean values, non significant deviations with regression coefficient less than unity. The genotype, LGG 403 had high mean, unit regression coefficient but the deviations from linear regression were significant. D12/333 recorded low mean value with significant deviations and linear regression coefficient less than unity ($b_i = 0.05790$). PDM 84-145 had unit regression slope with high mean value and non significant deviations. The genotypes, LGG 407, LGG 410, LGG 426, PDM 54 and ML 267 with high mean recorded linear regressions greater than one and the deviations were non significant. MH 309, PS 16, K 851, and UPM 79-4-12 recorded non significant deviations with regression coefficients less than one, PDM 84-155 recorded non

significant deviations with linear slopes greater than one. LGG 127 and UPM 83-10 have recorded linear slopes greater than one. LGG 127 and UPM 83-10 have recorded linear regressions less than unity and around unity, respectively along with significant deviations from linear regressions.

4.2.5.7 Pod length (cm)

The pod length ranged from 6.46 (MUG 125) to 7.76 cm (K 851) with a general mean of 6.96 cm over environments (Table 4.22 and Fig. 10). Four genotypes K 851 (7.76), LGG 426 (7.35), PDM 84-155 (7.48), PS 16 (7.13) and ML 131 (7.01) have recorded significantly greater pod length over general mean. Linear regression slopes ranged from 0.5765 (LGG 426) to 1.9672 (LGG 403), while, the deviations from linear regression slopes ranged from -0.0004 (ML 131) to 0.1632 (PDM 84-155). Both linear and non linear regression coefficients were significant for all the genotypes except for ML 131 and K 851. The genotypes. ML 131 and K 851 had unit regression coefficient, non significant deviations from regression and high mean values. While LGG 426 and PDM 84-145 and Pusa 105 with high mean and significant deviations with regression coefficient less the unity. PS 16 and UPM 83-10 had high mean with linear regressions greater than unity and significant deviations. The rest of the genotypes have recorded

Table 4.22: Stability parameters of mungbean genotypes for pod length (cm)

S.No.	Variety	X	bi	s^2_{di}
1	MUG 125	6.46	1.0973	0.0105**
2	LGG 403	6.79	1.9672	0.0428**
3	LGG 407	6.91	0.7404	0.0273**
4	LGG 410	6.91	0.8923	0.0291**
5	LGG 426	7.35	0.5765	0.0337**
6	PDM 84-145	7.03	0.7308	0.0209**
7	PDM 84-155	7.48	0.8325	0.1632**
8	D12/333	6.78	0.6041	0.0145**
9	MH 309	6.81	0.6045	0.0195**
10	ML 131	7.01	0.9841	-0.0064
11	LGG 127	6.76	0.5917	0.0139**
12	PS 16	7.13	1.3974	0.0697**
13	UPM 83-10	6.97	1.4348	0.0554**
14	LGG 450	6.91	0.9432	0.0114**
15	PDM 54	6.64	1.4645	0.0265**
16	Pusa 105	7.05	0.5183	0.0102**
17	K 851	7.76	1.0233	0.0004
18	ML 26-10-3	6.83	1.2893	0.0020*
19	ML 267	6.84	0.8815	0.0026*
20	UPM 79-4-12	6.76	1.4229	0.0889**
	General mean	6.96	1.0000	
	S.E (m)	0.09	0.2983	

* Significant at 5% level of probability

** Significant at 1% level of probability

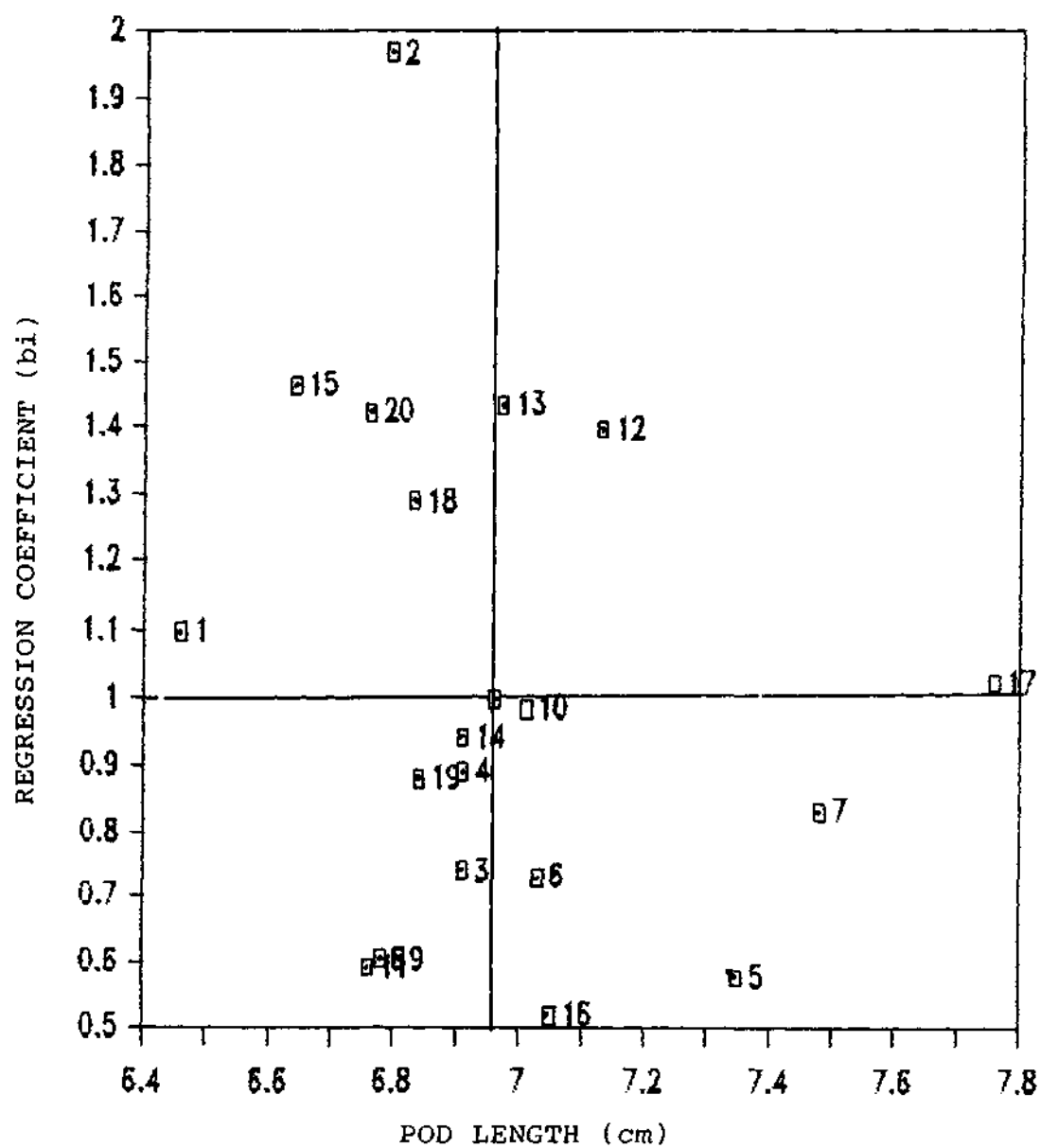


Fig.10: PARAMETERS OF STABILITY PLOTTED AGAINST THE MEAN PERFORMANCE OF INDIVIDUAL GENOTYPE

DOT IN THE SQUARE BOX INDICATES THE SIGNIFICANT DEVIATIONS FROM REGRESSION

SERIAL NUMBERS 1 TO 20 INDICATES GENOTYPES.

low mean and significant deviations with either regression slopes greater than one (UPM 83-10, PDM 54, ML 267 and UPM 79-4-12) or less than one (LGG 407, LGG 410, D12/333, MH 309, ML 26-10-3 and LGG 127) or equal to one (MUG 125, LGG 450 and LGG 403).

4.2.5.8 Seeds per pod (g)

The stability parameters for the number of seed per pod are presented in Table 4.23 and Fig. 11. The number of seeds per pod ranged from 9.87 (D12/333) to 11.77 (K 851) among the genotypes studied over six environments with a mean value of 10.52 (LGG 426). K 851 (11.77), ML 131 (10.82), LGG 127 (10.89), PS 16 (10.86) and PDM 84-145 recorded more number of seeds per pod. Linear regression coefficients ranged from -0.7087 (UPM 79-4-12) to 2.1835 (LGG 426) while deviations from regression ranged from -0.0182 (LGG 410) to 1.1163 (D12/333) among the genotypes. The genotype D12/333 with lowest number of seeds per pod had recorded a regression coefficient of 0.6783 ($b_i < 1$) with significant deviations from regression slope ($S^2_{di} = 1.1163$). Whereas UPM 83-10, LGG 407, PS 16 and LGG 426 with high mean had regression coefficient greater than unity and significant deviations from regression slope. LGG 127 had high mean and linear regressions less than 1.00 with significant deviations from regression slope. ML 131 recorded high mean with non significant deviations from

Table 4.23: Stability parameters of mungbean genotypes for seeds per pod

S.No.	Variety	X	bi	S^2_{di}
1	MUG 125	10.26	0.08827	0.0730**
2	LGG 403	10.39	0.6225	0.4232**
3	LGG 407	10.69	1.2519	0.0570*
4	LGG 410	10.39	0.8103	-0.0182
5	LGG 426	11.14	2.1835	0.0853**
6	PDM 84-145	10.53	1.0298	0.1029
7	PDM 84-155	10.62	0.7451	-0.0150
8	D12/333	9.87	0.6783	1.1163**
9	MH 309	10.43	1.1952	-0.0128
10	ML 131	10.82	1.3762	0.0048
11	LGG 127	10.89	0.8269	0.1978**
12	PS 16	10.86	1.9349	0.1711**
13	UPM 83-10	10.56	1.7356	0.1819**
14	LGG 450	10.41	0.5916	0.0214
15	PDM 54	9.94	1.7086	-0.0173
16	Pusa 105	10.48	0.6112	-0.0093
17	K 851	11.77	1.0245	0.0728
18	ML 26-10-3	10.33	0.9175	0.072**
19	ML 267	10.16	-0.6160	0.2776**
20	UPM 79-4-12	9.94	-0.7087	0.2175**
	General mean	10.52	1.0000	
	S.E (m)	0.19	0.4148	

* Significant at 5% level of probability

** Significant at 1% level of probability

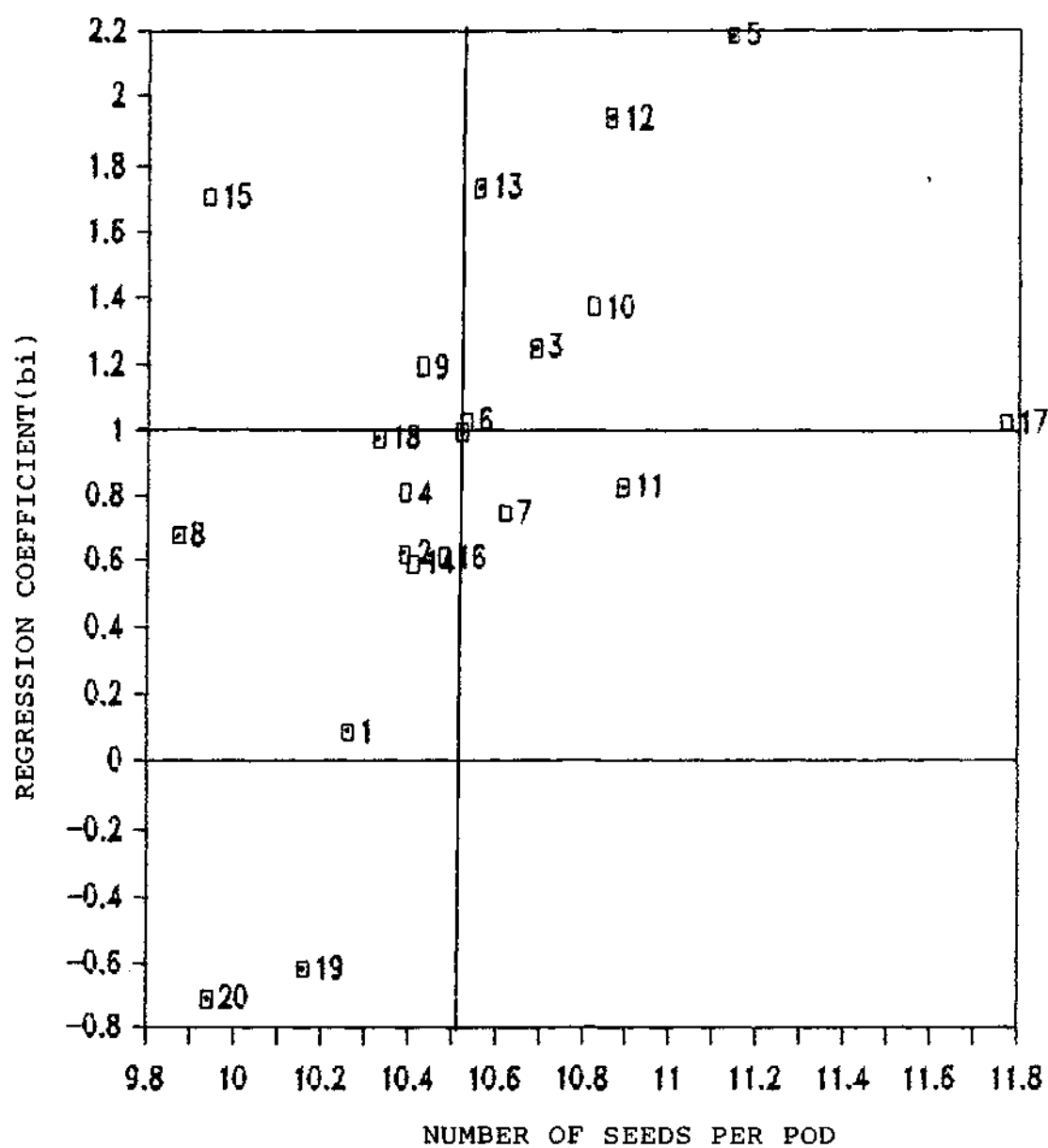


Fig.11 : PARAMETERS OF STABILITY PLOTTED AGAINST THE MEAN PERFORMANCE OF INDIVIDUAL GENOTYPE

DOT IN THE SQUARE BOX INDICATES THE SIGNIFICANT DEVIATIONS FROM REGRESSION.

SERIAL NUMBER 1 TO 20 INDICATES GENOTYPES.

linear regression and regression coefficients greater than unity (1.3762). PDM 84-145 and K 851 with high mean and unit regression coefficient had non significant deviations from regression coefficient. The remaining genotypes with significant deviation from the regression slope along with regression coefficients either greater than one (MH 309, and PDM 54) or less than one (UPM 79-4-12, PDM 84-155, ML 267, ML 26-10-3, MUG 125, LGG 403. Three genotypes LGG 410, LGG 450 and pusa 105 with low mean, regression coefficients less than one have non significant deviations.

4.2.5.9 1000 seed weight (g)

Stability parameters for this character are presented in Table 4.24 and Fig. 12. The mean 1000 seed weight ranged from 28.61 g (D12/333) to 37.75 g (k 851) among the genotype with a general mean of 33.87 g. Linear regression coefficients ranged from -0.5017 (PDM 84-155) to 1.9957 (D12/333) while, the deviations from regression coefficient ranged from -0.0761 (ML 26-10-3) to 0.9751 (LGG 403). Eight genotypes viz., LGG 407, LGG 410, PDM 84-155, PDM 84-145, LGG 450, PDM 54, Pusa 105 and K 851 recorded significantly higher 1000 seed weight over the general mean. Of these, three genotypes viz., LGG 410, LGG 450, and PDM 54 recorded regression coefficient around unity with non significant deviations. Two genotypes, PDM 84-145 and PDM 84-155

Table 4.24: Stability parameters of mungbean genotypes for 1000 seed weight (g)

S.No.	Variety	X	bi	s^2_{di}
1	MUG 125	32.31	1.2942	0.0009
2	LGG 403	32.22	1.5408	0.9751**
3	LGG 407	35.39	1.5559	-0.0140
4	LGG 410	36.00	1.0117	-0.0502
5	LGG 426	33.17	1.1339	-0.0685
6	PDM 84-145	36.81	0.8387	0.0290
7	PDM 84-155	30.36	-0.5017	-0.0033
8	D12/333	28.61	1.9957	-0.0380
9	MH 309	32.94	0.8041	-0.0520
10	ML 131	32.56	0.3757	0.0221
11	LGG 127	32.11	0.2023	0.1563**
12	PS 16	32.89	1.2343	0.2059**
13	UPM 83-10	31.56	-0.1499	0.4381**
14	LGG 450	36.06	1.0260	-0.0528
15	PDM 54	36.94	1.0359	0.1038
16	Pusa 105	36.58	1.8048	0.2087**
17	K 851	37.75	1.5969	0.2075**
18	ML 26-10-3	31.72	0.5173	-0.0761
19	ML 267	33.61	0.7604	-0.0361
20	UPM 79-4-12	31.78	1.7661	0.0065
	General mean	33.87	1.0000	
	S.E (m)	0.19	0.4554	

** Significant at 1% level of probability

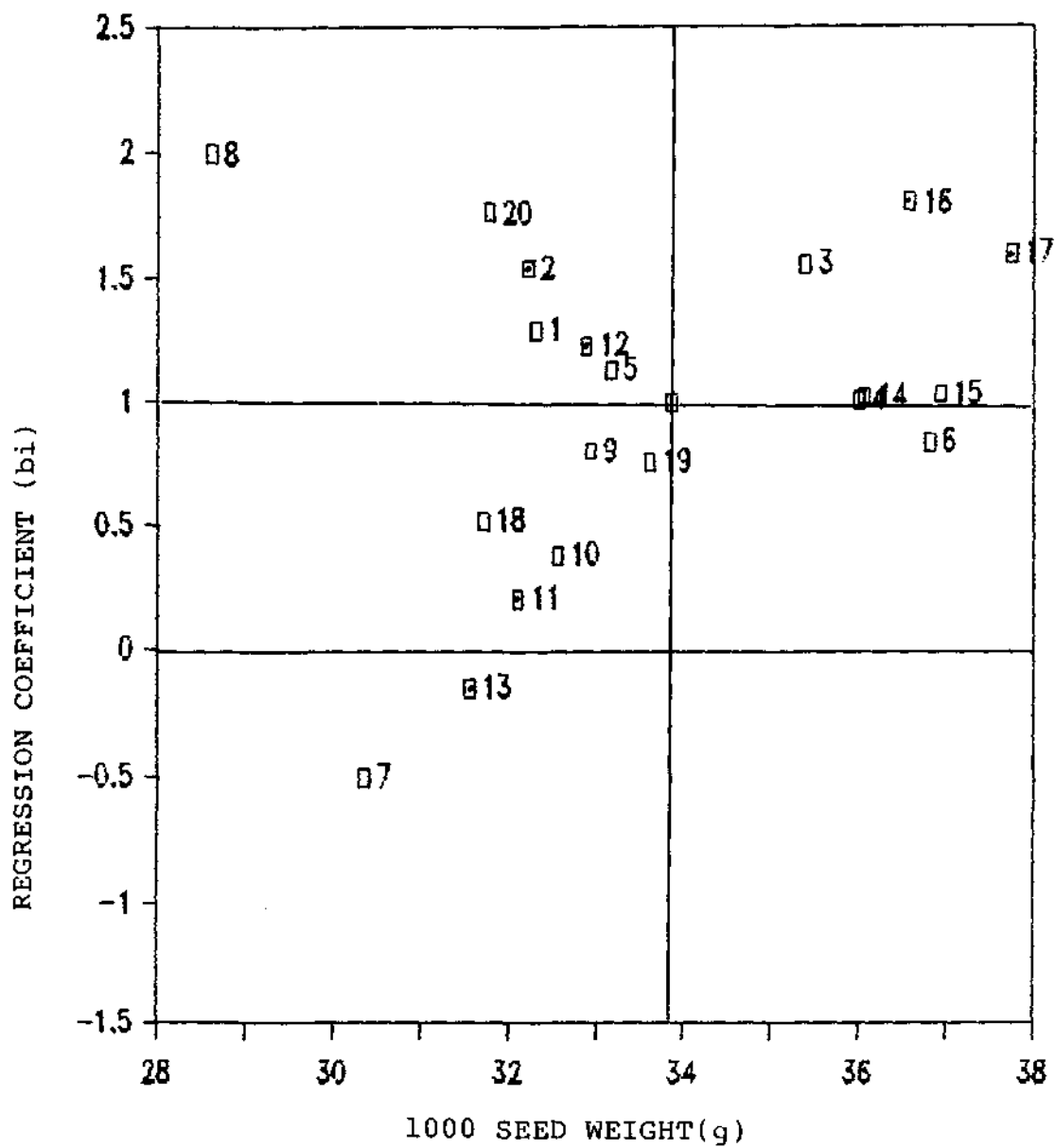


Fig.12 : PARAMETERS OF STABILITY PLOTTED AGAINST THE MEAN PERFORMANCE OF INDIVIDUAL GENOTYPE

DOT IN THE SQUARE BOX INDICATES THE SIGNIFICANT DEVIATIONS FROM REGRESSION

SERIAL NUMBER 1 TO 20 INDICATES GENOTYPES.

recorded linear regression coefficients less than unity and non significant deviations while, K 851, LGG 407 and Pusa 105 recorded regression coefficients greater than unity with significant deviations. The remaining genotypes with low mean and non significant deviations showed regression coefficients either less than unity (MH 309, ML 131, ML 26-10-3 and ML 267) or greater than unity (MUG 125, LGG 426, D12/333 and UPM 79-4-12). Two genotypes LGG 127 and UPM 83-10 with low mean and significant deviations showed linear regression coefficients below unity.

4.2.5.10 Shoot dry weight (g)

Stability parameters for this trait are presented in Table 4.25 and Fig. 13. Average shoot dry weight per plant over six environments ranged from 10.24 g (D12/333) to 20.41 g (LGG 410) with a general mean of 15.39 g. The linear regression coefficients were significant among the genotypes and ranged from 0.5643 (D12/333) to 1.4195 (LGG 410). Deviations from linear regressions ranged from -0.2533, (LGG 403) to 3.5602 (UPM 79-4-12) and were significant only in LGG 407, LGG 450, LGG 127, Pusa 105 and UPM 79-4-12. Nine genotypes viz., LGG 407, (19.91 g), LGG 410 (20.41 g), LGG 450 (19.63 g), Pusa 105 (18.47 g), PDM 54 (16.46 g), PDM 84-145 (17.13 g), LGG 426 (15.93 g), K 851 (15.89 g) and ML 267 (16.36 g) have recorded higher mean shoot

Table 4.25: Stability parameters of mungbean genotypes for shoot dry weight (g)

S.No.	Variety	$\bar{X}$	b_i	s^2_{di}
1	MUG 125	14.03	0.9630	-0.1075
2	LGG 403	15.48	0.9666	-0.2533
3	LGG 407	19.91	1.3994	0.0895
4	LGG 410	20.41	1.4195	0.5680**
5	LGG 426	15.93	1.2195	-0.0320
6	PDM 84-145	17.13	0.9993	0.0213
7	PDM 84-155	14.56	1.2598	0.0657
8	D12/333	10.24	0.5643	0.0816
9	MH 309	14.42	0.8358	0.0545
10	ML 131	15.51	1.1756	-0.0977
11	LGG 127	12.24	0.6410	1.1171**
12	PS 16	12.69	0.9374	0.2519
13	UPM 83-10	13.51	0.9485	-0.0618
14	LGG 450	19.63	0.8141	0.6923**
15	PDM 54	16.46	1.0218	0.0581
16	Pusa 105	18.47	0.6143	0.6486**
17	K 851	15.84	1.0389	0.0456
18	ML 26-10-3	12.69	0.9256	-0.0098
19	ML 267	16.36	1.0620	-0.2141
20	UPM 79-4-12	12.37	0.8244	3.5602**
	General mean	15.39	1.0000	
	S.E (m)	0.35	0.0870	

** Significant at 1% level of probability

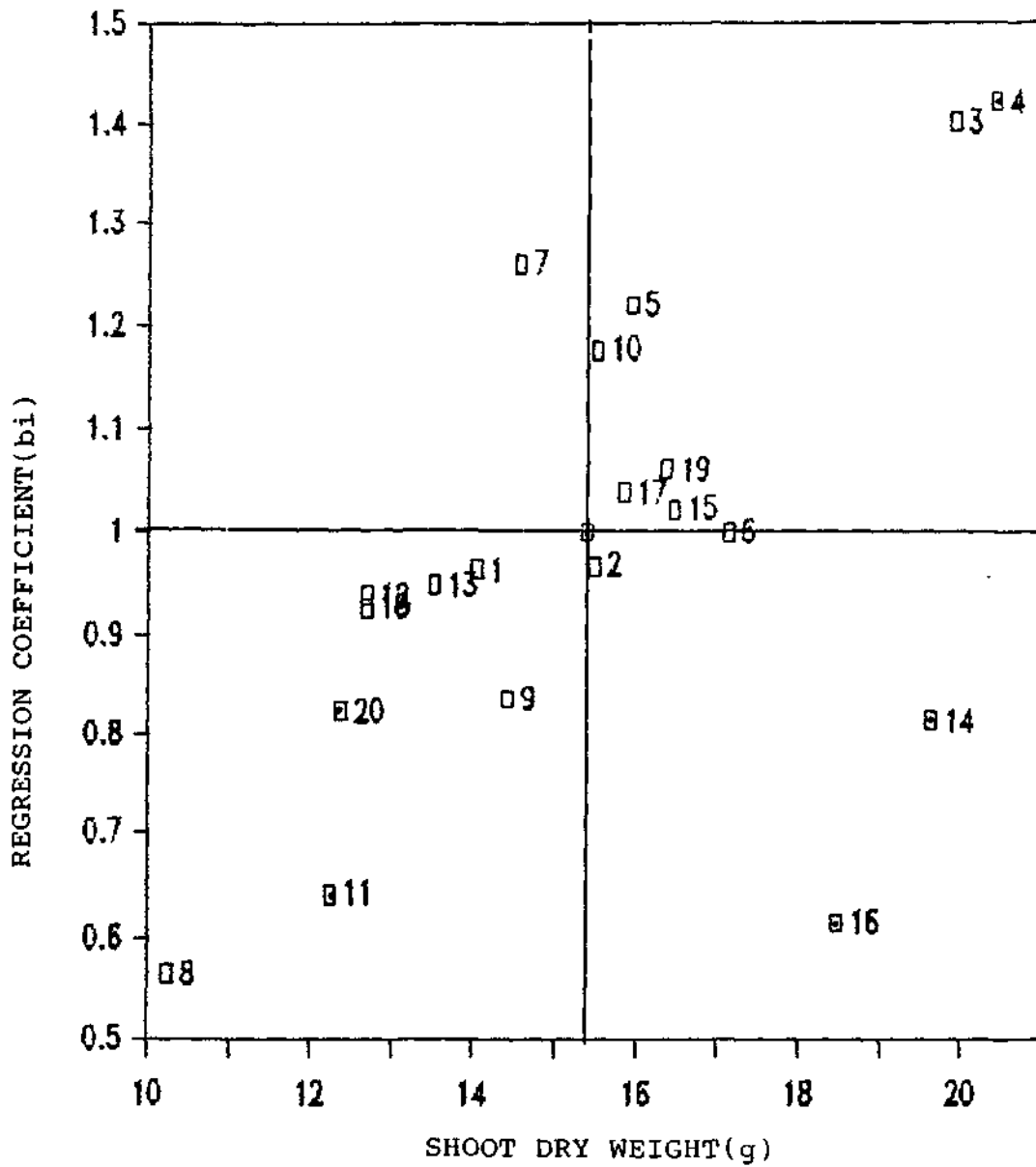


Fig.13: PARAMETERS OF STABILITY PLOTTED AGAINST THE MEAN PERFORMANCE OF INDIVIDUAL GENOTYPE

DOT IN THE SQUARE BOX INDICATES THE SIGNIFICANT DEVIATIONS FROM REGRESSION

SERIAL NUMBER 1 TO 20 INDICATES GENOTYPES.

dry weight over general mean. Of these, K 851, ML 267, PDM 54 and PDM 84-145 recorded b_i values around unity and non significant S^2_{di} values. Genotypes LGG 407 and LGG 426 recorded non significant deviations but with linear regressions greater than unity. While, LGG 450 and Pusa 105 recorded significant deviations and linear regressions less than unity. The genotype LGG 410 recorded higher shoot dry weight, regression coefficient greater than unity ($b_i=1.4195$) and significant deviations from linear regression ($S^2_{di} = 0.5680$). Two genotypes, LGG 127 and UPM 79-4-12 with low mean and regression coefficients less than unity had significant deviations from linear regressions. The remaining genotypes recorded low mean and non significant deviations with regression coefficients greater than unity (PDM 84-155 and ML 131) or less than unity (MUG 125, LGG 403, MH 309, D12/333, UPM 83-10 and ML26-10-3).

4.2.5.11 Seed protein (%)

Stability parameters for seed protein are presented in Table 4.26 and Fig. 14. Mean seed protein over six environments ranged from 23.59 (UPM 83-10) to 27.47 per cent (LGG 426). Seven genotypes viz., LGG 426 (27.49%), LGG 403 (27.47%), LGG 407 (25.70%), LGG 410 (25.18%), MUG 125 (25.08%), D12/333 (25.36%) and pusa 105 (25.66%) have recorded significantly higher seed protein over general mean. Linear regression

Table 4.26: Stability parameters of mungbean genotypes for seed protein (%)

S.No.	Variety	X	bi	S^2_{di}
1	MUG 125	25.08	0.9951	-0.1035
2	LGG 403	27.47	0.8433	-0.0992
3	LGG 407	25.70	0.9101	0.0086
4	LGG 410	25.18	0.7815	-0.0706
5	LGG 426	27.49	0.5185	0.0556
6	PDM 84-145	23.79	0.9376	0.4083**
7	PDM 84-155	24.29	1.6313	0.1070
8	D12/333	25.36	1.0275	-0.0175
9	MH 309	23.05	1.0317	0.1487
10	ML 131	24.30	1.9778	0.1402
11	LGG 127	24.83	1.4010	-0.0814
12	PS 16	24.49	1.5884	0.0930
13	UPM 83-10	23.59	1.9559	0.5567**
14	LGG 450	24.24	0.6431	-0.0839
15	PDM 54	24.55	0.9900	-0.0483
16	Pusa 105	25.66	1.0133	-0.0789
17	K 851	24.61	0.6554	0.0901
18	ML 26-10-3	24.06	0.9136	-0.1299
19	ML 267	24.60	1.1351	-0.1272
20	UPM 79-4-12	24.04	1.9699	0.8625**
	General mean	24.85	1.0000	
	S.E (m)	0.21	0.4130	

** Significant at 1% level of probability

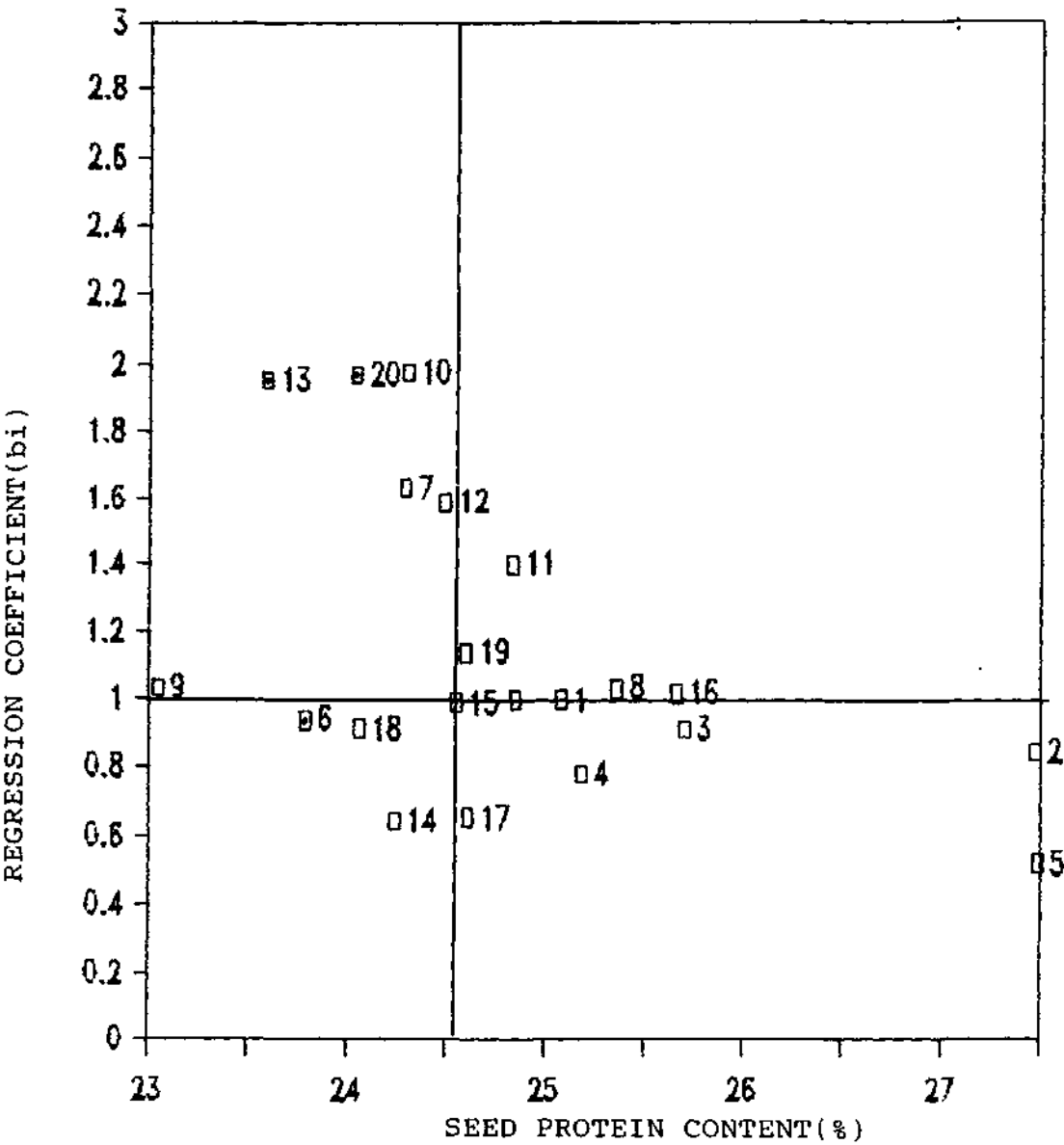


Fig.14: PARAMETERS OF STABILITY PLOTTED AGAINST THE MEAN PERFORMANCE OF INDIVIDUAL GENOTYPE

DOT IN THE SQUARE BOX INDICATES THE SIGNIFICANT DEVIATIONS FROM REGRESSION.

SERIAL NUMBER 1 TO 20 INDICATES GENOTYPES

coefficients ranged from 0.0101 (LGG 407) to 1.9699 (ML 26-10-3) while the deviations from linear regression ranged from -0.1272 (ML 267) to 0.8625 (UPM 79-4-12).

Genotypes, LGG 426, LGG 403, LGG 407 and LGG 410 with high mean and non significant deviations recorded linear regressions less than unity. Three genotypes viz., MUG 125, D12/333 and Pusa 105 showed linear regression coefficients around unity with non significant deviations from regression slopes. The genotype PDM 84-145 with low mean recorded regression coefficient less than unity. While, UPM 83-10 and UPM 79-4-12 had low mean and regression coefficients greater than one showed significant deviations from the regression slope. Whereas, PDM 54, ~~ML 131~~ and ML 267 recorded low mean value with regression coefficient around unity and non significant deviations. The genotypes PDM 84-155, LGG 127, PS 16 had ~~non~~ significant deviations from linear regression with 'bi' values greater than one, whereas MH 309, LGG 450, K 851 and ML 26-10-3 showed non significant deviations with 'bi' values less than one.

4.2.5.12 Shoot nitrogen content (%)

Shoot nitrogen content varied from 1.98 (ML 26-10-3) to 2.66 per cent (LGG 410) with a general mean of 2.29 per cent over six environments (Table 4.27 and Fig.

15). Linear regression coefficients ranged from -0.5197 (LGG 450) to 1.9641 (MH 309). The deviations from linear regression coefficient ranged from -0.0017 (UPM 74-4-12) to 0.0236 (LGG 450). Nine genotypes, LGG 426, LGG 403, PDM 84-145, K 851, ML 267, LGG 410, LGG 407, LGG 450 and Pusa 105 have recorded higher shoot nitrogen over general mean. Of these, LGG 403, LGG 407, LGG 410 and ML 267 have recorded linear regressions greater than unity ($b_i > 1$) with non significant ' S^2_{di} '. Whereas UPM 79-4-12, D12/333, LGG 127, PS 16 and PDM 54 have recorded low mean value with non significant deviations and regression coefficients greater than unity. The genotypes LGG 450, Pusa 105 and PDM 84-145 with high mean value showed significant deviations from regression slopes and linear regression coefficients less than unity ($b_i < 1$). The genotype LGG 426 showed high mean (2.55 %), regression coefficient around unity and non significant deviations from regression slope. The genotype UPM 83-10 recorded low mean with linear regression coefficient less than one and non significant deviations. MUG 125 recorded low mean value with regression coefficients around unity and significant deviations. PDM 84-155 and ML 131 recorded low mean with regression coefficients less than unity and significant deviations from regression. K 851 recorded high mean with linear regressions greater than unity and significant deviations.

Table 4.27: Stability parameters of mungbean genotypes for shoot nitrogen (%)

S.No.	Variety	$\bar{X}$	b_i	s^2_{di}
1	MUG 125	2.05	1.0771	0.0059*
2	LGG 403	2.45	1.4945	-0.0007
3	LGG 407	2.62	1.3505	-0.0013
4	LGG 410	2.66	1.2148	0.0014
5	LGG 426	2.55	1.1167	-0.0013
6	PDM 84-145	2.40	0.0564	0.0154**
7	PDM 84-155	2.31	0.5427	0.0043*
8	D12/333	2.28	1.5634	0.0018
9	MH 309	2.19	1.9641	0.0046*
10	ML 131	2.19	-0.2525	0.0104**
11	LGG 127	2.05	1.3943	0.0001
12	PS 16	2.04	1.4027	0.0020
13	UPM 83-10	2.07	1.1710	-0.0009
14	LGG 450	2.60	-0.5197	0.0236**
15	PDM 54	2.28	2.1416	0.0031
16	Pusa 105	2.49	-0.6220	0.0477**
17	K 851	2.36	1.5801	0.0107**
18	ML 26-10-3	1.98	0.9560	0.0009
19	ML 267	2.36	1.2420	0.0015
20	UPM 79-4-12	1.99	1.1271	-0.0017
	General mean	2.29	1.0000	
	S.E (m)	0.04	0.5729	

* Significant at 5% level of probability

** Significant at 1% level of probability

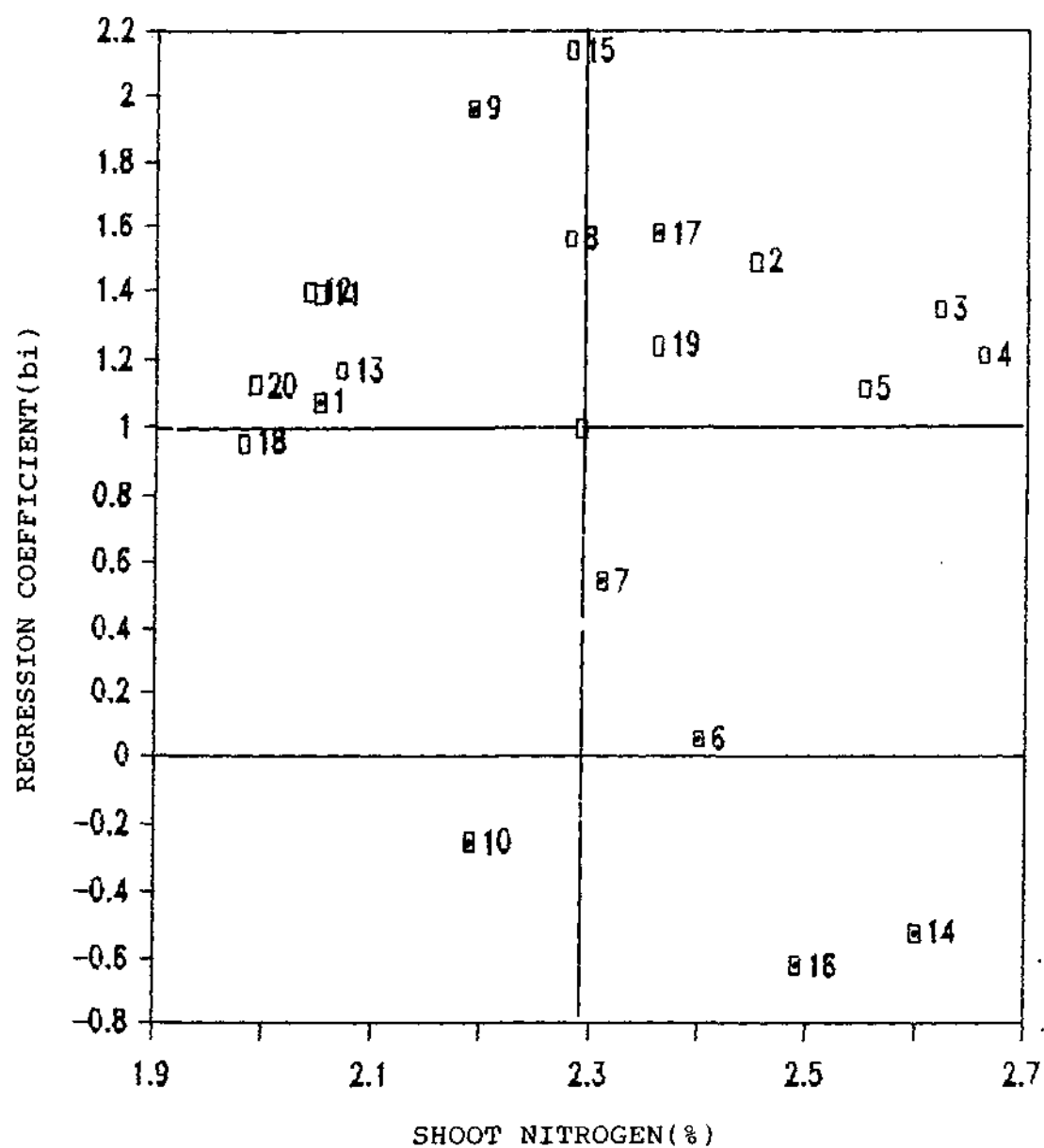


Fig.15: PARAMETERS OF STABILITY PLOTTED AGAINST THE MEAN PERFORMANCE OF INDIVIDUAL GENOTYPE

DOT IN THE SQUARE BOX INDICATES THE SIGNIFICANT DEVIATIONS FROM REGRESSION.

SERIAL NUMBERS 1 TO 20 INDICATES GENOTYPES

4.2.5.13 Grain yield

The stability parameters for grain yield are presented in table 4.28 and Fig. 16. Mean grain yield ranged from 670 (D12/333) to 1332 Kg/ha (LGG 410) with a general mean of 1006 Kg/ha over six environments. Nine genotypes LGG 410, LGG 407, LGG 450, Pusa 105, PDM 84-145, LGG 426, PDM 54, ML 267, and K 851 have recorded significantly higher grain yield over general mean. Linear regression coefficients ranged from 0.5523 (D12/333) to 1.4378 (LGG 410) while the deviations from linear regressions ranged from -287.7498 (MUG 125) to 15369.5840 (LGG 450). Among the superior genotypes, K 851, PDM 54, PDM 84-145 and ML 267 had linear regression coefficients around unity with non significant deviations from linear regression. Genotypes ML 131, LGG 410 and LGG 426 had linear regressions greater than unity while, Pusa 105 had linear regressions less than unity along with non significant deviations from regression coefficient. LGG 450 had high mean and regression coefficients less than one, and LGG 407 with high mean and regression coefficients greater than unity showed significant deviations from regression coefficient. MUG 125, LGG 403, D 12/333, MH 309, PS 16, UPM 83-10 and ML 26-10-3 have recorded low mean with regression coefficients less than unity and non

Table 4.28: Stability parameters₁ of mungbean genotypes for grain yield (kg ha⁻¹)

S.No.	Variety	X	bi	s^2_{di}
1	MUG 125	920	0.9798	-287.7498
2	LGG 403	1017	0.9440	-30.2005
3	LGG 407	1298	1.3721	738.0612*
4	LGG 410	1332	1.4378	56.4506
5	LGG 426	1087	1.1986	9163.3252**
6	PDM 84-145	1117	0.9951	524.3746
7	PDM 84-155	975	1.2886	304.6821
8	D12/333	670	0.5523	31.3646
9	MH 309	945	0.9508	207.5385
10	ML 131	1018	1.1569	-112.9096
11	LGG 127	797	0.5983	1045.5829**
12	PS 16	830	0.9829	188.3193
13	UPM 83-10	870	0.9694	-162.2934
14	LGG 450	1202	0.8958	15369.584**
15	PDM 54	1070	1.0363	230.2573
16	Pusa 105	1185	0.7093	448.8561
17	K 851	1057	1.0228	152.1633
18	ML 26-10-3	837	0.8778	220.7865
19	ML 267	1065	1.0300	-98.1794
20	UPM 79-4-12	828	0.9512	7375.2881**
	General mean	1006	1.0000	
	S.E (m)	3468	0.38	

X_j = Mean b_i = Regression coefficient

S^2_d = Deviation from regression coefficient

* Significant at 5% level of probability

** Significant at 1% level of probability

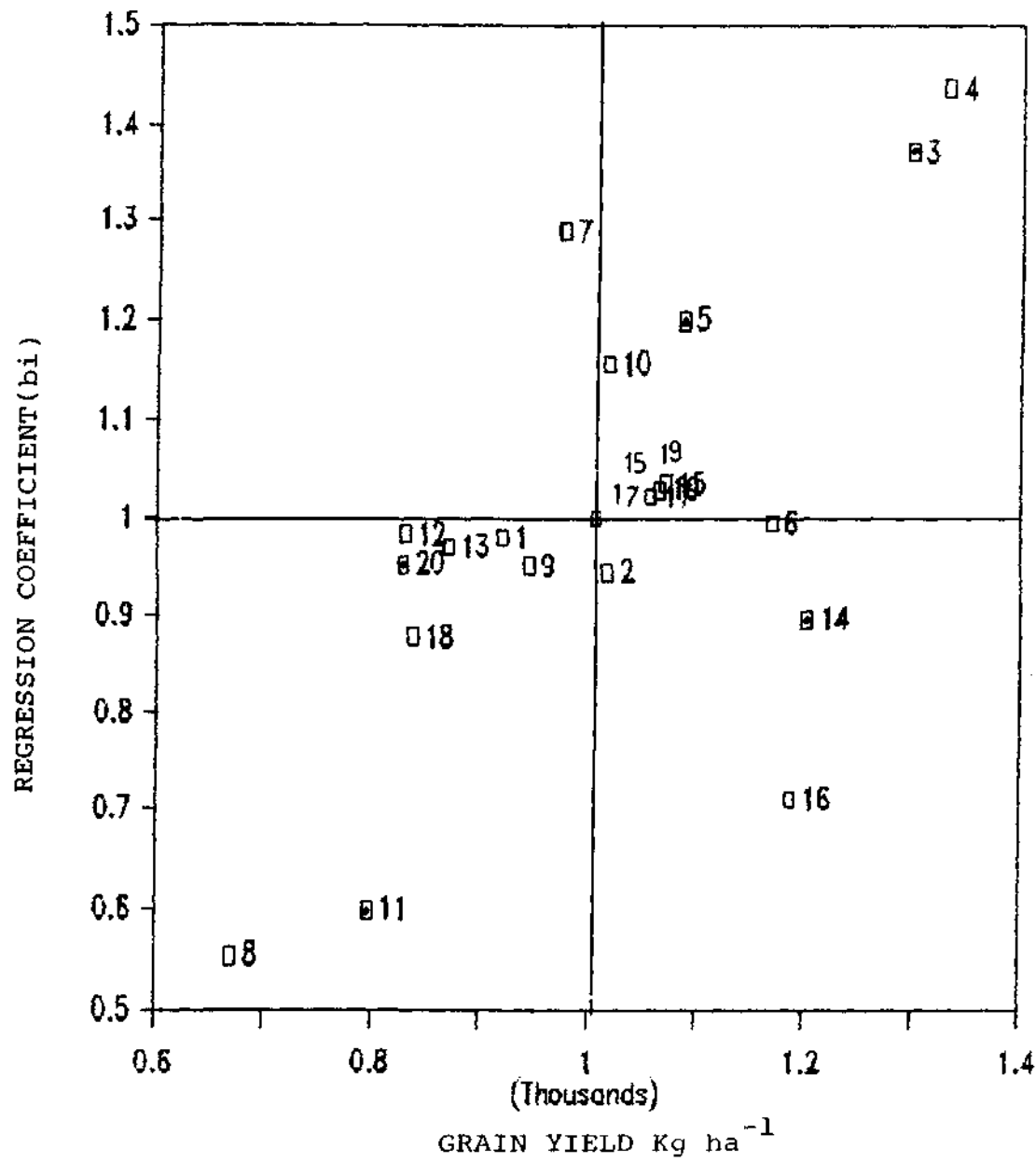


Fig.16: PARAMETERS OF STABILITY PLOTTED AGAINST THE MEAN PERFORMANCE OF INDIVIDUAL GENOTYPE

DOT IN THE SQUARE BOX INDICATES THE SIGNIFICANT DEVIATIONS FROM REGRESSION

SERIAL NUMBERS 1 TO INDICATES GENOTYPES.

significant deviations, while PDM 84-155 had recorded low mean, regression coefficients greater than unity and non significant deviations. Two genotypes LGG 127 and UPM 79-4-12 with low mean, regression coefficients less than 1.00 have recorded significant deviations from linear regression coefficient.

4.2.6 Association analysis among stability parameters

Association analysis among stability parameters indicated significant positive correlation between mean performance and linear regression coefficients for plant height, number of branches per plant, number of pods per plant, number of seeds per pod, shoot dry weight and seed yield per plot (table 4.29).

Correlation between mean performance and deviations from linear regression coefficient was positive and significant only in case of pod length. Correlation between linear regression coefficient (b_i) and non linear regression coefficient (S^2_{di}) was significantly positive in case of seed protein and significantly negative for shoot nitrogen.

4.2.7 Correlation coefficients and path analysis in different environments

Phenotypic as well as genotypic correlation coefficients calculated between yield and yield



Fig. 17. ML 267 - STABLE GENOTYPE

Table 4.29: Correlation coefficients among stability parameters for different characters

S.No.	Character	X		X		bi
		Vs	bi	Vs	S d	Vs
1	Days to 50% flowering	-0.0405		0.3815		-0.3106
2	Days to maturity	-0.3312		-0.3143		0.0617
3	Plant height (cm)	0.7865**		0.0880		0.2274
4	Number of branches per plant	0.5459*		0.3244		0.0385
5	Number of clusters per plant	0.1956		-0.3930		0.1412
6	Number of pods per plant	0.5052*		-0.2848		-0.4552
7	Pod length (cm)	-0.2388		0.6814**		0.1573
8	Seeds per pod	0.5198*		-0.3485		-0.1912
9	1000 seed weight (g)	-0.0324		-0.1012		0.0901
10	Shoot dry weight (g)	0.5283*		-0.1631		-0.3140
11	Seed protein (%)	-0.3211		-0.3954		0.5112*
12	Shoot nitrogen (%)	-0.2182		0.3119		-0.7412**
13	Grain yield (g)	0.5693**		-0.1584		-0.2205

X = Mean
S d = Deviation from regression coefficient
bi = regression coefficient
* Significant at 5% level of probability
** Significant at 1% level of probability

component traits and among themselves in each of the six environments studied are presented in the tables 4.30 to 4.35.

In general the genotypic correlations were higher than the phenotypic correlations.

Grain yield was found to be significantly positively correlated with the number of clusters per plant, number of pods per plant, 1000 seed weight, shoot dry weight and shoot nitrogen phenotypically under all the environments. Association between grain yield and plant height was positively significant in E2 and E3 only. Positive and significant correlation of grain yield with days to 50% flowering and days to maturity was recorded under E2 at phenotypic level. Grain yield showed significant and positive correlation with number of branches per plant only in E3. Grain yield was not found to be associated with pod length and seeds per pod under any of the environments. Genotypic correlations of grain yield with pod length and number of seeds per pod were higher than phenotypic correlations.

Association analysis among yield component traits revealed that days to 50% flowering had significant positive correlation with days to maturity in all the environments except in E5, with plant height it showed significantly positive association with number

Table 4.30: Phenotypic (P) and Genotypic (G) correlation coefficients between yield and yield components under E1 (Kharif, 1987)

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Days to 50% flowering	1.0000	0.6980**	0.5385**	-0.1165	0.1593	0.1509	-0.1595	-0.1879	-0.0037	0.0697	0.2420	-0.1845	0.0678
	G	1.0000	0.5555	-0.1144	0.2052	0.2468	-0.1557	-0.1881	-0.0125	0.0825	0.3055	-0.2391	0.0822
Days to maturity		1.0000	0.5110**	-0.1906	-0.0138	0.2170	-0.1130	-0.0534	-0.1716	0.0696	0.2635	-0.1821	0.0673
		1.0000	0.5312	-0.2348	-0.0074	0.3509	-0.1197	-0.0543	-0.1776	0.0741	0.3473	-0.2221	0.0722
Plant height (cm)			1.0000	0.5110**	0.3727*	0.1113	0.1728	-0.0136	0.2120	0.1878	-0.0738	-0.2117	0.1866
			1.0000	0.5312	0.3967	0.1605	0.1865	-0.0179	0.2328	0.1989	-0.1008	-0.2422	0.1987
Number of branches per plant				1.0000	0.0839	-0.0926	-0.2782	-0.3019	-0.2528	-0.2482	0.0276	-0.1272	-0.2540
Number of clusters per plant					1.0000	0.1145	-0.3496	-0.4050	-0.2701	-0.2877	0.0045	-0.2016	-0.2968
Number of pods per plant						1.0000	-0.0489	-0.0352	0.3333*	0.3957**	-0.0773	0.0328	0.3915**
Pod length (cm)							-0.0261	-0.0326	0.3944	0.4013	-0.0433	0.0129	0.3942
							-0.1749	-0.0334	0.3949**	0.7420**	0.0735	0.4603**	0.7445**
							-0.2121	-0.0985	0.6062	0.9934	0.3399	0.7770	0.9933
Seeds per pod							1.0000	0.6851**	0.2692	0.1326	-0.0188	0.2431	0.1357
							1.0000	0.7245	0.2974	0.1615	-0.0612	0.2869	0.1648
1000 seed weight (g)								1.0000	0.1822	0.1952	-0.0160	0.1715	0.2004
								1.0000	0.1852	0.1865	0.0066	0.1881	0.1912
Shoot dry weight (g)									1.0000	0.7683**	0.1755	0.5219**	0.7665**
									1.0000	0.8120	-0.2554	0.5810	0.8110
Shoot nitrogen (%)										1.0000	-0.0427	0.6794**	0.9993**
										1.0000	0.0337	0.7476	0.9998
Seed protein (%)											1.0000	0.0611	0.0297
											1.0000	0.1392	0.0480
Grain yield per plant (g)												1.0000	0.6865**
												1.0000	0.7547
													1.0000

P = Phenotypic correlation coefficients ; G = Genotypic correlation coefficients
 * = Significant at 5% level ; ** = Significant at 1% level

Table 4.31: Phenotypic (P) and Genotypic (G) correlation coefficients between yield and yield components under E2 (Rabi uplands, 1987-88)

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Days to 50% flowering	P 1.0000	0.8207**	0.3497*	0.1459	-0.0035	0.2930	-0.0414	0.1754	0.0643	0.3719**	0.2636	0.2756	0.3602*
	G 1.0000	0.9210	0.3799	0.1830	-0.0060	0.3363	-0.0386	0.2397	0.0833	0.4090	0.3124	0.3100	0.3976
Days to maturity		1.0000	0.3460*	0.1284	0.0727	0.4453**	-0.1188	0.1061	0.0509	0.4596**	0.2288	0.4127**	0.4494**
		1.0000	0.3563	0.1583	0.0745	0.4582	-0.1209	0.1224	0.0499	0.4699	0.2574	0.4372	0.4582
Plant height (cm)			1.0000	0.1434	0.1434	0.3065*	0.1730	0.4249**	0.2900	0.5034**	0.2814	0.1545	0.5127**
			1.0000	0.0655	0.1615	0.3395	0.1804	0.5026	0.3070	0.5226	0.2898	0.1669	0.5310
Number of branches per plant				1.0000	0.4982**	0.1756	-0.1200	-0.1220	-0.2305	-0.0342	0.0956	-0.0725	-0.0342
				1.0000	0.6055	0.1963	-0.1634	-0.2252	-0.2666	-0.0203	0.1016	-0.0716	-0.0282
Number of clusters per plant					1.0000	0.5789**	-0.3963**	-0.1956	-0.0030	0.3857**	0.2471	0.3820*	0.3816*
					1.0000	0.5820	-0.4090	-0.2199	0.0109	0.3780	0.3759	0.3611	0.3728
Number of pods per plant						1.0000	-0.2398	-0.1664	0.3271*	0.8089**	0.1078	0.6466**	0.8105**
						1.0000	-0.2544	-0.1732	0.3414	0.8330	0.1697	0.7128	0.8335
Pod length (cm)							1.0000	0.4477**	0.4419**	0.0425	-0.1405	0.0115	0.0522
							1.0000	0.5702	0.4465	0.0462	-0.1713	0.0202	0.0557
Seeds per pod								1.0000	0.2841	0.1939	0.1427	-0.0134	0.2068
								1.0000	0.3729	0.2639	0.1708	-0.0399	0.2810
1000 seed weight (g)									1.0000	0.6736**	-0.0866	0.4187**	0.6757**
									1.0000	0.7011	-0.1242	0.4578	0.7003
Shoot dry weight (g)										1.0000	0.0459	0.6720**	0.9986**
										1.0000	0.0968	0.7095	0.9994
Seed protein (%)											1.0000	0.4685**	0.0418
											1.0000	0.5470	0.0942
Shoot nitrogen (%)												1.0000	0.6595**
												1.0000	0.6994
Grain yield per plant (g)													1.0000
													1.0000

P = Phenotypic correlation coefficients ; G = Genotypic correlation coefficients
 * = Significant at 5% level ; ** = Significant at 1% level

Table 4.32: Phenotypic (P) and Genotypic (G) correlation coefficients between yield and yield components under E3 (Rabi Rice Fallows, 1987-88)

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Days to 50% flowering	P 1.0000	0.9489**	0.4943**	0.0045	0.3153**	0.2298	-0.1276	-0.1502	0.0824	0.2160	0.0690	0.0789	0.2196
	G 1.0000	1.0065	0.5629	-0.0207	0.3473	0.2572	-0.1351	-0.1643	0.0781	0.2308	0.0579	0.0863	0.2363
Days to maturity		1.0000	0.5138**	0.0287	0.3512**	0.2435	-0.1121	-0.1250	0.1143	0.2510	0.0874	0.1213	0.2561
		1.0000	0.5683	0.0013	0.3799	0.3080	-0.1182	-0.1496	0.1088	0.2720	0.0737	0.1358	0.2797
Plant height (cm)			1.0000	0.0396	0.5048**	0.5096**	-0.1754	-0.1445	0.2477	0.4816**	0.2353	0.3465*	0.4950**
			1.0000	0.1006	0.5370	0.5611	-0.1891	-0.1575	0.2477	0.5146	0.2498	0.3680	0.5260
Number of branches per plant				1.0000	0.3293*	0.4553**	0.2142	0.1185	-0.0188	0.3517*	0.3693*	0.5435**	0.3525*
				1.0000	0.3786	0.5608	0.2402	0.1601	-0.0442	0.4023	0.4588	0.6509	0.4072
Number of clusters per plant					1.0000	0.8087*	-0.0752	0.0102	0.1919	0.7787**	0.3017	0.7288**	0.7797**
					1.0000	0.8721	-0.0742	0.0116	0.2005	0.8054	0.4313	0.7777	0.8073
Number of pods per plant						1.0000	-0.0576	0.0344	0.2838	0.8789**	0.2143	0.7481**	0.8786**
						1.0000	-0.0600	0.0306	0.3063	0.9039	0.2592	0.7933	0.9017
Pod length (cm)							1.0000	0.6997**	0.4420**	0.1387	0.2811	0.4064**	0.1546
							1.0000	0.7205	0.4678	0.1398	0.2991	0.4200	0.1556
Seeds per pod								1.0000	0.2708	0.2414	0.1724	0.3686**	0.2436
								1.0000	0.2833	0.2466	0.1936	0.3864	0.2453
1000 seed weight (g)									1.0000	0.5524**	-0.0988	0.4841**	0.5556**
									1.0000	0.5749	-0.1076	0.5162	0.5796
Shoot dry weight (g)										1.0000	0.2061	0.8883**	0.9987**
										1.0000	0.2508	0.9109	0.9954
Seed protein (%)											1.0000	0.3661*	0.2213
											1.0000	0.4240	0.2673
Shoot nitrogen (%)												1.0000	0.8942**
												1.0000	0.9162
Grain yield per plant (g)													1.0000
													1.0000

P = Phenotypic correlation coefficients ; G = Genotypic correlation coefficients
 * = Significant at 5% level ; ** = Significant at 1% level

Table 4.33: Phenotypic (P) and Genotypic (G) correlation coefficients between yield and yield components under E4 (Kharif, 1988)

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Days to 50% flowering	P 1.0000 G 1.0000	0.1128 0.1542	0.5479** 0.5664	0.8755** 0.5975	0.1128 0.1542	0.3301* 0.4531	-0.1187 -0.1268	-0.2299 -0.2673	0.0476 0.0525	0.1563 0.2276	-0.0316 -0.0437	-0.0455 -0.0532	0.1908 0.2257
Days to maturity		1.0000 1.0000	0.4498** 0.4902	-0.0659 -0.0772	0.1633 0.2259	0.3756** 0.5490	-0.0480 -0.0772	-0.1333 -0.1522	0.0784 0.1219	0.2379 0.3508	0.0252 0.0504	-0.0054 0.0033	0.2853 0.3384
Plant height (cm)			1.0000 1.0000	0.5491** -0.5755	0.2496 0.2719	0.2514 0.3079	0.1973 0.1986	0.0713 0.0754	0.3162* 0.3277	0.2332 0.2813	-0.1584 -0.1681	0.0030 0.0087	0.2623 0.2788
Number of branches per plant				1.0000 1.0000	0.0634 0.0808	-0.0820 -0.0540	-0.3164** -0.3370	-0.3818* -0.4019	-0.2867 -0.2937	-0.1912 -0.2119	-0.0441 -0.0312	-0.1030 -0.0924	0.2183 -0.1921
Number of clusters per plant					1.0000 1.0000	0.4929* 0.4638	-0.0571 -0.0351	-0.1963 -0.1977	0.2486 0.2662	0.4346** 0.3592	0.0549 0.0397	0.1124 0.1833	0.4384** 0.4016
Number of pods per plant						1.0000 1.0000	-0.0351 -0.1424	-0.1977 -0.1494	0.2662 0.4027**	0.3592 0.8427**	0.0397 0.0785	0.1833 0.5480**	0.4016 0.8474**
Pod length (cm)							-0.1724 1.0000	-0.1724 0.5985**	0.4817 0.2899	0.9196 0.0926	0.1096 0.0233	0.7854 0.0087	0.9696 0.1013
Seeds per pod							1.0000 1.0000	0.6161 1.0000	0.3054 0.1452	0.1676 0.1397	0.0518 0.1634	0.0139 0.0456	0.1330 0.1220
1000 seed weight (g)								1.0000 1.0000	0.1502 1.0000	0.1755 0.6498**	0.1592 0.0459	0.0784 0.4882**	0.1385 0.6856**
Shoot dry weight (g)									1.0000 1.0000	0.7493 1.0000	0.0614 0.1342	0.5241 0.6379**	0.7253 0.9584**
Seed protein (%)										1.0000 1.0000	0.0994 1.0000	0.8663 0.4020*	1.0239 0.1182
Shoot nitrogen (%)											1.0000 1.0000	0.4885 1.0000	0.1304 0.6984**
Grain yield per plant (g)												1.0000 1.0000	0.8347 1.0000

P = Phenotypic correlation coefficients ; G = Genotypic correlation coefficients
 * = Significant at 5% level ; ** = Significant at 1% level

Table 4.34: Phenotypic (P) and Genotypic (G) correlation coefficients between yield and yield components under E5 (Rabi uplands, 1988-89)

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Days to 50% flowering	1.0000	0.7166**	0.4510**	0.0169	0.0527	0.1280	0.3847*	0.1896	0.1082	0.2686	-0.1035	-0.0507	0.2762
G	1.0000	0.8562	0.5220	0.0408	0.0689	0.2515	0.4324	0.1873	0.1172	0.2972	-0.1509	-0.0700	0.3055
Days to maturity		1.0000	0.6533**	0.3204*	0.2804	0.3295*	0.2438	0.0912	0.1205	0.2792	0.0000	0.0467	0.2868
Plant height (cm)			1.0000	0.3531	0.3012	0.3697	0.2706	0.0822	0.1259	0.3030	0.0401	0.0315	0.3056
Number of branches per plant				1.0000	0.4434**	0.2683	0.1935	0.1653	-0.0541	0.1182	-0.0864	-0.1611	0.1219
Number of clusters per plant					1.0000	0.2822	0.1810	0.1863	-0.0603	0.1131	-0.0810	-0.1615	0.1175
Number of pods per plant						0.2401	-0.1725	-0.2848	0.3583*	0.2521	-0.0025	0.2558	0.2620
Pod length (cm)						0.3068	-0.1999	-0.3312	0.4163	0.2807	-0.0706	0.3156	0.3001
Seeds per pod													
1000 seed weight (g)													
Shoot dry weight (g)													
Seed protein (%)													
Shoot nitrogen (%)													
Grain yield per plant (g)													

P = Phenotypic correlation coefficients ; G = Genotypic correlation coefficients
 * = Significant at 5% level ; ** = Significant at 1% level

Table 4.35: Phenotypic (P) and Genotypic (G) correlation coefficients between yield and yield components under E6 (Rabi Rice Fallows, 1988-89)

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Days to 50% flowering	P 1.0000	0.8009**	0.2801	0.1150	0.2669	0.1651	-0.2469	-0.1900	0.1478	0.1169	-0.2628	0.0624	0.0866
	G 1.0000	0.8653	0.3229	0.0967	0.2799	0.1655	-0.2584	-0.1945	0.1715	0.1206	-0.3543	0.0911	0.0909
Days to maturity		1.0000	0.5500**	0.1179	0.4568**	0.2827	-0.2315	-0.0600	0.0966	0.2194	-0.0383	0.2068	0.1562
		1.0000	0.5749	0.2209	0.4911	0.3100*	-0.2367	-0.0516	0.1145	0.2318	-0.0633	0.2781	0.1635
Plant height (cm)			1.0000	-0.0474	0.3826*	0.2368	-0.2291	-0.1245	0.0696	0.2835	0.1368	0.1433	0.2129
			1.0000	-0.1003	0.4643	0.3040	-0.2479	-0.1392	0.0418	0.3182	0.1273	0.1422	0.2628
Number of branches per plant				1.0000	0.3231*	0.1097	0.3073*	-0.0255	0.1237	0.1407	0.1143	0.3972*	0.1072
				1.0000	0.4162	0.2012	0.4403	-0.0555	0.1507	0.2092	0.1030	0.5208	0.1717
Number of clusters per plant					1.0000	0.7788**	-0.1587	-0.0346	0.2686	0.7161**	0.2933	0.6580**	0.6738**
					1.0000	0.8507	-0.1742	-0.0256	0.3079	0.7405	0.4473	0.8056	0.6881
Number of pods per plant						1.0000	-0.1630	0.0091	0.3538*	0.8185**	0.3119*	0.6951**	0.8087**
Pod length (cm)							-0.1721	0.0057	0.4032	0.8567	0.5028	0.8447	0.8466
							1.0000	0.6171**	0.4112**	0.0984	0.1766	0.2758	0.1240
Seeds per pod								0.6362	0.4339	0.0970	0.2155	0.2835	0.1268
								1.0000	0.1451	0.1085	0.1140	0.1894	0.1414
1000 seed weight (g)									1.0000	0.1070	0.1438	0.2040	0.1418
										0.6233**	0.0374	0.4790**	0.6608**
Shoot dry weight (g)										0.6567	0.0554	0.5292	0.6967
										1.0000	0.2646	0.7445**	0.9801**
Seed protein (%)											0.3626	0.8237	0.9846
											1.0000	0.4822**	0.2768
Shoot nitrogen (%)												1.0000	0.3899
													0.7575**
Grain yield per plant (g)													0.8523
													1.0000
													1.0000

P = Phenotypic correlation coefficients ; G = Genotypic correlation coefficients

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

of branches per plant only under E4, number of clusters per plant only in E3, with shoot dry weight and shoot nitrogen in E2. Significantly positive association between days to 50% flowering with number of pods per plant (E2 and E4) and number of seeds per pod (E1 and E2) was recorded in two environments only.

Days to maturity recorded significantly positive association with plant height in all the environments, with number of pods per plant in all the environments except E3 and E6, with number of branches per plant only under E5 with number of seeds per pod in E1 and with shoot nitrogen in E2. While positive and significant association between days to maturity with number of clusters per plant (E3 and E6) and shoot dry weight (E2 and E4) was observed in two environments.

Plant height showed significantly positive association with number of clusters per plant (E1, E3, E5 and E6) and number of pods per plant (E1, E2, E3 and E4) in four environments. While with 1000-seed weight (E2 and E3) in two environments. Whereas, with number of seeds per pod (E2) and shoot nitrogen (E3) only in one environment.

Number of branches per plant recorded significantly positive association with number of clusters per plant in all the environments except E1 and

E4 whereas with number of pods per plant in three environments (E3, E5 and E6). Number of branches per plant recorded significant and positive association with pod length and shoot nitrogen in two environments (E3 and E5). Significantly positive correlation of this trait with number of seeds per pod (E1), 1000 seed weight (E5), shoot dry weight and shoot nitrogen (E3) was observed only in one environment at phenotypic level.

Number of clusters per plant recorded significantly positive correlation with shoot dry weight under all the environments. Whereas with number of pods per plant in all the environments except in E1. Number of clusters per plant recorded significant positive association with number of seeds per pod (E2, E3 and E5) and 1000 seed weight (E1, E2 and E6) in three environments whereas with shoot nitrogen (E2, E3, E5 and E6) in four environments.

Number of pods per plant showed significant and positive association with shoot dry weight in all the environments. Whereas with shoot nitrogen in all the environments except in E5. Significant and positive association of pods per plant with 1000 seed weight was observed in four environments (E1, E2, E4 and E6) while with number of seeds per pod in two environments (E1 and E6).

Positive and significant correlation between pod length and number of seeds per pod was observed in all the environments. Pod length also found to be positively correlated with 1000 seed weight in four environments (E2, E3, E4 and E6) and with shoot nitrogen only in one environment (E3).

Number of seeds per pod had significant positive association with 1000 seed weight only in E2 and with seed protein and shoot nitrogen in E3 only.

Significant and positive association of 1000 seed weight with shoot dry weight and shoot nitrogen was recorded in all the environments.

The association between shoot dry weight with seed protein, shoot dry weight with shoot nitrogen, and seed protein with shoot nitrogen were found to be significantly positive under all the environments.

Significant negative association between number of clusters per plant and pod length (E2 and E5), number of branches per plant with plant height (E4), pod length and number of seeds per pod (E4) were recorded.

Path coefficient analysis: Genotypic as well as phenotypic path coefficient analysis were carried out separately for the six environments and are given in

Table 4.37: Phenotypic path coefficient analysis for grain yield under E1 (Kharif, 1987)

	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Correlation with grain yield
Days to 50% flowering	-0.0013	-0.0078	0.0071	0.0007	-0.0003	0.0016	0.0012	-0.0020	0.0002	0.0681	0.0035	-0.0031	0.0678
Days to maturity	-0.0009	-0.0112	0.0067	0.0011	0.0000	0.0024	0.0010	-0.0006	0.0020	0.0680	0.0018	-0.0031	0.0673
Plant height (cm)	-0.0007	0.0057	0.0132	0.0010	-0.0007	0.0012	-0.0015	-0.0001	0.0010	0.1835	-0.0011	-0.0035	0.1865
Number of branches per plant	0.0002	0.0021	-0.0044	-0.0060	-0.0002	-0.0003	0.0024	-0.0033	-0.0002	-0.2426	0.0004	-0.0021	-0.2940
Number of clusters per plant	-0.0002	0.0002	0.0029	-0.0005	-0.0020	0.0029	0.0004	-0.0004	0.0020	0.3867	-0.0011	0.0005	0.3915
Number of pods per plant	-0.0002	-0.0024	0.0015	0.0003	-0.0005	0.0109	0.0015	-0.0004	0.0030	0.7251	0.0011	0.0047	0.7445
Pod length (cm)	0.0002	0.0013	0.0023	0.0017	0.0001	-0.0020	-0.0087	0.0044	0.0030	0.1296	-0.0003	0.0041	0.1357
Seeds per pod	0.0002	0.0006	-0.0002	0.0009	0.0001	-0.0004	-0.0060	0.0108	0.0009	0.1907	-0.0002	0.0029	0.2004
1000 seed weight (g)	0.0000	0.0019	0.0028	0.0015	-0.0007	0.0023	-0.0023	0.0020	0.0020	0.7508	-0.0025	0.0087	0.7665
Shoot dry weight (g)	-0.0001	-0.0008	0.0015	0.0015	-0.0008	0.0081	-0.0012	0.0021	0.0010	0.9772	-0.0006	0.0114	0.9993
Seed protein (%)	-0.0003	-0.0030	-0.0010	-0.0002	0.0002	0.0008	0.0001	-0.0002	0.0001	-0.0417	0.0145	0.0010	0.0297
Shoot nitrogen (%)	0.0002	0.0020	-0.0028	0.0004	-0.0001	0.0050	-0.0021	0.0019	0.0004	0.6640	0.0009	0.0168	0.6865

Residual effect 0.0306

Table 4.38: Genotypic path coefficient analysis for grain yield under E2 (Rabi uplands, 1987-88)

	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Correlation with grain yield
Days to 50% flowering	-0.0299	-0.0095	-0.0018	-0.0008	0.0001	0.0311	-0.0001	0.0110	0.0008	0.3837	0.0030	-0.0091	0.3976
Days to maturity	-0.0276	-0.0103	-0.0017	-0.0007	-0.0011	0.0424	-0.0002	0.0056	0.0005	0.4409	0.0025	-0.0128	0.4582
Plant height (cm)	-0.0114	0.0037	-0.0047	-0.0003	-0.0024	0.0314	0.0003	0.0231	0.0031	0.4902	0.0028	-0.0049	0.5310
Number of branches per plant	-0.0055	0.0016	-0.0003	-0.0042	-0.0090	0.0182	-0.0002	-0.0104	-0.0027	-0.0191	0.0010	0.0021	-0.0285
Number of clusters per plant	0.0002	0.0008	-0.0008	-0.0025	-0.0149	0.0539	-0.0007	-0.0101	0.0001	0.3546	0.0036	-0.0114	0.3728
Number of pods per plant	-0.0101	0.0047	-0.0016	-0.0008	-0.0086	0.0926	-0.0004	-0.0080	0.0035	0.7814	0.0016	-0.0208	0.8335
Pod length (cm)	0.0012	-0.0012	-0.0008	0.0006	0.0061	-0.0236	0.0016	0.0262	0.0045	0.0434	-0.0016	-0.0006	0.0557
Seeds per pod	-0.0072	0.0013	-0.0023	0.0009	0.0033	-0.0160	0.0009	0.0460	0.0038	0.2476	0.0016	0.0012	0.2810
1000 seed weight (g)	-0.0025	0.0005	-0.0014	0.0011	-0.0002	0.0316	0.0007	0.0171	0.0102	0.6577	-0.0012	-0.0134	0.7003
Shoot dry weight (g)	-0.0122	0.0048	-0.0024	0.0001	-0.0056	0.0771	0.0001	0.0121	0.0071	0.9381	0.0009	-0.0207	0.9994
Seed protein (%)	-0.0094	0.0026	-0.0014	-0.0004	-0.0056	0.0157	-0.0003	0.0079	-0.0013	0.0927	0.0096	-0.0160	0.0942
Shoot nitrogen (%)	-0.0093	0.0045	-0.0008	0.0003	-0.0058	0.0660	0.0000	-0.0018	0.0046	0.6656	0.0053	-0.0292	0.6994

Residual path 0.0011

Table 4.39: Phenotypic path coefficient analysis for grain yield under E2 (Rabi uplands, 1987-88)

	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Correlation with grain yield
Days to 50% flowering	-0.0155	-0.0006	0.0017	-0.0004	0.0100	0.0153	-0.0004	0.0032	0.0003	0.3619	0.0023	-0.0077	0.3602
Days to maturity	-0.0127	-0.0007	0.0016	-0.0004	-0.0005	0.0233	-0.0012	0.0019	0.0003	0.4472	0.0020	-0.0115	0.4494
Plant height (cm)	-0.0054	-0.0002	0.0047	-0.0002	-0.0010	0.0161	0.0017	0.0078	-0.0011	0.4898	0.0023	-0.0043	0.5127
Number of branches per plant	-0.0023	-0.0001	0.0003	-0.0028	-0.0036	0.0092	-0.0012	-0.0022	0.0000	-0.0333	0.0008	0.0020	-0.0342
Number of clusters per plant	0.0001	-0.0001	0.0007	-0.0014	-0.0072	0.0302	-0.0039	-0.0037	0.0000	0.3753	0.0022	-0.0106	0.3816
Number of pods per plant	-0.0046	-0.0003	0.0015	-0.0005	-0.0041	0.0524	-0.0024	-0.0030	0.0016	0.7871	0.0010	-0.0180	0.8105
Pod length (cm)	0.0006	0.0001	0.0008	0.0003	0.0028	-0.0126	0.0099	0.0082	0.0022	0.0414	-0.0012	-0.0003	0.0522
Seeds per pod	-0.0027	-0.0001	0.0020	0.0003	0.0014	-0.0087	0.0044	0.0183	0.0014	0.1887	0.0013	0.0004	0.2068
1000 seed weight (g)	-0.0010	0.0000	0.0014	0.0006	0.0000	0.0171	0.0044	0.0052	0.0050	0.6554	-0.0008	-0.0117	0.6757
Shoot dry weight (g)	-0.0058	-0.0003	0.0024	0.0001	-0.0028	0.0424	0.0044	0.0035	0.0033	0.9730	0.0004	-0.0187	0.9986
Seed protein (%)	-0.0041	-0.0002	0.0012	-0.0003	-0.0018	0.0056	0.0014	0.0026	-0.0004	0.0447	0.0088	-0.0131	0.0418
Shoot nitrogen (%)	-0.0043	-0.0003	0.0007	0.0002	-0.0027	0.0339	0.0001	-0.0002	0.0021	0.6538	0.0041	-0.0279	0.6595

Residual path 0.0544

Table 4.40: Genotypic path coefficient analysis for grain yield under E3 (Rabi Rice Fallows, 1987-88)

	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Correlation with grain yield
Days to 50% flowering	0.0816	-0.0754	0.0077	0.0004	-0.0065	0.0025	-0.0011	0.0015	0.0002	0.2200	0.0003	0.0051	0.2363
Days to maturity	0.0821	-0.0749	0.0077	0.0000	-0.0071	0.0030	-0.0010	0.0014	0.0002	0.2593	0.0009	0.0081	0.2797
Plant height (cm)	0.0459	-0.0426	0.0137	-0.0019	-0.0101	0.0055	-0.0016	0.0015	0.0005	0.4305	0.0030	0.0216	0.5261
Number of branches per plant	-0.0017	-0.0001	0.0014	-0.0188	-0.0071	0.0055	0.0020	-0.0015	-0.0001	0.3835	0.0054	0.0388	0.4072
Number of clusters per plant	0.0285	-0.0285	0.0073	-0.0071	-0.0187	0.0085	-0.0005	-0.0003	0.0007	0.8816	0.0031	0.0473	0.8073
Number of pods per plant	0.0210	-0.0231	0.0076	-0.0105	-0.0163	0.0098	-0.0006	-0.0001	0.0004	0.7677	0.0091	0.0463	0.9017
Pod length (cm)	-0.0110	0.0089	-0.0026	-0.0045	0.0011	-0.0007	0.0083	-0.0067	0.0010	0.1333	0.0035	0.0250	0.1556
Seeds per pod	-0.0134	0.0112	-0.0021	-0.0030	-0.0006	0.0001	0.0060	-0.0093	0.0006	0.2390	0.0023	0.0230	0.2498
1000 seed weight (g)	0.0064	-0.0081	0.0034	0.0008	-0.0057	0.0020	0.0039	-0.0026	0.0022	0.5480	-0.0013	0.0308	0.5796
Shoot dry weight (g)	0.0188	-0.0204	0.0070	-0.0076	-0.0169	0.0079	0.0012	-0.0023	0.0013	0.9532	0.0030	0.0543	0.9994
Seed protein (%)	0.0023	-0.0055	0.0034	-0.0086	-0.0049	0.0042	0.0025	-0.0018	-0.0002	0.2391	0.0119	0.0253	0.2675
Shoot nitrogen (%)	0.0073	-0.0102	0.0049	-0.0122	-0.0149	0.0076	0.0039	-0.0036	0.0011	0.8683	0.0050	0.0596	0.9162

Table 4.42: Genotypic path coefficient analysis for grain yield under E4 (Kharif, 1988)

	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Correlation with grain yield
Days to 50% flowering	-3.6125	2.2359	0.3320	0.0121	-0.1234	1.0990	-0.0345	0.1455	0.0909	0.1003	0.2257	0.2196
Days to maturity	-3.6034	2.2416	0.2874	0.0072	-0.1809	1.3317	-0.0210	0.0829	0.0247	-0.0063	0.3384	0.2561
Plant height (cm)	-2.0461	1.0989	0.5862	0.0535	-0.2176	0.7468	0.0541	-0.0411	0.0648	-0.0163	0.2788	0.4950
Number of branches per plant	0.4709	-0.1731	-0.3374	-0.0929	-0.0647	-0.1320	-0.0918	0.2188	-0.0580	0.1744	-0.1921	0.3529
Number of clusters per plant	-0.5569	0.5064	0.1594	-0.0075	-0.8006	1.1250	0.0096	0.1076	0.0526	-0.3458	0.4016	0.7747
Number of pods per plant	-1.6368	1.2307	0.1805	0.0051	-0.3713	2.4255	-0.0451	0.0939	0.0952	-1.4817	0.9393	0.8784
Pod length (cm)	0.4579	-0.1730	0.1164	0.0313	0.0281	-0.4017	0.2723	-0.3355	0.0604	-0.0261	0.1330	0.1546
Seeds per pod	0.9655	-0.3412	0.0442	0.0373	0.1583	-0.4182	0.1678	-0.5446	0.0297	-0.1478	0.1385	0.2436
1000 seed weight (g)	-0.1896	0.2732	0.1921	0.0273	-0.2131	1.1685	0.0832	-0.0818	0.1976	-0.9887	0.1293	0.5556
Shoot dry weight (g)	-0.8224	0.7864	0.1649	0.0197	-0.2876	2.2304	0.0456	-0.0956	0.1481	-1.6342	1.0239	0.9987
Seed protein (%)	0.1569	0.1129	-0.0986	0.0029	-0.0317	0.2659	0.0141	-0.0922	-0.0121	-0.9215	0.1304	0.2215
Shoot nitrogen (%)	0.1921	0.0074	0.0051	0.0086	-0.1467	1.9051	0.0038	-0.0427	0.1036	-1.8865	0.8347	0.8944

Residual path 0.0002

Table 4.43: Phenotypic path coefficient analysis for grain yield under E4 (Kharif, 1988)

	Days to 50% flowering	Days to 50% flo-maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Correlation with grain yield
Days to 50% flowering	-0.0161	0.1145	-0.0127	0.0013	0.0077	0.0609	-0.0005	-0.0170	0.0059	0.0840	0.0023	-0.0095	0.1908
Days to maturity	-0.0405	0.1303	-0.0104	0.0007	0.0712	0.0694	-0.0002	-0.0098	0.0097	0.1279	-0.0018	-0.0011	0.2853
Plant height (cm)	-0.0253	0.0586	-0.0232	0.0060	0.0171	0.0464	0.0008	0.0053	0.0391	0.1254	0.0113	0.0006	0.2623
Number of branches per plant	0.0054	-0.0086	0.0127	-0.0109	0.0043	-0.0151	-0.0013	-0.0282	-0.0355	-0.1028	0.0032	-0.0215	-0.1983
Number of clusters per plant	-0.0052	0.0213	-0.0058	-0.0007	0.0685	0.0910	-0.0002	-0.0145	0.0308	0.2337	-0.0039	0.0235	0.4384
Number of pods per plant	-0.0152	0.0489	-0.0058	0.0009	0.0337	0.1846	-0.0006	-0.0110	0.0499	0.4531	-0.0056	0.1145	0.8474
Pod length (cm)	0.0053	-0.0063	-0.0046	0.0034	-0.0039	-0.0263	0.0041	0.0442	0.0359	0.0498	-0.0024	0.0018	0.1013
Seeds per pod	0.0106	-0.0174	-0.0017	0.0042	-0.0134	-0.0276	0.0025	0.0739	0.0180	0.0751	-0.0117	0.0095	0.1220
1000 seed weight (g)	-0.0022	0.0102	-0.0073	0.0031	0.0170	0.0744	0.0012	0.0107	0.1238	0.3494	0.0033	0.1020	0.6856
Shoot dry weight (g)	-0.0072	0.0310	-0.0054	0.0021	0.0298	0.1556	0.0004	0.0103	0.0805	0.5377	-0.0096	0.1333	0.9584
Seed protein (%)	0.0015	0.0033	0.0037	0.0005	0.0038	0.0145	0.0001	0.0121	-0.0057	0.0722	-0.0716	0.0840	0.1182
Shoot nitrogen (%)	0.0021	-0.0007	-0.0001	0.0011	0.0077	0.1012	0.0000	0.0034	0.0604	0.3430	-0.0288	0.2090	0.6984
Residual path 0.2048													

Table 4.44: Genotypic path coefficient analysis for grain yield under E5 (Rabi uplands, 1988-89)

	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Correlation with grain yield
Days to 50% flowering	0.1902	-0.1204	0.1795	-0.0058	-0.0094	-0.1190	-0.1312	-0.0206	0.0108	0.3447	0.0215	-0.0345	0.3055
Days to maturity	0.1629	-0.1406	0.2439	-0.0220	-0.0412	-0.1150	-0.0821	-0.0090	0.0117	0.3514	-0.0057	0.0155	0.3096
Plant height (cm)	0.0993	-0.0997	0.3439	-0.0098	-0.0613	-0.1336	-0.0549	-0.0205	-0.0056	0.1311	0.0115	-0.0830	0.1175
Number of branches per plant	0.0078	-0.3001	0.0237	-0.1429	-0.0483	-0.1452	0.0607	0.0364	0.0386	0.3255	0.0101	0.1555	0.3001
Number of clusters per plant	0.0131	-0.0423	0.1539	-0.0504	-0.1369	-0.3717	0.1245	0.0498	0.0245	0.6502	-0.0197	0.1567	0.5517
Number of pods per plant	0.0478	-0.0520	0.0971	-0.0438	-0.1075	-0.4733	0.0099	0.0251	0.0456	1.0613	-0.0340	0.3350	0.9113
Pod length (cm)	0.0823	-0.0380	0.0623	0.0286	0.0562	0.0155	-0.3034	-0.0911	0.0277	0.2831	-0.0025	0.1316	0.2522
Seeds per pod	0.0356	-0.0116	0.0641	0.0473	0.0621	0.1079	-0.2515	-0.1099	0.0276	0.0848	0.0182	0.0044	0.0790
1000 seed weight (g)	0.0223	-0.0177	-0.0207	-0.0596	-0.0362	-0.2333	-0.0909	-0.0327	0.0926	0.8572	0.0066	0.2569	0.7445
Shoot dry weight (g)	0.0565	-0.0426	0.0389	-0.0401	-0.0768	-0.4331	-0.0741	-0.0080	0.0684	1.1597	-0.0145	0.3651	0.9995
Seed protein (%)	-0.0287	-0.0056	-0.0278	0.0101	-0.0189	-0.1128	-0.0053	0.0140	-0.0043	0.1181	-0.1425	0.3037	0.1000
Shoot nitrogen (%)	-0.0133	-0.0044	-0.0579	-0.0451	-0.0435	-0.3217	-0.0810	-0.0010	0.0483	0.8592	-0.0878	0.4928	0.7444

Residual path 0.0001

Table 4.45: Phenotypic path coefficient analysis for grain yield under E5 (Rabi uplands, 1988-89)

	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Correlation with grain yield
Days to 50% flowering	0.0120	-0.0026	0.0131	0.0001	-0.0021	0.0027	-0.0068	-0.0013	0.0021	0.2595	0.0017	-0.0021	0.2762
Days to maturity	0.0086	-0.0036	0.0189	0.0005	-0.0110	0.0044	-0.0043	-0.0006	0.0023	0.2697	0.0000	0.0019	0.2868
Plant height (cm)	0.0054	-0.0024	0.0290	0.0002	-0.0174	0.0036	-0.0034	-0.0011	-0.0010	0.1142	0.0014	-0.0066	0.1219
Number of branches per plant	0.0002	-0.0004	0.0019	-0.0032	-0.0125	0.0037	0.0030	0.0019	0.0069	0.2435	0.0000	0.0105	0.2620
Number of clusters per plant	0.0006	-0.0010	0.0128	0.0012	-0.0391	0.0101	0.0069	0.0030	0.0049	0.5414	-0.0011	0.0119	0.5517
Number of pods per plant	0.0024	0.0012	0.0078	0.0009	-0.0294	0.0135	0.0007	0.0015	0.0086	0.8379	-0.0015	0.0228	0.8640
Pod length (cm)	0.0046	-0.0009	0.0056	-0.0006	0.0154	-0.0005	-0.0176	-0.0053	0.0055	0.2275	-0.0004	0.0102	0.2434
Seeds per pod	0.0023	-0.0003	0.0048	-0.0011	0.0172	-0.0031	-0.0138	-0.0068	0.0054	0.0639	0.0019	0.0005	0.0709
1000 seed weight (g)	0.0013	-0.0004	-0.0016	0.0013	-0.0101	0.0061	-0.0051	-0.0019	0.0192	0.7009	0.0008	0.0202	0.7308
Shoot dry weight (g)	0.0032	-0.0010	0.0034	0.0009	-0.0219	0.0117	-0.0042	-0.0004	0.0139	0.9661	-0.0009	0.0282	0.9990
Seed protein (%)	-0.0012	0.0000	-0.0025	0.0000	-0.0025	0.0012	-0.0005	0.0008	-0.0009	0.0502	-0.0167	0.0194	0.0473
Shoot nitrogen (%)	-0.0006	-0.0002	-0.0047	0.0009	-0.0113	0.0074	-0.0044	-0.0001	0.0094	0.6606	-0.0079	0.0412	0.6906

Residual path 0.0330

Table 4.46: Genotypic path coefficient analysis for grain yield under E6 (Rabi Rice Fallows, 1988-89)

	Days to 50% flo- wering	Days to Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Correlation with grain yield	
Days to 50% flowering	-0.0092	-0.0894	0.0176	-0.0343	-0.0215	-0.0347	-0.0115	0.0252	-0.0086	0.0779	0.0916	0.0877	0.0909
Days to maturity	-0.0080	-0.1033	0.0313	-0.0783	-0.0376	-0.0650	-0.0105	0.0067	-0.0058	0.1497	0.0164	0.2679	0.1635
Plant height (cm)	-0.0030	-0.0594	0.0545	0.0355	-0.0356	-0.0637	-0.0110	0.0180	-0.0021	0.2055	-0.0329	0.1370	0.2628
Number of branches per plant	-0.0009	-0.0228	-0.0055	-0.3543	-0.0319	-0.0422	0.0196	0.0072	-0.0076	0.1351	-0.0266	0.5017	0.1717
Number of clusters per plant	-0.0026	-0.0507	0.0253	-0.1475	-0.0767	-0.1785	-0.0077	0.0033	-0.0155	0.4782	-0.1157	0.7760	0.6881
Number of pods per plant	-0.0015	-0.0320	0.0166	-0.0713	-0.0652	-0.2096	-0.0076	0.0007	-0.0203	0.5533	-0.1301	0.8137	0.8466
Pod length (cm)	0.0024	0.0245	-0.0135	-0.1560	0.0134	0.0361	0.0444	-0.0825	-0.0219	0.0626	-0.0557	0.2730	0.1268
Seeds per pod	0.0018	0.0053	-0.0076	0.0197	0.0020	0.0012	0.0283	-0.1296	-0.0075	0.0891	-0.0372	0.1965	0.1418
1000 seed weight (g)	-0.0016	-0.0118	0.0023	-0.0534	-0.0236	-0.0845	0.0193	-0.0193	-0.0504	0.4241	-0.0143	0.5097	0.6964
Shoot dry weight (g)	-0.0011	-0.0239	0.0173	-0.0741	-0.0568	-0.1796	0.0043	-0.0139	-0.0331	0.8458	-0.0938	0.7934	0.9846
Seed protein (%)	0.0033	0.0065	0.0069	-0.0365	-0.0343	-0.1054	0.0096	-0.0186	-0.0028	0.2342	-0.2587	0.5855	0.3897
Shoot nitrogen (%)	-0.0008	-0.0287	0.0077	-0.1845	-0.0618	-0.1770	0.0126	-0.0264	-0.0267	0.5319	-0.1572	0.9633	0.8523

Table 4.47: Phenotypic path coefficient analysis for grain yield under E6 (Rabi Rice Fallows, 1988-89)

	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Correlation with grain yield	
Days to 50% flowering	0.0569	-0.0838	-0.0074	-0.0050	0.0011	0.0038	0.0155	-0.0100	0.0153	0.0992	-0.0050	0.0059	0.0866
Days to maturity	0.0456	-0.1046	-0.0145	-0.0051	0.0019	0.0065	0.0145	-0.0032	0.0100	0.1862	-0.0007	0.0196	0.1562
Plant height (cm)	0.0159	-0.0576	-0.0263	0.0021	0.0016	0.0055	0.0144	-0.0066	0.0072	0.2405	0.0026	0.0136	0.2129
Number of branches per plant	0.0065	-0.0123	0.0012	-0.0435	0.0014	0.0025	-0.0193	-0.0014	0.0128	0.1193	0.0022	0.0377	0.1072
Number of clusters per plant	0.0152	-0.0478	-0.0101	-0.0141	0.0042	0.0179	0.0100	-0.0018	0.0278	0.6074	0.0055	0.0624	0.6768
Number of pods per plant	0.0094	-0.0296	-0.0062	-0.0048	0.0033	0.0230	0.0102	0.0005	0.0367	0.6943	0.0059	0.6590	0.8087
Pod length (cm)	-0.0141	0.0242	0.0060	-0.0134	-0.0007	-0.0038	-0.0628	0.0327	0.0426	0.0835	0.0033	0.0262	0.1240
Seeds per pod	-0.0108	0.0063	0.0033	0.0011	-0.0001	0.0002	-0.0387	0.0530	0.0150	0.0921	0.0022	0.0180	0.1414
1000 seed weight (g)	0.0084	-0.0101	-0.0018	-0.0054	0.0011	0.0081	-0.0258	0.0077	0.1037	0.5287	0.0007	0.0154	0.6608
Shoot dry weight (g)	0.0067	-0.0230	-0.0075	-0.0061	0.0030	0.0189	-0.0062	0.0057	0.0646	0.8483	0.0050	0.0706	0.9801
Seed protein (%)	-0.0150	0.0040	-0.0036	-0.0050	0.0012	0.0072	-0.0111	0.0060	0.0039	0.2244	0.0189	0.0457	0.2768
Shoot nitrogen (%)	0.0036	-0.0216	-0.0038	-0.0173	0.0028	0.0160	-0.0173	0.0100	0.0496	0.6315	0.0091	0.0949	0.7575

Residual path 0.1533

Tables 4.36 to 4.47. The direct and indirect effects of yield components on yield are described below.

Shoot dry weight was found to have maximum direct positive effect on grain yield under all the environments studied except the genotypic paths under E4, where the number of pods per plant exerted high positive direct effect on yield. Pods per plant also exerted direct positive effect on grain yield to a certain extent under all the environments. While shoot nitrogen had showed direct effect on grain yield except in E2 and E4. Number of seeds per pod showed positive direct effect on grain yield only at phenotypic paths under three environments viz., E4, E5 and E6.

Number of branches per plant showed negative direct effect on yield in all the environments. Days to 50% flowering, number of seeds per pod and shoot nitrogen showed negative direct effect in the genotypic paths under E4.

Number of pods per plant, 1000 seed weight and shoot nitrogen exerted positive indirect effects through shoot dry weight both at genotypic and phenotypic level under all the environments except the genotypic paths in E4.

Experiment No.3**4.3 COMBINING ABILITY STUDIES**

Twenty cross combinations were made in a line x tester design utilizing four lines viz., Pusa 105, ML 267, K 851 and DL2/333 and five testers viz., PDM 54, MH 309, LGG 410, LGG 450 and UPM 79-4-12 during kharif 1987. A part of the crossed seed of each cross was used to raise F_1 generation during rabi 1987-88 to advance the material. The F_1 and F_2 generations of the 20 crosses along with the parents, were studied during kharif 1988, to study the gene actions governing the inheritance of the yield and yield component traits of Mungbean through combining ability analysis.

Data were collected on 1) days to 50 % flowering, 2) days to maturity, 3) plant height (cm), 4) number of branches per plant, 5) number of clusters per plant, 6) number of pods per plant, 7) pod length (cm), 8) number of seeds per pod, 9) 1000 seed weight (g), 10) shoot dry weight at harvest (g), 11) seed protein (%), 12) shoot nitrogen at flowering (%) and 13) grain yield per plant (g).

Heterosis was calculated over mid parent and better parent is furnished in Table 4.51. Inbreeding depression/vigour at F_2 generation was calculated as per procedures developed by Singh and Singh (1981) and is

presented in Table 4.52). Combining ability analysis for the crosses derived in the line x tester design was done following Kempthorne (1957) model. Estimates of variances due to general combining ability (gca) and specific combining ability (sca), 'gca' for parents and 'sca' for crosses both in F_1 and F_2 generations are presented in Table 4.53 and 4.58.

The inbreeding depression was not significant for any trait studied in any of the 20 F_2 populations. Correlation coefficients and character contributions through path coefficient analysis have been worked out between yield and yield components and among the yield components for parents, F_1 's and F_2 's separately and are presented in Tables 4.59 to 4.67. The results are described in detail hereunder :

4.3.1 Mean performance and heterosis

Analysis of variance revealed significant differences among the parents and crosses for all the characters studied (Appendix XXVI and XXVII) both in F_1 and F_2 generations. Significant differences were also observed due to parents verses crosses for all the characters except for plant height in F_1 generation and for seed protein in F_2 generation.

Mean performance of parents and crosses at F_1 and F_2 generations are presented in Tables 4.48 to

Table 4.48: Mean performance of mungbean parents for yield and yield components

Parent	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight(g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Lines													

Pusa 105	32.00	65.00	90.33	1.37	5.00	24.33	7.17	10.80	36.33	19.80	25.45	2.53	8.37
ML 267	30.00	62.00	64.00	1.13	5.47	25.67	7.13	9.87	34.00	17.23	24.57	2.53	7.40
K 851	30.00	61.00	78.67	1.00	5.07	19.00	7.80	12.47	38.00	20.00	24.62	2.43	8.22
D12/333	29.00	60.00	47.00	1.40	4.33	17.33	6.90	10.20	28.83	12.67	25.03	2.37	5.22
Testers													

PDM 54	29.67	60.00	73.67	1.10	4.87	23.00	7.13	10.60	37.00	23.00	24.83	2.50	7.95
MH 309	29.33	60.00	81.67	1.27	5.00	24.00	7.20	10.70	33.17	18.27	21.63	2.33	7.30
LGG 410	35.00	67.00	86.63	1.47	5.13	30.00	7.10	10.80	36.50	23.33	24.92	2.63	9.20
LGG 450	31.00	62.00	84.00	1.53	6.00	26.67	7.17	11.00	36.10	22.33	24.37	2.63	9.00
UPM 79-4-12	34.00	66.00	79.00	1.27	5.00	20.33	7.10	9.73	32.85	13.23	24.05	2.07	5.47
General mean													
S.E.m	31.11	62.56	76.11	1.28	5.09	23.37	7.19	10.68	34.75	18.87	24.38	2.45	7.57
C.D. at 5%	0.15	0.02	0.69	0.04	0.15	1.24	0.04	0.08	0.23	0.42	0.30	0.04	0.06
C.V. (%)	0.48	0.07	2.07	0.13	0.48	3.78	0.13	0.26	0.68	1.28	0.96	0.13	0.26
	0.84	0.50	1.59	6.05	4.97	9.17	0.88	1.96	1.13	3.84	2.14	3.16	1.78

Table 4.49: Mean performance of mungbean F1 hybrids (LxT programme) for yield and yield components

Cross	Days to 50% flo- wering	Days to matu- rity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Pusa 105 x PDM 54	30.00	60.67	82.00	1.63	5.37	26.67	7.40	10.90	37.50	24.00	25.27	2.60	9.75
Pusa 105 x MH 309	29.67	61.00	86.00	1.17	5.47	26.67	7.30	10.80	36.00	22.53	24.20	2.53	9.03
Pusa 105 x LGG 410	31.67	63.67	87.67	1.40	5.60	30.33	7.37	10.97	37.50	26.97	25.43	2.72	11.27
Pusa 105 x LGG 450	30.67	62.00	86.67	1.60	5.80	28.33	7.27	11.07	37.17	25.87	25.23	2.70	10.33
Pusa 105 x UPM 79-4-12	32.00	63.67	82.67	1.33	5.13	24.00	7.30	10.60	35.17	19.77	24.77	2.43	7.75
ML 267 x PDM 54	29.33	60.00	71.00	2.20	5.27	24.67	7.27	10.60	35.50	20.47	24.77	2.67	8.23
ML 267 x MH 309	29.00	60.00	73.33	1.60	5.40	25.00	7.30	10.37	34.17	18.00	23.30	2.57	7.45
ML 267 x LGG 410	32.00	63.33	74.67	1.30	5.83	29.00	7.30	10.73	35.83	24.70	24.60	2.67	10.20
ML 267 x LGG 450	29.67	61.67	75.00	1.50	5.80	29.33	7.23	10.80	36.00	24.27	24.73	2.65	9.80
ML 267 x UPM 79-4-12	30.00	63.33	73.00	1.23	5.13	23.00	7.23	9.93	34.67	16.47	24.37	2.37	6.87
K 851 x PDM 54	29.00	59.33	75.00	1.27	5.13	23.33	7.63	11.33	38.00	22.33	24.90	2.50	9.25
K 851 x MH 309	29.00	59.67	77.67	1.23	5.27	25.00	7.57	11.07	37.83	22.80	23.80	2.47	9.35
K 851 x LGG 410	31.00	63.00	79.00	1.40	5.33	29.00	7.57	11.73	38.33	27.83	24.87	2.65	11.55
K 851 x LGG 450	29.67	60.33	81.00	1.40	5.43	29.67	7.57	12.00	37.50	27.47	24.43	2.70	11.33
K 851 x UPM 79-4-12	30.00	62.00	77.67	1.27	5.20	23.33	7.57	10.93	36.17	20.27	24.53	2.47	8.52
D12/333 x PDM 54	29.00	59.00	63.00	2.03	4.93	23.33	7.10	10.40	35.00	19.37	24.93	2.52	7.63
D12/333 x MH 309	28.67	59.33	66.33	1.40	5.00	23.67	7.20	10.33	33.67	16.53	23.17	2.42	6.63
D12/333 x LGG 410	31.33	62.67	69.00	1.63	5.20	28.33	7.10	10.73	34.50	23.23	25.47	2.67	9.53
D12/333 x LGG 450	29.33	60.33	68.67	1.60	5.67	26.00	7.07	10.80	34.50	21.00	24.80	2.58	8.52
D12/333 x UPM 79-4-12	30.67	62.67	65.00	2.07	4.87	22.33	6.97	10.00	32.83	15.23	24.83	2.42	6.27
General mean	30.08	61.38	75.72	1.51	5.30	26.65	7.32	10.80	35.89	22.46	24.62	2.56	8.95
S.E.m	0.22	0.29	0.72	0.05	0.09	0.91	0.03	0.05	0.28	0.57	0.27	0.04	0.21
C.D. at 5%	0.63	0.85	2.08	0.14	0.27	2.53	0.08	0.15	0.81	1.63	0.77	0.12	0.61
C.V. (%)	1.26	0.84	1.66	5.48	3.16	6.12	0.65	0.81	1.36	4.49	1.88	2.82	4.12

Table 4.50: Mean performance of mungbean F_2 hybrids (LxT programme) for yield and yield components

Cross	Days to 50% flowering	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Pusa 105 x PDM 54	30.33	60.67	1.63	5.33	24.67	7.37	10.67	37.00	22.17	25.10	2.62	9.43
Pusa 105 x MH 309	30.00	61.33	1.17	5.47	26.33	7.27	10.73	35.50	21.87	24.17	2.50	8.97
Pusa 105 x LGG 410	31.33	64.00	1.33	5.57	30.67	7.33	10.93	36.67	26.57	25.13	2.68	11.23
Pusa 105 x LGG 450	30.67	62.33	1.60	5.97	27.67	7.23	11.07	36.83	23.53	24.99	2.64	10.23
Pusa 105 x UPM 79-4-12	31.67	63.67	1.37	5.07	23.00	7.33	10.47	34.33	18.20	24.53	2.37	7.33
ML 267 x PDM 54	29.00	60.33	2.20	5.13	24.67	7.27	10.20	36.00	19.07	24.93	2.45	7.83
ML 267 x MH 309	29.33	60.00	1.63	5.30	24.00	7.23	10.33	34.17	18.23	23.10	2.35	7.43
ML 267 x LGG 410	31.67	63.67	1.33	5.83	27.67	7.33	10.53	35.83	24.90	24.28	2.65	10.13
ML 267 x LGG 450	30.00	62.00	1.50	5.73	28.67	7.23	10.67	35.83	24.00	24.50	2.65	9.67
ML 267 x UPM 79-4-12	30.33	63.33	1.27	4.93	22.67	7.30	9.93	33.67	15.87	24.37	2.30	6.83
K 851 x PDM 54	29.33	60.00	1.13	5.13	22.00	7.57	11.47	37.83	21.77	25.23	2.53	8.63
K 851 x MH 309	29.00	60.00	1.20	5.13	23.67	7.60	11.30	37.50	22.53	24.03	2.57	9.13
K 851 x LGG 410	31.00	63.33	1.33	5.13	27.67	7.57	11.67	38.00	27.17	25.15	2.65	11.13
K 851 x LGG 450	29.67	60.67	1.37	5.70	26.33	7.53	11.53	38.00	26.50	24.33	2.65	10.93
K 851 x UPM 79-4-12	30.00	62.00	1.20	5.07	23.00	7.53	11.07	36.33	19.90	24.40	2.37	8.13
D12/333 x PDM 54	29.33	60.00	1.93	4.93	22.00	7.17	10.40	35.00	18.07	24.93	2.53	7.53
D12/333 x MH 309	29.00	60.00	1.40	4.97	23.33	7.17	10.93	34.17	16.83	23.40	2.43	6.93
D12/333 x LGG 410	31.00	63.33	1.57	5.20	26.33	7.13	10.60	34.50	23.60	24.98	2.62	9.53
D12/333 x LGG 450	29.33	60.67	1.57	5.47	23.00	7.13	10.67	34.40	20.60	24.90	2.58	8.47
D12/333 x UPM 79-4-12	30.67	62.67	2.00	4.97	22.00	7.00	10.07	32.50	15.83	25.13	2.33	6.33
General mean	30.13	61.70	1.49	5.28	24.82	7.31	10.76	35.70	21.36	24.58	2.52	8.73
S.E.m	0.24	0.26	0.04	0.09	0.91	0.03	0.05	0.24	0.35	0.41	0.03	0.13
C.D. at 5%	0.70	0.74	0.13	0.27	1.29	0.09	0.15	0.68	1.01	1.17	0.08	0.34
C.V. (%)	1.40	0.73	5.33	3.17	6.37	0.73	0.87	1.15	2.85	2.88	2.04	2.33

Table 4.51: Estimates of heterosis in mungbean over mid parent (MP) and better parent (BP) in per cent

Cross	Days to 50% flowering		Days to maturity		Plant height (cm)		Number of branches per plant		Number of clusters per plant		Number of pods per plant		Pod length (cm)	
	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP
Pusa 105 x PDM 54	-2.69*	1.11	-2.93**	1.12	0.12	-9.22**	32.50**	18.98**	8.92*	7.40	12.72	9.67	3.50**	3.21**
Pusa 105 x MH 309	-3.23**	1.16	-2.40**	1.67*	--	-4.79**	-11.36*	-14.59**	9.40*	9.40*	10.39	9.62	1.67**	1.39**
Pusa 105 x LGG 410	-5.46**	-1.03	-3.50**	-2.05**	-0.75	-2.94*	-1.41	-4.76	10.67*	2.00	9.65	1.10	3.37**	2.79**
Pusa 105 x LGG 450	-4.16**	-1.06	-2.36**	--	-0.56	-4.05**	10.34*	4.57	--	-8.33**	11.10	6.22	1.39**	1.39**
Pusa 105 x UPM 79-4-12	-3.03**	--	0.27	-2.05**	-2.35	-8.48**	0.76	-2.92	2.60	2.60*	7.43	-1.36	2.38**	1.81**
ML 267 x PDM 54	-1.68	-3.14	-1.63*	--	2.65	-3.62**	98.20**	94.69**	1.93	-3.66	1.40	-3.89	1.96**	1.96**
ML 267 x MH 309	-2.23*	-1.13	-1.64*	--	0.22	-10.21**	33.33**	25.98	3.25	-1.28	0.68	-2.61	1.96**	1.39**
ML 267 x LGG 410	-1.54	6.67**	-1.81**	2.14**	-1.10	-13.51**	--	-11.56	0.57	-2.56	4.20	-3.33	2.67**	2.38**
ML 267 x LGG 450	-2.72*	-1.10	-0.58	-0.53	0.90	-10.71**	12.78*	-1.96	1.22	-3.33	4.43	2.47	1.12*	0.84
ML 267 x UPM 79-4-12	-6.27**	--	-1.05	2.15**	1.63	-7.59**	2.50	-3.15	-1.91	-6.21	-5.47	-10.40	1.69**	1.40**
K 851 x PDM 54	-2.78*	-2.26*	-1.95**	-1.12	-1.52	-4.66**	20.95**	15.45	3.22	1.18	11.10	1.43	2.28**	-2.18**
K 851 x MH 309	-2.23*	-1.13	-1.37	-0.55	-3.12*	-4.84**	8.85	-3.15	4.77	3.94	16.28	4.17	0.93	-2.95**
K 851 x LGG 410	-4.62**	3.33*	-1.05	3.82**	-4.24**	-8.49**	13.82*	4.76	4.50	3.89	18.37*	-3.33	1.61**	-2.95**
K 851 x LGG 450	-2.72*	-1.10	-1.90**	-1.09	-0.41	-3.57**	11.11*	-8.49	-1.81	-9.50*	21.26*	3.75	1.20*	-2.95**
K 851 x UPM 79-4-12	-6.25**	--	-0.80	1.64*	-1.16	-16.83**	12.39*	--	3.38	2.56	18.66*	14.76	1.61**	-2.95**
D12/333 x PDM 54	-1.09	--	-1.67*	-1.67*	4.43**	-14.48**	62.40**	45.00	7.17	1.23	15.72	1.43	1.28*	-0.42**
D12/333 x MH 309	-1.68	-1.14	-1.12	-1.12	3.11*	-18.78**	5.26	--	7.30	--	14.57	-1.37	2.13**	--
D12/333 x LGG 410	-2.09*	8.03**	-1.31	4.45**	3.53**	-20.07**	13.99*	10.88	9.94*	1.36	19.74*	-5.57	1.43**	--
D12/333 x LGG 450	-2.23	1.14	-1.10	0.55	4.84**	-18.25**	9.59*	4.57	9.88*	-5.50	18.18*	-2.51	0.57	-1.39**
D12/333 x UPM 79-4-12	-1.06	5.76**	-0.52	4.45**	3.17**	-17.72**	55.84**	47.86	4.51	-2.60	18.52*	-0.84	-0.43	-1.83**
Average heterosis	-3.03	0.77	-1.52	0.57	0.25	-9.35	18.89	9.12	4.33	-0.19	10.04	1.09	1.80	--

Contd..

Contd..

Cross	Number of seeds per pod		1000 seed weight (g)		Shoot dry weight (g)		Seed protein (%)		Shoot nitrogen (%)		Grain yield per plant (g)	
	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP
Pusa 105 x PDM 54	1.87**	0.92	2.29	1.35	12.15**	4.35	0.52	-0.71	3.17	2.77	19.48**	16.49**
Pusa 105 x MH 309	1.41**	--	3.60**	-0.91	18.39**	13.79**	2.80	-4.91	4.11	--	15.96**	8.48*
Pusa 105 x LGG 410	2.52**	1.57*	2.99*	2.74*	25.09**	15.60**	0.99	-0.08	5.43*	3.42	26.08**	20.32**
Pusa 105 x LGG 450	2.50**	0.64	2.65*	2.31	22.84**	15.85**	1.28	-0.86	4.65*	2.66	19.00**	14.78**
Pusa 105 x UPM 79-4-12	4.23**	-1.85**	1.71	-3.19**	19.75**	-0.15	0.08	-2.67	5.65*	-3.95	11.27**	-8.00
ML 267 x PDM 54	3.62**	--	--	-4.05**	1.79	-11.00**	0.28	-0.24	5.95*	5.53*	7.30*	3.52
ML 267 x MH 309	0.88	-3.08**	1.76	0.50	1.41	-1.48	0.87	-5.17	5.76*	1.58	1.77	1.08
ML 267 x LGG 410	3.87**	-0.64	1.65	-1.81	21.79**	0.59	-0.57	-1.28	3.49	1.52	22.89**	10.87**
ML 267 x LGG 450	3.54**	-1.82**	2.71*	-0.28	22.69**	8.69**	1.06	0.65	2.71	0.76	19.51**	8.89**
ML 267 x UPM 79-4-12	1.22	0.61	3.77**	1.97	8.14	-4.41	0.25	-0.81	3.04	-6.32*	6.84	-7.16
K 851 x PDM 54	-1.73*	-9.14**	1.33	--	3.86	-2.91	0.73	0.28	1.63	--	13.86**	11.92**
K 851 x MH 309	-4.40**	-11.23**	6.32**	-0.45	19.18**	14.00**	2.94	-3.37	3.78	1.65	20.88**	14.11**
K 851 x LGG 410	0.86	-5.93**	2.90*	0.87	28.49**	19.29**	0.40	-0.20	4.74*	0.76	32.95**	25.81**
K 851 x LGG 450	2.30**	-3.79**	1.21	-1.31	29.82**	23.02**	-0.24	-0.77	6.72**	2.66	31.74**	25.89**
K 851 x UPM 79-4-12	-1.62*	-12.35**	2.15	-4.81**	22.03**	1.35	0.82	-0.36	9.78**	1.65	21.64**	1.22
D12/333 x PDM 54	--	-1.89**	6.35**	-5.40**	8.58	-15.78**	--	-0.39	3.70	0.80	19.76**	-0.88
D12/333 x MH 309	-1.15	-3.46**	8.61**	1.51	6.85	-9.52*	-0.69	-7.43	2.98	2.10	6.71	-8.49
D12/333 x LGG 410	2.19**	-0.65	5.63**	-5.48**	29.06**	-0.43	2.00	1.76	6.50**	2.69	32.18**	3.59
D12/333 x LGG 450	1.89**	-1.82**	6.28**	-4.43**	20.08**	-5.96	0.40	-0.92	3.20	-0.77	19.83**	-5.33
D12/333 x UPM 79-4-12	0.30	-1.96**	6.49**	--	17.01**	15.12*	1.18	-0.79	9.00**	2.11	17.41**	14.63**
Average heterosis	1.12	-3.05	3.43	-1.07	17.25	4.27	0.73	-1.40	4.89	1.18	18.63	7.92

Table 4.52: Inbreeding depression in per cent in F_2 generation of '20' crosses

Cross	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Pusa 105 x PDM 54	-1.10	---	---	---	0.74	7.49	0.40	2.11	7.63	0.67	-0.77	3.28
Pusa 105 x MH 309	-1.11	-0.54	-1.16	---	---	1.27	0.41	0.65	2.93	0.12	1.18	3.21
Pusa 105 x LGG 410	1.07	-0.52	0.37	-19.82	0.54	-1.12	0.54	0.36	1.48	1.18	1.47	3.17
Pusa 105 x LGG 450	---	-0.53	---	---	-8.54	2.33	0.55	---	9.04	0.95	2.22	3.26
Pusa 105 x UPM 79-4-12	1.03	---	-1.21	-3.00	1.17	4.17	-0.41	1.23	7.94	0.97	2.47	4.54
ML 267 x PDM 54	1.12	-0.55	0.46	---	2.66	---	---	0.38	6.84	-0.64	8.24	3.22
ML 267 x MH 309	-1.14	---	2.73	-1.87	1.85	4.00	0.96	0.38	-1.28	0.86	8.56	3.67
ML 267 x LGG 410	1.03	-0.54	-0.44	-2.31	---	4.58	-0.41	0.18	-0.81	1.30	0.75	3.68
ML 267 x LGG 450	-1.11	-0.54	---	---	1.21	6.07	---	1.20	1.11	0.93	---	3.32
ML 267 x UPM 79-4-12	1.10	---	3.19	-3.25	3.89	1.43	-0.97	---	3.64	---	2.95	3.03
K 851 x PDM 54	1.10	-1.13	-1.33	11.02	---	5.70	0.77	-1.23	2.51	-1.32	-0.80	3.65
K 851 x MH 309	-1.14	-0.55	-2.14	2.44	2.66	5.32	-0.39	-2.08	1.18	-0.97	-4.05	2.67
K 851 x LGG 410	---	---	0.85	5.00	3.75	4.59	---	0.51	2.37	1.04	---	3.71
K 851 x LGG 450	---	-0.56	1.23	2.14	-4.97	4.84	0.53	3.92	3.53	0.41	1.85	3.53
K 851 x UPM 79-4-12	---	---	---	5.51	2.50	4.41	0.53	1.41	1.83	0.53	4.05	3.28
D12/333 x PDM 54	-1.14	-1.69	2.11	4.93	---	5.70	-0.99	---	6.71	---	-0.39	4.82
D12/333 x MH 309	-0.87	-1.13	-2.02	---	1.40	1.44	0.42	0.58	-1.81	-0.99	-0.41	3.29
D12/333 x LGG 410	1.05	-1.05	1.45	3.68	---	7.06	0.42	1.21	-1.59	1.92	1.87	3.31
D12/333 x LGG 450	---	-0.56	1.45	1.87	3.53	11.54	0.85	1.20	1.90	-0.40	---	3.58
D12/333 x UPM 79-4-12	---	---	0.51	3.38	-2.05	1.48	0.43	-0.70	-3.94	-1.21	3.72	3.48

4.50. Heterosis over mid parent and better parent in F_1 generation are presented in Table 4.51 and are described character wise.

4.3.1.1 Days to 50% flowering

D 12/333 (29.00) among the lines and MH 309 (29.33) among the testers were earliest to flower while, the tester LGG 410 (35.00) was late to flower. Days to 50% flowering ranged from 28.67 (D 12/333 x MH 309) to 32.0 (Pusa 105 x UPM 79-4-12) in F_1 generation while in F_2 generation it ranged from 29.0 (D12/333 x MH 309) to 31.67 (Pusa 105 x UPM 79-4-12 and ML 267 x LGG 410). Seven crosses viz., ML 267 x PDM 54, ML 267 x MH 309, K 851 x PDM 54, K 851 x MH 309, D 12/333 x PDM 54, D12/333x MH 309 and D 12/333 x LGG 450 both in F_1 and F_2 flowered significantly earlier. Heterosis for days to flower ranged from -1.06 (D 12/333x UPM 79-4-12) to -6.27 (ML 267 x UPM 79-4-12) and from -2.26 (K 851 x PDM 54) to 8.03 (D 12/333 x LGG 410) in F_1 generation over mid and better parent, respectively. Significant negative heterosis (desired direction) over better parent was observed only in K 851 x PDM 54 and over mid parent in 15 crosses. Average heterosis for days to 50% flowering was -3.03 and 0.77 over mid and better parent, respectively. Inbreeding depression in F_2 ranged from -1.3 (Pusa 105 x UPM 79-4-12) to -1.12 (ML267 x LGG410).

4.3.1.2 Days to maturity

D12/333 (60.00) among the lines and MH 309 (67.0) among the testers matured earlier. The tester, LGG 410 (67.00) was late to mature among the parents. In F_1 generation, days to maturity ranged from 59.0 (D 12/333 x PDM 54) to 63.67 days (Pusa 105 x UPM 79-4-12 and Pusa 105 x LGG 410) while in F_2 generation it ranged from 60.00 (ML 267 x MH 309, K 851 x PDM 54, K 851 x MH 309, D 12/333 x PDM 54 and D 12/333 x MH 309) to 64.0 days (Pusa 105 x LGG 410). Eight crosses viz., ML 267 x PDM 54, ML 267 x MH 309, K 851 x PDM 54, K 851 x MH 309, K 851 x LGG 450, D 12/333 x PDM 54, D 12/333 x MH 309 and D 12/333 x LGG 450 matured significantly earlier both in F_1 and F_2 generations. Heterosis over mid parent ranged from -3.50 (Pusa 105 x LGG 410) to 0.27 (Pusa 105 x UPM 79-4-12), while it ranged from -2.05 (Pusa 105 x UPM 79-4-12 and Pusa 105 x LGG 410) to 4.45 (D 12/333 x LGG 410 and D12/333 x UPM 79-4-12) over better parent. The cross Pusa 105 x LGG 410 recorded significantly negative heterosis both over mid and better parent. Average heterosis over mid and better parents was -1.52 and 0.57 respectively. Inbreeding depression in F_2 ranged from -1.04 (D12/333 x PDM 54) to -0.52 (Pusa 105 x MH 309).

4.3.1.3 Plant height (cm)

Tester LGG 410 was the tallest (86.33 cm) and the line D 12/333 was the shortest (47.00 cm) among the parents. Mean plant height of F_1 ranged from 63.0 cm (D 12/333 x PDM 54) to 87.67 cm (Pusa 105 x LGG 410) and from 61.67 cm (D 12/333 x PDM 54) to 87.0 cm (Pusa 105 x LGG 410) in F_2 generation. Nine crosses Pusa 105 x PDM 54, Pusa 105 x MH 309, Pusa 105 x LGG 410, Pusa 105 x LGG 450, Pusa 105 x UPM 79-4-12, K 851 x PDM 54, K 851 x MH 309, K 851 x LGG 410, K 851 x LGG 450, and K 851 x UPM 79-4-12 recorded significantly higher plant height both in F_1 and F_2 generations. Heterosis over mid parent ranged from -4.24 (K 851 x LGG 410) to 4.84 per cent (D 12/333 x LGG 450) and over better parent, it ranged from -2.94 (Pusa 105 x LGG 410) to -20.07 per cent (D 12/333 x LGG 410). Significant positive heterosis over mid parent for plant height was recorded only in 5 crosses viz., D 12/333 x PDM 54, D 12/333 x MH 309, D 12/333 x LGG 410, D 12/333 x LGG 450 and D 12/333 x UPM 79-4-12. Average heterosis over mid and better parents was 0.25 and -9.35 per cent respectively. Inbreeding depression at F_2 generation ranged from 0.37 (Pusa 105 x LGG 410) to 3.19 per cent (ML 267 x UPM 79-4-12).

4.3.1.4 Number of branches per plant

Average number of branches per plant ranged from 1.0 to 1.53 among the parents. The lines D 12/333 (1.37) and Pusa 105 (1.40) and testers LGG 410 (1.47) and LGG 450 (1.53) recorded more number of branches per plant. The mean number of branches per plant ranged from 1.17 (Pusa 105 x MH 309) to 2.20 (ML 267 x PDM 54) in F_1 generation, while in F_2 it ranged from 1.13 (K 851 x PDM 54) to 2.20 (ML 267 x PDM 54). Three crosses viz. ML 267 x PDM 54, D 12/333 x PDM 54 and D 12/333 x UPM 79-4-12 recorded significantly higher number of branches per plant both in F_1 and F_2 generations.

Heterosis over mid parent for the number of branches per plant ranged from -11.36 (Pusa 105 x MH 309) to 98.2 per cent (ML 267 x PDM 54) and over better parent from -14.59 (Pusa 105 x MH 309) to 94.69 per cent (ML 267 x PDM 54). Average heterosis over mid and better parent was 18.89 and 9.42 per cent respectively. Though 13 crosses recorded significantly positive heterosis over the mid parent, only 7 crosses viz., (Pusa 105 x PDM 54), (ML 267 x PDM 54), (ML 267 x MH 309), (K 851 x PDM 54), (D 12/333 x PDM 54), (D 12/333 x LGG 410), and (D12/333 x UPM 79-4-12) recorded significant positive heterosis over better parents. The inbreeding depression ranged from 1.87 (D12/333 x LGG 450) to 11.02 per cent (K 851 x PDM 54) in F_2 generation.

4.3.1.5 Number of clusters per plant

Among the parents the line ML 267 (5.47) and the tester LGG 450 (6.0) recorded more number of clusters per plant. Mean number of clusters per plant ranged from 4.87 (D 12/333 x UPM 79-4-12) to 5.80 (ML 267 x LGG 450) in F_1 generation while it ranged from 4.93 (D 12/333 x PDM 54 and ML 267 x UPM 79-4-12) to 5.97 (Pusa 105 x LGG 450) in F_2 generation. Four crosses viz., Pusa 105 x LGG 410, Pusa 105 x LGG 450, ML 267 x LGG 410 and ML 267 x LGG 450 have recorded significantly higher number of clusters per plant both in F_1 and F_2 generations, whereas, D 12/333 x LGG 450 in F_1 only and K 851 x LGG 450 in F_2 only have recorded significantly higher number of clusters per plant. Heterosis over mid and better parent ranged from -1.91 (ML 267 x UPM 79-4-12) to 10.67 per cent (Pusa 105 x LGG 410) and from -9.50 (K 851 x LGG 450) to 12.00 per cent (Pusa 105 x LGG 410) respectively. Four crosses showed significant positive heterosis over mid parent for the number of clusters per plant, but only two crosses viz., Pusa 105 x MH 309 and Pusa 105 x LGG 410 recorded significant positive heterosis over the better parent. Average heterosis was 4.33 to -0.19 per cent over mid and better parents respectively. The inbreeding depression ranged from 0.54 (Pusa 105 x LGG 410) to 3.89 per cent (ML 267 x UPM 79-4-12).

4.3.1.6 Number of pods per plant

The number of pods per plant ranged from 17.33 to 30.00 among the parents. The line ML 267 (25.67) and the tester LGG 410 (30.00) had more number of pods per plant (Table 4.48). The average number of pods per plant ranged from 22.33 (D 12/333 x UPM 79-4-12) to 30.33 (Pusa 105 x LGG 410) in F_1 generation (Table 4.49) while in F_2 it ranged from 22.0 (K 851 x PDM 54, D12/333 x PDM 54 and D 12/333 x UPM 79-4-12) to 30.67 (Pusa 105 x LGG 410) (Table 4.50). Seven crosses viz., Pusa 105 x LGG 410, Pusa 105 x LGG 450, ML 267 x LGG 410, ML 267 x LGG 450, K 851 x LGG 410, K 851 x LGG 450 and D 12/333 x LGG 450 recorded significantly higher number of pods per plant both in F_1 and F_2 generations, while Pusa 105 x MH 309 recorded significantly higher number of pods in F_2 generation only. Heterosis over mid parent, ranged from -5.47 (ML 267 x UPM 79-4-12) to 21.20 (K 851 x LGG 450) and it ranged from -10.40 (ML 267 x UPM 79-4-12) to 14.76 per cent (K 851 x UPM 79-4-12) over better parent. Six crosses viz., K 851 x LGG 410, K 851 x LGG 450, K 851 x UPM 79-4-12, D12/333 x LGG 410, D 12/333 x LGG 450 and D 12/333 x UPM 79-4-12 recorded significant positive heterosis over mid parent and none over the better parent. Average heterosis over mid and better parent was 10.4 and 1.09 per cent respectively. In F_2 generation, in breeding depression

ranged from 1.27 (Pusa 105 x MH 309) to 11.54 per cent (D 12/333 x LGG 450).

4.3.1.7 Pod length (cm)

K 851 (7.80 cm) among lines and MH 309 (7.17 cm) among testers recorded higher pod length. Mean pod length in F_1 generation ranged from 6.97 (D 12/333 x UPM 79-4-12) to 7.63 cm (K 851 x PDM 54) while it ranged from 7.00 cm (D 12/333 x UPM 79-4-12) to 7.60 cm (K 851 x MH 309) in F_2 generation. Among the crosses, K 851 x PDM 54, K 851 x MH 309, K 851 x LGG 450, and K 851 x UPM 79-4-12, have recorded significantly higher pod length both in F_1 and F_2 generations. Heterosis for the pod length ranged from 0.43 (D 12/333 x UPM 79-4-12) to 3.50 per cent (Pusa 105 x PDM 54) over the mid parent and from -2.95 (K 851 x LGG 410, K 851 x LGG 450 and K 851 x UPM 79-4-12) to 3.21 per cent (Pusa 105 x PDM 54) over the better parent. Average heterosis was 1.80 per cent over mid parent. 17 crosses recorded positive heterosis for pod length over mid parent, but only 9 crosses viz., Pusa 105 x PDM 54, Pusa 105 x MH 309, Pusa 105 x LGG 410, Pusa 105 x LGG 450, Pusa 105 x UPM 79-4-12, ML 267 x PDM 54, ML 267 x MH 309, ML 267 x LGG 410 and ML 267 x UPM 79-4-12 recorded positive and significant heterosis over better parent (Table 4.51). Inbreeding depression in F_2 generation ranged from 0.40 (Pusa 105 x PDM 54) to 0.96 per cent (ML 267 x MH 309).

4.3.1.8 Number of seeds per pod

K 851 (12.47), Pusa 105 (10.80), LGG 410 (10.80) and LGG 450 (11.0) recorded higher number of seeds per pod among the parents while D 12/333 (9.73) had fewer number of seeds per pod. Mean number of seeds per pod ranged from 9.93 (ML 267 x UPM 79-4-12) to 12.0 (K 851 x LGG 450) in F_1 generation while it ranged from 9.93 (ML 267 x UPM 79-4-12) to 11.67 (K 851 x LGG 450) at F_2 generation. Six crosses viz., Pusa 105 x LGG 410, Pusa 105 x LGG 450, K 851 x PDM 54, K 851 x MH 309, K 851 x LGG 410 and K 851 x LGG 450 have recorded significantly higher number of seeds per pod both in F_1 and F_2 , whereas two crosses K 851 x UPM 79-4-12 and D12/333 x PDM 54 also recorded significantly higher number of seeds per pod only F_2 generation. Heterosis over mid parent ranged from -4.40 (K 851 x MH 309) to 4.23 (ML 267 x PDM 54) and over better parent it ranged from -12.35 (K 851 x UPM 79-4-12) to 1.57 per cent (Pusa 105 x LGG 410). The average heterosis over mid and better parents was 1.12 and -3.05 per cent, respectively. Eleven crosses viz., Pusa 105 x PDM 54, Pusa 105 x MH 309, Pusa 105 x LGG 410, Pusa 105 x LGG 450, Pusa 105 x UPM 79-4-12, ML 267 x PDM 54, ML 267 x LGG 410, ML 267 x LGG 450, K 851 x LGG 450, D 12/333 x LGG 410 and D 12/333 x LGG 450 have recorded significant positive heterosis over better parent. Inbreeding

depression in F_2 generation ranged from 0.18 (ML 267 x LGG 410) to 3.92 per cent (K 851 x LGG 450).

4.3.1.9 1000 seed weight (g)

The average 1000 seed weight ranged from 28.33 g (D12/333) to 38.0 g (K 851) among lines (Table 4.48) while in testers it ranged from 32.89 g (UPM 79-4-12) to 37.0 g (PDM 54). The average 1000 seed weight in F_1 generation (Table 4.49) ranged from 32.83 g (D12/333 x UPM 79-4-12) to 38.33 g (K 851 x LGG 410), while, in F_2 it ranged (Table 4.50) from 32.50 (D 12/333 x UPM 79-4-12) to 38.0 g (K 851 x LGG 410 and K 851 x LGG 450). Heterosis over mid parent ranged from 1.21 (K 851 x LGG 450) to 8.61 per cent (D 12/333 x MH 309) while over better parent it ranged from -5.48 (D12/333 x LGG 410) to 2.74 per cent (Pusa 105 x LGG 410). The average heterosis over mid and better parent was 3.43 and -1.07 per cent, respectively. Twelve crosses showed significant positive heterosis over mid parent. But only Pusa 105 x LGG 410 showed significant positive heterosis over better parent. Inbreeding depression in F_2 ranged from 0.29 (D12/333 x LGG 450) to 2.89 per cent (ML 267 x UPM 79-4-12).

4.3.1.10 Shoot dry weight (g)

The testing LGG 410 recorded highest shoot dry weight among the parents (23.33 g) whereas the line

D12/333 recorded lowest shoot dry weight (13.23 g) at maturity. In F_1 generation, it ranged from 15.23 g (D12/333 x UPM 79-4-12) to 27.83 g (K 851 x LGG 410) while in F_2 generation from 15.83 g (D 12/333 x UPM 79-4-12) to 27.17 g (K 851 x LGG 410). Crosses Pusa 105 x LGG 410, Pusa 105 x LGG 450, ML 267 x LGG 410, ML 267 x LGG 450, K 851 x LGG 410, K 851 x LGG 450 and D 12/333 x LGG 410 recorded significantly higher shoot dry weight both in F_1 and F_2 generations, whereas, Pusa 105 x PDM 54 recorded significantly higher shoot dry weight only in F_1 generation. Heterosis over mid parent ranged from 1.41 (ML 267 x MH 309) to 29.82 per cent (K 851 x LGG 450) and over better parent it ranged from -15.78 (D12/333 x PDM 54) to 23.02 per cent (K 851 x LGG 450). Average heterosis over mid and better parent was 17.25 and 4.27 per cent, respectively. Eight crosses viz., Pusa 105 x MH 309, Pusa 105 x LGG 410, Pusa 105 x LGG 450, ML 267 x LGG 450, K 851 x MH 309, K 851 x LGG 410, K 851 x LGG 450 and D 12/333 x UPM 79-4-12 recorded significantly positive heterosis over better parent for shoot dry weight, though 14 crosses recorded significant positive heterosis over the mid parent. Inbreeding depression in F_2 generation ranged from 1.11 (ML 267 x LGG 450) to 9.04 per cent (Pusa 105 x LGG 450) for this trait.

4.3.1.11 Seed protein content (%)

Among the lines, Pusa 105 (25.45%) and D 12/333 (25.03%), and testers LGG 410 (24.92%) and PDM 54 (24.83%) were superior in seed protein content. Average seed protein content in F_1 ranged from 23.17 (D 12/333 x MH 309) to 25.47 per cent (D 12/333 x LGG 410) while in F_2 it ranged from 23.40 (D 12/333 x MH 309) to 25.23 per cent (ML 267 x PDM 54). Two crosses viz., Pusa 105 x LGG 410 (25.43%) and D 12/333 x LGG 410 (25.47%) have recorded significantly higher seed protein content in F_1 generation. Average heterosis over mid and better parent was 0.73 and -1.40 per cent, respectively. None of the crosses recorded significant heterosis for this trait either over mid parent or better parent.

4.3.1.12 Shoot nitrogen content (%)

Pusa 105 (2.53) and ML 267 (2.53) among the lines and LGG 410 (2.63) and LGG 450 (2.63) among the testers have recorded higher shoot nitrogen content. Mean shoot nitrogen at flowering ranged from 2.37 (ML 267 x UPM 79-4-12) to 2.72 per cent (Pusa 105 x LGG 410) in F_1 and from 2.33 (D 12/333 x UPM 79-4-12) to 2.68 per cent (Pusa 105 x LGG 410) in F_2 generation. Pusa 105 x LGG 410, Pusa 105 x LGG 450, and K 851 x LGG 450 have recorded significantly higher shoot nitrogen both in F_1 and F_2 generations, whereas, Pusa 105 x PDM 54, ML 267 x

LGG 410, ML 267 x LGG 450, K 851 x LGG 410, K 851 x LGG 450 and D 12/333 x LGG 410 have recorded significantly higher shoot nitrogen only in F_2 generation. Heterosis ranged from 1.63 (K 851 x PDM 54) to 9.78 per cent (K 851 x UPM 79-4-12) over mid parent and from -6.32 (ML 267 x UPM 79-4-12) to 5.53 per cent (ML 267 x PDM 54) over better parent. Ten crosses recorded significantly positive heterosis over mid parent while over better parent only ML 267 x PDM 54 showed significant positive heterosis. Average heterosis was 4.89 and 1.80 per cent over mid and better parents, respectively. Inbreeding depression in F_2 generation ranged from 0.75 (ML 267 x LGG 410) to 8.24 per cent (ML 267 x PDM 54).

4.3.1.13 Grain yield (g)

Among the lines K 851 (8.22 g) and Pusa 105 (8.37 g) and testers LGG 410 (9.2 g) and LGG 450 (9.0 g) have recorded higher grain yield per plant (Table 4.48). The yield per plant ranged from 6.27 g (D 12/333 x UPM 79-4-12) to 11.58 g (K 851 x LGG 410) in F_1 generation (Table 4.49) and from 6.38 (D 12/333 x UPM 79-4-12) to 11.20 g (Pusa 105 x LGG 410) in F_2 generation (Table 4.50). Seven crosses viz., Pusa 105 x PDM 54, Pusa 105 x LGG 410, Pusa 105 x LGG 450, ML 267 x LGG 410, ML 267 x LGG 450, K 851 x LGG 410 and K 851 x LGG 450 have recorded significantly higher grain yield both in F_1 and F_2 generations. Whereas two crosses,

K 851 x MH 309 and D12/333 x LGG 410 were superior for grain yield only in F_2 generation. Heterosis over mid parent ranged from 6.71 (D12/333 x MH 309) to 32.95 per cent (K 851 x LGG 410) while over better parent it ranged from -8.49 (D12/333 x MH 309) to 25.89 per cent (K 851 x LGG 450). Significant positive heterosis was recorded over mid parent in 17 crosses, but only 11 crosses viz., Pusa 105 x PDM 54, Pusa 105 x MH 309, Pusa 105 x LGG 410, Pusa 105 x LGG 450, ML 267 x LGG 410, ML 267 x LGG 450, K 851 x PDM 54, K 851 x MH 309, K 851 x LGG 410, K 851 x LGG 450 and D12/333 x UPM 79-4-12 have recorded significant positive heterosis over better parent (Table 4.51). The average heterosis over the mid parent was 18.83 and it was 7.92 per cent over the better parent for grain yield. Inbreeding depression in F_2 generation ranged from 0.31 (D12/333 x LGG 410) to 5.65 per cent (K 851 x PDM 54).

4.3.2 Combining ability analysis

Combining ability analysis of 20 crosses derived from a line x tester 4 x 5 programme indicated that the mean squares due to lines and testers differed significantly for all the characters studied both in F_1 and F_2 generations (Tables 4.53 and 4.54). Mean squares due to line x tester interactions were significant in F_1 generation for days to 50% flowering, number of branches

per plant, pod length, number of seeds per pod and grain yield per plant and in F_2 generation, interactions of line x tester were significant for plant height, number of branches per plant, pod length, number of seeds per pod, shoot dry weight, shoot nitrogen and grain yield per plant.

The mean squares due to lines were higher compared to testers for plant height, number of branches per plant, pod length, seeds per pod, 1000 seed weight both in F_1 and F_2 generations. Whereas, for other traits the variances due to testers were higher than lines.

Estimates of variance components, degree of dominance and heritability (narrow sense) are presented in Table 4.53 and 4.54 for F_1 and F_2 generations, respectively. The derived 'gca' effects for parents and 'sca' effects for crosses in F_1 and F_2 generations are presented in table 4.55 to 4.58 and are presented below characterwise.

4.3.2.1 Days to 50% flowering

Estimates of variances due to 'sca' were greater than 'gca' in F_1 generation while in F_2 the 'gca' variance was higher than 'sca' variance for this trait. The degree of dominance was found to be 0.774 in F_1 and 0.670 in F_2 generation. The heritability was

Appendix 4.53: ANOVA for combining ability (mean squares) for grain yield and its components in F₁ generation

Source of variation	Degrees of freedom	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Lines	3	3.616**	6.774**	919.351**	0.524**	0.244**	15.527**	0.624**	2.994**	35.249**	89.810**	1.068**	0.017**	14.981**
Testers	4	11.916**	30.609**	54.193**	0.323**	0.412**	68.433**	0.011**	1.217**	7.736**	124.386**	4.145**	0.139**	21.679**
Lines x testers	12	0.450**	0.230	1.947	0.168**	0.055	0.722	0.007**	0.055**	0.558	1.846	0.190	0.008	0.322**
Error	38	0.143	0.264	1.575	0.007	0.058	5.199	0.002	0.008	0.238	0.970	0.215	0.005	0.137
Estimates of variance components														
2gca		0.085	0.217	4.549	0.003	0.003	0.484	0.003	0.021	0.204	0.158	0.028	0.001	0.119
2sca		0.102	-0.110	0.124	0.054	-0.001	-1.492	0.001	0.015	0.107	0.292	-0.008	0.001	0.061
Degree of dominance		0.774	-0.513	0.116	3.000	0.517	0.707	0.517	0.617	0.512	0.355	0.217	0.707	0.391
Heritability (n.s)		40.963	62.170	84.260	8.955	9.375	15.696	66.666	63.636	54.183	64.728	20.664	25.000	66.775

** Significant at 5% level of probability

Table 4.54: Anova for combining ability (mean squares) for grain yield and its components in F₂ generation

Source of variation	Degrees of freedom	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Lines	3	3.156**	4.509**	978.358**	0.574**	0.381**	25.084**	0.259**	31.865**	63.261**	0.852**	0.023**	11.687**
Testers	4	7.858**	27.232**	48.673**	0.257**	0.872**	55.350**	0.696**	10.675**	124.864**	3.431**	0.193**	27.461**
Lines x testers	12	0.336	0.345	3.230**	0.168**	0.027	2.472	0.063**	0.328	2.245**	0.291	0.006**	0.332**
Error	38	0.178	0.203	0.734	0.006	0.048	4.685	0.009	0.169	0.369	0.500	0.003	0.043
Variance components													
σ^2_{gca}		0.059	0.184	4.773	0.002	0.007	0.429	0.019	0.209	1.035	0.022	0.001	0.184
σ^2_{sca}		0.053	0.047	0.832	0.054	-0.007	-0.738	0.180	0.053	0.625	-0.069	0.001	0.096
Degree of dominance		0.670	0.357	0.295	3.674	-0.717	-0.927	0.688	0.356	0.549	-1.252	0.707	0.510
Heritability (h ² s)		33.811	59.547	85.907	6.250	22.580	15.478	58.462	65.312	67.558	8.088	33.333	72.580

** Significant at 1% level of probability

Table 4.55: Estimates of general combining ability gca effects of parents in F1 generation

Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Lines													
Pusa 10S	0.717**	0.817**	9.283**	-0.087*	0.142*	1.350*	0.012	0.062	0.775**	1.872**	0.360*	0.032	0.626**
ML 267	-0.083	0.283	-2.317	0.053	0.185	-0.050	-0.048	-0.318**	-0.658**	-1.175**	-0.267	0.019	-0.444**
K 851	-0.350**	-0.517**	2.350**	-0.200**	-0.028	-0.183	0.265**	0.608**	1.675**	2.185**	-0.113	-0.007	1.003**
D12/333	-0.283**	-0.583**	-9.317**	0.233**	-0.168*	-1.117*	-0.228**	-0.352**	-1.792**	-2.882**	0.020	0.044**	-1.184**
S.E.	0.098	0.133	0.324	0.021	0.062	0.589	0.012	0.023	0.126	0.254	0.120	0.019	0.096
S.E. (G1-Gj)	0.138	0.188	0.458	0.030	0.088	0.833	0.017	0.032	0.178	0.360	0.169	0.026	0.135
Testers													
PDM 54	-0.750**	-1.633**	-2.967**	0.270**	-0.127	1.350**	0.035**	0.003	0.608**	-0.413	0.347**	0.007	-0.194
MH 309	-1.000**	-1.383**	0.117	-0.163**	-0.018	-0.767	0.027	-0.163**	-0.475**	-1.988**	-1.003**	-0.068*	-0.802**
LGG 410	1.417**	1.783**	1.667**	-0.080**	0.265**	3.317**	0.018	0.237**	0.650**	3.728**	0.472**	0.111**	1.635**
LGG 450	-0.250*	-0.300*	2.117**	0.012	0.298**	1.483*	-0.032*	0.362**	0.400**	2.695**	0.180	-0.094**	1.035**
UPM 79-4-12	0.563**	1.533**	-1.133**	-0.038	-0.218**	-2.683**	-0.048**	-0.438**	-1.183**	-4.022**	0.005	-0.143**	-1.673**
S.E.	0.109	0.148	0.362	0.024	0.070	0.658	0.014	0.025	0.141	0.284	0.134	0.021	0.107
S.E. (G1-Gj)	0.154	0.210	0.512	0.034	0.098	0.931	0.019	0.036	0.199	0.402	0.169	0.029	0.151

* Significant at 5% level of probability

** Significant at 1% level of probability

Table 4.56: Estimates of general combining ability (gca) effects of parents in F2 generation

Genotypes	Days to 50% flo- wering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Lines													
Pusa 105	0.667**	0.700**	9.467**	-0.067*	0.203**	1.650**	-0.008	0.012	0.863**	1.107**	0.206	0.039**	0.642**
ML 267	-0.067	0.167	-2.867**	0.200**	0.210**	0.117	-0.042**	0.428**	-0.605**	0.947**	-0.343	-0.043**	-0.422**
K 851	-0.333**	-0.500**	2.867**	-0.240**	0.043	0.283	0.245**	0.645**	1.830**	2.213**	0.427	0.028	0.818**
D12/333	-0.267*	-0.367**	-9.467**	0.267**	-0.170**	-1.483**	-0.195**	-0.228**	-1.590**	-2.373**	0.090	-0.023	-1.038**
S.E.	0.109	0.116	0.221	0.020	0.057	0.559	0.014	0.024	0.106	0.157	0.183	0.013	0.054
S.E. (G1-Gj)	0.194	0.164	0.313	0.029	0.080	0.790	0.019	0.034	0.150	0.222	0.258	0.019	0.076
Testers													
PDM 54	-0.633**	1.450**	-2.817**	0.238**	0.143*	1.483*	0.037*	-0.078	0.755**	-1.093**	0.470**	0.006	0.434**
MH 309	-0.800**	-1.367**	0.433	-0.137**	-0.060	-0.483	0.020	-0.063	-0.370*	-1.493**	0.905**	0.060	-0.660**
LGG 410	1.117**	1.883**	1.683**	-0.095**	0.232*	3.267**	-0.027	0.172**	0.547**	4.198**	0.304	0.127**	1.708**
LGG 450	-0.217*	-0.283*	1.933**	0.022	0.440**	1.850**	-0.032*	0.222**	0.563**	2.298**	0.102	0.109**	1.028**
UPM 79-4-12	0.533**	1.217**	-1.233**	-0.028	-0.268**	-2.150**	-0.023	-0.378**	-1.495**	-3.910**	0.029	-0.182**	-1.622**
S.E.	0.122	0.130	0.247	0.023	0.064	0.625	0.015	0.027	0.119	0.175	0.204	0.029	0.060
S.E. (G1-Gj)	0.172	0.184	0.350	0.032	0.090	0.884	0.022	0.038	0.168	0.248	0.289	0.038	0.065

* Significant at 5% level of probability

** Significant at 1% level of probability

Table 4.57: Estimates of specific combining ability (SCA) effects of crosses in F₁ generation

Cross	Days to 50% flo- wering	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Pusa 105 x PDM 54	-0.050	0.100	-0.033	0.063	0.817*	0.038	0.225	0.030	0.587	-0.060	-0.003	0.353*
Pusa 105 x MH 309	-0.133	0.183	0.883	-0.097*	0.633*	-0.053*	-0.192	0.097	0.695	0.223	0.005	0.293*
Pusa 105 x LGG 410	-0.550	-0.317*	0.800	0.053	0.422**	0.022	0.183	-0.137**	-0.588	-0.018	0.009	0.613**
Pusa 105 x LGG 450	0.117	0.100	-0.450	0.162**	0.350*	-0.028	0.100	0.162**	-0.655	0.073	0.009	0.283*
Pusa 105 x UPM 79-4-12	0.617	-0.067	1.200*	-0.055	-0.517**	0.002	-0.317	0.172**	-0.038	-0.218	0.020	-0.213
ML 267 x PDM 54	0.083	0.567	0.567	0.363**	0.007	-0.035	-0.342	0.110*	0.100	0.067	0.007	-0.089
ML 267 x MH 309	0.001	-0.283	-0.183	0.197**	-0.033	0.007	-0.592*	0.043	0.792*	-0.050	0.052	-0.211
ML 267 x LGG 410	0.583**	-0.117	-0.600	-0.187**	-0.117	0.015	-0.050	0.010	0.192	-0.225	-0.028	0.043
ML 267 x LGG 450	-0.083	0.300	-0.517	-0.078	0.650*	-0.002	0.367	-0.048	0.792*	0.200	-0.028	0.243*
ML 267 x UPM 79-4-12	-0.583**	0.133	0.733	-0.295**	-0.117	0.015	0.617*	-0.115*	-0.292	0.008	-0.073	0.623**
K 851 x PDM 54	0.017	0.100	-0.100	-0.317**	-0.983	0.018	-0.175	-0.083	1.393*	0.047	-0.063	-0.513*
K 851 x MH 309	0.267	0.183	-0.517	0.083	0.100	-0.040	0.742**	-0.183**	0.648	0.297	-0.022	0.222
K 851 x LGG 410	-0.150	0.350*	-0.933	0.167**	0.617*	-0.032	0.117	0.083	-0.035	-0.112	-0.018	0.615**
K 851 x LGG 450	0.183	-0.233	0.817	0.075	0.517*	0.018	-0.467	0.225**	0.635	-0.253	0.049	0.333*
K 851 x UPM 79-4-12	-0.317	-0.400*	0.733	-0.008	0.350*	0.035	-0.217	-0.042	0.148	0.022	0.053	0.021
D12/333 x PDM 54	-0.050	-0.167	-0.433	0.017	-0.050	-0.022	0.292	-0.057	0.707*	-0.053	-0.010	0.301*
D12/333 x MH 309	-0.133	-0.083	-0.183	-0.183**	-0.300	0.087*	0.042	0.043	-0.552	-0.070	-0.035	-0.291*
D12/333 x LGG 410	0.117	0.083	0.733	-0.033	0.283	-0.005	-0.250	0.043	0.432	0.355	0.036	0.221
D12/333 x LGG 450	-0.217	-0.467*	0.150	-0.158**	-0.417*	0.012	0.001	-0.015	0.768*	-0.020	-0.031	0.293*
D12/333 x UPM 79-4-12	0.283	0.333	-0.267	0.358**	0.483*	-0.072**	-0.083	-0.015	0.182	0.188	0.040	0.413**
S.E.m	0.218	0.297	0.725	0.048	0.108	0.027	0.281	0.051	0.569	0.268	0.042	0.213
S.E. (S.D-SKL)	0.309	0.419	1.025	0.068	0.112	0.039	0.398	0.072	0.804	0.379	0.059	0.302

* Significant at 5% level

** Significant at 1% level

Table 4.58: Estimates of specific combining ability (SCA) effects of crosses in F₂ generation

Cross	Days to 50% flo- wering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Pusa 105 x PDM 54	0.167	-0.283	-0.050	-0.025	-0.003	-0.317	0.033	-0.028	0.178	0.793*	-0.156	0.049	0.437**
Pusa 105 x MH 309	0.001	0.300	-0.300	-0.117*	0.047	0.350	-0.042	-0.103	-0.197	0.893*	0.286	-0.002	0.217
Pusa 105 x LGG 410	-0.583*	-0.283	0.450	0.008	0.655**	0.933*	0.001	-0.012	0.053	-0.098	0.044	-0.006	0.662**
Pusa 105 x LGG 450	0.083	0.217	-0.133	0.158**	0.647**	0.850*	-0.042	0.072	0.203	1.232**	0.106	-0.027	0.258*
Pusa 105 x UPM 79-4-12	0.333	0.050	0.033	-0.025	0.145**	-1.317*	0.050	0.072	-0.238	-0.357	-0.281	-0.014	-0.458**
ML 267 x PDM 54	-0.433	-0.083	0.950	0.375**	-0.010	1.217*	-0.033	-0.055	0.145	-0.253	0.226	-0.036	-0.132
ML 267 x MH 309	0.067	-0.500*	-1.633**	0.183**	0.073	-0.450	-0.042	-0.063	0.563*	-0.687*	-0.232	-0.070*	-0.253*
ML 267 x LGG 410	0.483*	-0.083	0.783	-0.158**	0.015	0.883*	0.033	0.028	0.187	0.288	-0.257	0.043	0.659**
ML 267 x LGG 450	0.150	0.417	0.533	-0.108*	0.007	0.917*	-0.008	0.112*	0.170	1.288**	0.161	0.061*	0.272*
ML 267 x UPM 79-4-12	0.267	0.250	-0.633	-0.292**	-0.085	1.117*	0.050	-0.022	0.062	-0.637	0.101	0.002	0.055
K 851 x PDM 54	0.167	0.250	0.550	-0.352**	0.043	-1.050	-0.020	0.138*	0.455*	-0.713*	0.136	-0.040	-0.489**
K 851 x MH 309	0.001	0.167	0.633	0.090	-0.040	-0.383	0.038	-0.170**	0.337	0.453	0.311	0.073**	0.207
K 851 x LGG 410	0.083	0.250	-1.617**	0.182**	-0.132*	1.133**	-0.020	0.088	-0.080	-0.605	0.203	-0.028	0.264*
K 851 x LGG 450	0.083	-0.517*	-0.200	0.098*	0.027	0.950*	0.005	-0.095	-0.097	0.628	-0.395	-0.009	0.298*
K 851 x UPM 79-4-12	-0.333	-0.417	0.633	-0.018	0.102*	0.917*	-0.003	0.038	0.295	0.237	-0.255	-0.003	0.248*
D12/333 x PDM 54	0.100	0.117	-1.450**	0.002	-0.030	0.150	0.020	-0.055	0.132	0.173	-0.207	0.027	0.184
D12/333 x MH 309	-0.067	0.033	1.030**	-0.157**	-0.080	0.483	0.045	0.337**	0.423*	-0.660	-0.365	-0.007	-0.170
D12/333 x LGG 410	0.017	0.117	0.383	-0.032	0.062	-0.267	-0.013	-0.105	-0.160	0.415	0.010	-0.010	0.642**
D12/333 x LGG 450	-0.317	-0.683*	-0.200	-0.148**	-0.080	1.183*	0.045	-0.088	-0.277	-0.665	0.128	-0.025	0.312**
D12/333 x UPM 79-4-12	0.267	0.117	-0.033	0.335**	0.128	0.817	-0.097**	-0.088	-0.118	0.757*	0.435	0.015	0.255*
S.E	0.244	0.260	0.495	0.046	0.070	0.450	0.031	0.054	0.237	0.351	0.408	0.030	0.120
S.E. (Sij-SKL)	0.345	0.368	0.700	0.065	0.115	0.575	0.043	0.076	0.335	0.496	0.577	0.042	0.170

* Significant at 5% level

** Significant at 1% level

moderate with 40.96 per cent in F_1 generation and 33.81 per cent in F_2 .

Lines D 12/333 (-0.283^*) and (-0.267^*) and K 851 (-0.350^* and -0.333^{**}) and testers, MH 309 (-1.000^{**} and -0.880^{**}), LGG 450 (-0.250^* and -0.217^*) and PDM 54 (-0.750^{**} and -0.633^{**}) recorded significant 'gca' effects in desired direction, whereas LGG 410, UPM 79-4-12 and Pusa 105 recorded positive 'gca' effects F_1 and F_2 generations, respectively. Two crosses i.e., ML 267 x UPM 79-4-12 (-0.583^{**}) and Pusa 105 x LGG 410 (-0.550^*) in F_1 and one cross in F_2 generation viz., Pusa 105 x LGG 450 (-0.588^*) recorded significantly negative 'sca' effects for days to 50% flowering. The cross ML 267 x LGG 410 showed significant positive 'sca' effect for this trait both in F_1 (0.583^*) and F_2 (0.483^*) generations (Tables 4.57 and 4.58).

4.3.2.2 Days to Maturity

The variance due to 'gca' was higher than 'sca' in both F_1 and F_2 generations for days to maturity. The degree of dominance was low with -0.503 and 0.357 in F_1 and F_2 generations respectively. High narrow sense heritability estimates of 62.17 and 59.55 per cent were recorded in F_1 and F_2 generations respectively. Among the lines D 12/333 (-0.583^{**} and 0.367^{**}) and K 851 (-0.511^{**} and -0.500^{**}) and testers MH 309 (-1.383^* and

-1.367**), PDM 54 (-1.633** and -1.450**) and LGG 450 (-0.300** and -0.283*) showed significant negative 'gca' effects for days to maturity (Tables 4.55 and 4.56). Other parents, Pusa 105, LGG 410 and UPM 79-4-12 were found to exert significant positive 'gca' effects. The crosses Pusa 105 x LGG 410 (-0.317*), K 851 x UPM 79-4-12 (-0.400*) and D 12/333 x LGG 450 (-0.467*) have recorded significant negative 'sca' effects for days to maturity in F_1 generation. Whereas, in F_2 generation ML 267 x MH 309 (-0.510*), K 851 x LGG 450 (-0.517*) and D 12/333 x LGG 450 (-0.683*) showed significant desirable 'sca' effects.

4.3.2.3 Plant height (cm)

Variance due to 'gca' was greater than 'sca' for plant height both at F_1 and F_2 generations. The degree of dominance was low both in F_1 (0.116) and F_2 (0.295). Heritability estimates were high for this trait both in F_1 (84.26 per cent) and F_2 (85.91 per cent) generations (Tables 4.53 and 4.54). Among the lines, Pusa 105 (9.283** and 9.467**) and K 851 (2.350** and 2.867*) and among testers, LGG 410 (1.667** and 1.683**) and LGG 450 (2.117** and 1.933**) showed significant positive 'gca' effects, whereas D12/333 (-9.317** and -9.467**) PDM 54 (-2.967** and -2.810**) and UPM 79-4-12 (-1.133** and -1.233**) showed significant negative 'gca' effects in both the generations.

(Tables 4.55 and 4.56). Pusa 105 x UPM 79-4-12 (1.200*) in F_1 and D 12/333 x MH 309 (1.300**) in F_2 have recorded significant positive 'sca' effects for plant height. While ML 267 x MH 309 (-1.633**) K 851 x LGG 410 (-1.617*) and D 12/333 x PDM 54 (-11.450*) showed significant negative 'sca' effects only in F_2 generation (Table 4.58).

4.3.2.4 Number of branches per plant

Variance due to 'sca' was higher than 'gca' for this trait both in F_1 and F_2 generations. The degree of dominance estimates were high i.e., 3.000 and 3.674 in F_1 and F_2 generations respectively. Heritability for this trait was estimated to be low in both F_1 (8.95) and F_2 (6.25) generations. D 12/333 (0.233** and 0.267**) and PDM 54 (0.270** and 0.238**) showed significant positive 'gca' effects in both the generations. Five crosses viz., ML 267 x PDM 54 (0.363** and 0.375**), D12/333 x UPM 79-4-12 (0.358** and 0.335**), ML 267 x MH 309 (0.197** and 0.183**), K 851 x LGG 410 (0.167** and 0.182**), Pusa 105 x LGG 450 (0.162** and 0.158**) have recorded positively significant 'sca' effects both in F_1 and F_2 generations. Whereas, K 851 x LGG 450 (0.098**) showed significant positive 'sca' effects only in F_2 generation for this trait.

4.3.2.5 Number of clusters per plant

Estimates of 'gca' variance was higher than 'sca' variance in both the generations for the number of clusters per plant. The heritability estimates were low both in F_1 (9.38) and F_2 (22.58) generations. The degree of dominance was found to be low with -0.408 in F_1 and -0.707 in F_2 generation.

Among the lines, Pusa 105 (0.142* and 0.203**) and ML 267 (0.185* and 0.210**) and testers, LGG 410 (0.265** and 0.232*) and LGG 450 (0.298** and 0.440**) have recorded significant positive 'gca' effects for this trait in both F_1 and F_2 generations. D12/333 (-0.168* and -0.170*) and UPM 79-4-12 (-1.117* and -1.483**) however showed significant negative 'gca' effects for this trait in both the generations. Three crosses viz., Pusa 105 x LGG 410 (0.422*), Pusa 105 x LGG 450 (0.212*) and D 12/333 x LGG 450 (0.235*) in F_1 and four crosses viz., Pusa 105 x LGG 410 (0.655*), Pusa 105 x LGG 450 (0.647*), Pusa 105 x UPM 79-4-12 (0.145**) and K 851 x UPM 79-4-12 (0.102*) in F_2 have recorded significant positive 'sca' effects for the number of clusters per plant.

4.3.2.6 Number of pods per plant

The 'gca' variance was higher compared to 'sca' variance both in F_1 and F_2 generations for this

character. Heritability estimates were found to be low both in F_1 (15.69) and F_2 (15.48) generations. The degree of dominance was high with -1.241 in F_1 and -0.927 in F_2 generations (Tables 4.53 and 4.54).

Among the lines Pusa 105 (1.350** and 1.650**) and testers PDM 54 (1.350* and 1.483*), LGG 410 (3.317** and 3.267**) and LGG 450 (1.483** and 1.850**) showed significant positive 'gca' effects. Six crosses viz., Pusa 105 x LGG 410 (0.483* and 0.933**), Pusa 105 x LGG 450 (0.350* and 0.850*), ML 267 x LGG 450 (0.650* and 0.917*), K 851 x LGG 410 (0.617* and 1.133**), K 851 x LGG 450 (0.517* and 0.950*) and K 851 x UPM 79-4-12 (0.350* and 0.917*) have recorded positively significant 'sca' effects both at F_1 and F_2 generations. Whereas, Pusa 105 x PDM 54 (0.817*) Pusa 105 x MH 309 (0.633*), D 12/333 x LGG 410 (0.417*) and D 12/333 x LGG 450 (0.483*) in F_1 and ML 267 x PDM 54 (1.217*), ML 267 x UPM 79-4-12 (1.133*), ML 267 x LGG 410 (0.833*) in F_2 only have recorded significant 'sca' effects (Tables 4.57 and 4.58).

4.3.2.7 Pod length (cm)

Variance due to 'gca' was greater than due to 'sca' variance in F_1 generation while in F_2 generation both 'gca' and 'sca' variances were equal. Degree of dominance was found to be 0.517 in F_1 and 0.707 in F_2

generations. Heritability for this trait was high in F_1 (66.66 per cent) and moderate in F_2 generation (44.44 per cent).

Among the lines K 851 (0.265* and 0.245**) and testers PDM 54 (0.035* and 0.037*) have recorded significant positive 'gca' effects for pod length. Only one cross in F_1 generation (D 12/333 x MH 309) has recorded significant positive 'sca' effect (0.087**) for pod length, whereas D 12/333 x UPM 79-4-12 recorded significant negative 'sca' effects in both F_1 and F_2 generations.

4.3.2.8 Number of seeds per pod

Variance due to 'gca' was greater than the variance due to 'sca' both in F_1 and F_2 generations (Table 4.53 and 4.54). The heritability estimates for this trait were high in F_1 (63.64 per cent) as well as in F_2 (58.46 per cent) generations. The degree of dominance was also high i.e., 0.617 and 0.688 in F_1 and F_2 generations respectively.

Among the lines, K 851 (0.608** and 0.645**) and testers, LGG 450 (0.237* and 0.172**) and LGG 410 (0.362** and 0.222**) were found to be good general combiners for the number of seeds per pod in both the generations, while ML 267 had recorded significant

positive 'gca' effects (0.428**) only in F_1 generation (Tables 4.55 and 4.56).

Two crosses namely, ML 267 x UPM 79-4-12 (0.617*) and K 851 x MH 309 (0.742**) have recorded significant positive 'sca' effects only in F_1 generation, and three crosses, namely, ML 267 x LGG 450 (0.112*), K 851 x PDM 54 (0.138**) and D 12/333 x MH 309 (0.337**) recorded significant positive 'sca' effects only in F_2 generations.

4.3.2.1 1000 seed weight (g)

Gca variance was greater than 'sca' for seed weight both in F_1 and F_2 generations. High heritability estimates were recorded for this trait both in F_1 (51.18 per cent) and F_2 (65.31 per cent) generations. The degree of dominance was estimated to be 0.512 and 0.356 in F_1 and F_2 generations, respectively.

Pusa 105 (0.775** and 0.863**), K 851 (1.675** and 1.830**) among the lines and PDM 54 (0.400** and 0.755**), LGG 410 (0.650** and 0.547**) and LGG 450 (0.400** and 0.563**) among the testers were found to be good general combiners for seed weight in both the generations. Four crosses viz., Pusa 105 x LGG 450 (0.162**), Pusa 105 x UPM 79-4-12 (0.172**), ML 267 x PDM 54 (0.110*) and K 851 x LGG 450 (0.225**) have recorded significant positive 'sca' effects in F_1

generation and three crosses viz., ML 267 x PDM 54 (0.563*), K 851 x PDM 54 (0.455*) and D 12/333 x MH 309 (0.423*) in F_2 generation have recorded significantly positive 'sca' effects for 1000 seed weight.

4.3.2.10 Shoot dry weight (g)

The 'gca' variances were greater than 'sca' variances in both the generations. High heritability estimates were recorded for shoot dry weight both in F_1 (64.73 per cent) and F_2 (67.56 per cent) generations. The degree of dominance was found to be low in F_1 (0.355) and moderate in F_2 (0.549).

Pusa 105 (1.872** and 1.107**), K 851 (2.185** and 2.213**) among the lines, LGG 410 (3.728** and 4.198**) and LGG 450 (2.695** and 2.298**) among the testers were found to be good general combiners for the shoot dry weight in both the generations. ML 267 has recorded significant 'gca' effect only in F_1 generation. Five crosses in F_1 viz., ML 267 x MH 309 (0.792*), ML 267 x LGG 410 (0.792*), K 851 x PDM 54 (1.393*), D12/333 x PDM 54 (0.707*) and D 12/333 x LGG 450 (0.768*) and five crosses in F_2 , Pusa 105 x PDM 54 (0.793*), Pusa 105 x MH 309 (0.893*), Pusa 105 x LGG 450 (1.232**), ML 267 x LGG 450 (1.288**) and D 12/333 x UPM 79-4-12 (0.757*) showed significant positive 'sca' effects.

4.3.2.11 Seed protein (%)

Variances due to 'gca' were greater than 'sca' for seed protein in both the generations. Estimates of narrow sense heritability were low for this trait in both F_1 (20.66) and F_2 (8.08). The degree of dominance was also low with -0.377 and -1.252 in F_1 and F_2 generations, respectively.

PDM 54 (0.347* and 0.470*) and LGG 410 (0.472** and 0.304*) have recorded significant positive 'gca' effects for seed protein in F_1 and F_2 generations, whereas Pusa 105 (0.360*) showed significant 'gca' effects only in F_1 generation. None of the crosses showed significant 'sca' effect either in F_1 or F_2 generations for seed protein content (Tables 4.57 and 4.58).

4.3.2.12 Shoot nitrogen (%)

The 'gca' and 'sca' variances were equal both in F_1 and F_2 generations for this trait. Moderate levels of heritability estimates were recorded for this trait with 25.00 and 33.33 per cent in F_1 and F_2 generations, respectively. The degree of dominance was high both in F_1 (0.707) and in F_2 (0.707) generations.

LGG 410 (0.111** and 0.127**) showed positive and significant 'gca' effects in both F_1 and F_2

generations. Whereas, Pusa 105 (0.039*) and LGG 450 (0.109**) have recorded significant 'gca' effects only in F_1 generation. Two crosses, ML 267 x LGG 450 (0.61**) and K 851 x MH 309 (0.079**) showed significantly positive 'sca' effects for shoot nitrogen only in F_2 generation.

4.3.2.13 Grain yield per plant

Estimates of 'gca' variances were greater than 'sca' variances for grain yield both in F_1 and F_2 generations. The heritability estimates were high for this trait both in F_1 (66.78) and F_2 (72.18). The degree of dominance was found to be 0.391 in F_1 and 0.510 in F_2 generations (Tables 4.53 and 4.54).

Pusa 105 (0.626** and 0.642**) and K 851 (1.003** and 0.818**) among the lines and PDM 54 (0.626** and 0.642**), LGG 410 (1.635** and 1.708**) and LGG 450 (1.035** and 1.028**) among the testers have recorded significant 'gca' effects in both the generations (Tables 4.55 and 4.56).

Eight crosses viz., Pusa 105 x PDM 54 (0.358* and 0.437**), Pusa 105 x LGG 410 (0.655** and 0.662**), Pusa 105 x LGG 450 (0.288* and 0.258*), ML 267 x LGG 450 (0.248* and 0.272*), K 851 x LGG 410 (0.615** and 0.264*), K 851 x LGG 450 (0.335* and 0.298**), D 12/333 x LGG 450 (0.295* and 0.312**) and D 12/333 x UPM 79-4-



Fig.18. LGG450-GOOD GENEREL COMBINER



Fig.19. PDM54-GOOD GENEREL COMBINER

Fig .20.PUSA-105
GOOD GENEREL COMBINER



Fig.21.LGG-410
GOOD GENEREL COMBINER



Fig.22.PUSA105×LGG410
GOOD SPECIFIC COMBINER



Fig.23.PUSA105×LGG450
GOOD SPECIFIC COMBINER



Fig.24. ML267×LGG450
GOOD SPECIFIC COMBINE



Fig.25. K851×LGG410 GOOD SPECIFIC COMBINER

12 (0.463** and 0.312**) have recorded significant 'sca' effects both in F_1 and F_2 generations. Whereas three crosses viz., Pusa 105 x MH 309 (0.299**), ML 267 x UPM 79-4-12 (0.623*), D 12/333 x PDM 54 (0.301*) in F_1 and three crosses Pusa 105 x UPM 79-4-12 (0.458**), K 851 x UPM 79-4-12 (0.248*) and D 12/333 x LGG 410 (0.642**) in F_2 generation only have recorded significant 'sca' effects for grain yield (Tables 4.57 and 4.58).

4.3.3 Correlation coefficients

Correlation coefficients between yield and yield components and among themselves were worked out for parents, F_1 s and F_2 s separately and are presented in Tables 4.59 to 4.61 respectively.

4.3.3.1 Correlation analysis in parents

Association analysis in parents revealed that seed yield was significantly and positively associated with plant height (0.6813*), clusters per plant (0.5149*), pods per plant (0.7595**), seeds per pod (0.4794*), 1000 seed weight (0.7787**), shoot dry weight (0.9920**), and shoot nitrogen (0.7866**), at phenotypic level, Genotypic correlations were also higher for the above character combinations (Table 4.59).

Among yield components significant positive association was observed between days to 50% flowering

Table 4.59: Phenotypic (P) and Genotypic (G) correlation coefficients between yield and yield components in parents

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Days to 50% flowering	P 1.0000 G 1.0000	0.9651** 0.9725	0.5803* 0.5662	0.2698 0.2920	0.1813 0.2048	0.5041* 0.5747	-0.1272 -0.1213	-0.0536 -0.0677	0.2561 0.2627	0.3110 0.3163	0.2619 0.2600	-0.0151 -0.0447	0.3465 0.3509
Days to maturity		1.0000 1.0000	0.5451* 0.5477	0.2620 0.2780	0.2313 0.2593	0.4753* 0.5460	-0.1317 -0.1356	-0.1128 -0.1185	0.2244 0.2270	0.2600 0.2647	0.2771 0.3366	-0.0100 -0.0107	0.3020 0.3037
Plant height (cm)			1.0000 1.0000	0.1034 0.1060	0.5243* 0.5896	0.4925* 0.5907	0.3691 0.3911	0.4814* 0.5077	0.7570** 0.7713	0.6917** 0.7041	-0.0781 -0.0994	0.2377 0.2563	0.6613** 0.6876
Number of branches per plant				1.0000 1.0000	0.2796 0.3692	0.4586 0.5433	-0.6171** -0.6815	0.2922 -0.3661	-0.2301 -0.2377	0.2043 0.2443	0.0753 0.0336	0.3173 0.4173	0.2693 0.2980
Number of clusters per plant					1.0000 1.0000	0.4760* 0.5293	0.1108 0.1598	0.0649 0.0981	0.4652 0.5015	0.5014** 0.5260	0.0007 0.0652	0.4585 0.5189	0.5147* 0.5413
Number of pods per plant						1.0000 1.0000	-0.1647 -0.1947	-0.0056 0.0167	0.3838 0.4363	0.7128** 0.8467	0.0400 0.4002	0.5714* 0.6980	0.7595** 0.8713
Pod length (cm)							1.0000 1.0000	0.8302** 0.8801	0.6028** 0.6281	0.2614 0.2783	-0.0879 -0.0698	0.0505 0.0402	0.2240 0.2367
Seeds per pod								1.0000 1.0000	0.6704** 0.7207	0.5114 0.5463	0.0324 0.0431	0.2866 0.3106	0.4794* 0.5096
1000 seed weight (g)									1.0000 1.0000	0.8108** 0.8220	0.1861 0.2735	0.4828* 0.5179	0.5096 0.7819
Shoot dry weight (g)										1.0000 1.0000	0.0987 0.2049	0.7684** 0.8259	0.9920** 0.9985
Seed protein (%)											1.0000 1.0000	0.2898 0.4563	0.1371 0.2116
Shoot nitrogen (%)												1.0000 1.0000	0.2116 0.7866**
Grain yield per plant (g)													0.8441 1.0000 1.0000

P = Phenotypic correlation coefficients ; G = Genotypic correlation coefficients
 * = Significant at 5% level ; ** = Significant at 1% level

and days to maturity, plant height, number of clusters per plant, number of pods per plant, seeds per pod, 1000 seed weight and shoot dry weight. Days to maturity was found to be significantly and positively associated with plant height and number of pods per plant. Plant height showed positive association with number of clusters per plant, number of pods per plant, seeds per pod, 1000 seed weight and shoot dry weight. Branches per plant had negative association with pod length. Number of clusters per plant was significantly positively associated with pods per plant and shoot dry weight. The number of pods per plant was found to be positively associated with shoot dry weight and shoot nitrogen. Pod length showed significant positive association with seeds per pod, 1000 seed weight. 1000 seed weight also had similar association with shoot dry weight and shoot nitrogen. Shoot dry weight had significant positive association with shoot nitrogen.

4.3.3.2 Association analysis at F_1 generation

Data collected from twenty F_1 hybrids were utilised to find out the character associations. Seed yield was found to be significantly and positively associated with days to flowering (0.3193*), plant height (0.6028**), number of clusters (0.5151**), pods per plant (0.7283**), pod length (0.5221**), seeds per pod (0.8300**), 1000 seed weight (0.7833**), shoot dry

Table 4.60: Phenotypic (P) and Genotypic (G) correlation coefficients between yield and yield components in F₁ generation

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Days to 50% flowering	1.0000	0.8492**	0.3669*	-0.1197	0.0392	0.4181**	0.0698	0.0624	0.3280*	0.4596*	0.2622	0.3193*
	G	0.9385	0.3875	-0.1419	0.1042	0.6039	0.0892	0.0594	0.3695	0.6279	0.3264	0.3525
Days to maturity		1.0000	0.3392*	-0.2217	0.0838	0.3126*	-0.0148	-0.0790	0.1804	0.3459*	0.0881	0.1829
		1.0000	0.3582	-0.2390	0.1298	0.4446	-0.0155	-0.0931	0.1993	0.4953	0.1319	0.1940
Plant height (cm)			1.0000	-0.5079**	0.3866*	0.4197**	0.6623**	0.5206**	0.6253**	0.1951	0.3286*	0.6028**
			1.0000	-0.5516	0.6743	0.6580	0.7140	0.5345	0.6640	0.2330	0.3915	0.6321
Number of branches per plant				1.0000	-0.2056	-0.1558	-0.4025**	-0.3254*	-0.2766	0.1972	0.1408	-0.2769
				1.0000	-0.3047	0.2454	-0.4169	-0.3469	-0.2836	0.3322	0.1825	-0.3003
Number of clusters per plant					1.0000	0.6344**	0.2800	0.3307*	0.5584**	-0.0176	0.5050**	0.5151**
					1.0000	0.7597	0.5125	0.5125	0.7180	0.3483	0.8226	0.7203
Number of pods per plant						1.0000	0.3704*	0.4371**	0.7379**	0.0481	0.7052**	0.7283**
						1.0000	0.8045	0.6515	0.9965	0.1412	0.0219	1.0000
Pod length (cm)							0.7844**	0.7277**	0.5017**	-0.1041	0.1129	0.5221**
							1.0000	0.7468	0.5252	-0.1030	0.1244	0.5463
Seeds per pod							0.8541	0.7664**	0.8217**	0.1782	0.4985**	0.8300**
							1.0000	0.8540	0.8625	0.2604	0.6128	0.8667
1000 seed weight (g)							1.0000	1.0000	0.7707**	0.2635	0.3567**	0.7633**
								1.0000	0.8458	0.3319	0.5080	0.8433
Shoot dry weight (g)									1.0000	0.3522*	0.7374**	0.9639**
									1.0000	0.5418	0.8647	1.0000
Seed protein (%)										1.0000	0.2845	0.3288*
										1.0000	0.6193	0.5222
Shoot nitrogen (%)											1.0000	0.7471**
											1.0000	0.8472
Grain yield per plant (g)												1.0000
												1.0000

P = Phenotypic correlation coefficients ; G = Genotypic correlation coefficients
 * = Significant at 5% level ; ** = Significant at 1% level

weight (0.9839**), seed protein (0.3288**), and shoot nitrogen (0.7471**), phenotypically. Genotypic correlations were higher for the above characters with grain yield (Table 4.60).

Association analysis among the yield components indicated that days to 50% flowering showed significantly positive correlation with days to maturity, plant height, pods per plant, shoot dry weight, seed protein and shoot nitrogen. Days to maturity was found to be positively associated with plant height, pods per plant and seed protein. Plant height had positive and significant association with clusters per plant, pods per plant, pod length, seeds per pod, 1000 seed weight, shoot dry weight and shoot nitrogen. Whereas it had significantly negative correlation with branches per plant. Branches per plant had significantly positive association only with seed protein, whereas it had negative association with pod length, seeds per pod and 1000 seed weight.

Clusters per plant showed significantly positive association with pods per plant, seeds per pod, 1000 seed weight, shoot dry weight and shoot nitrogen. While it was significantly positive only with seeds per pod and seed protein. Significantly positive association was also observed between pods per plant and seeds per pod, 1000 seed weight, shoot dry weight and

shoot nitrogen, whereas pod length showed significantly positive association with seeds per pod, 1000 seed weight and shoot dry weight.

Seeds per pod had significantly positive correlation with 1000 seed weight, shoot dry weight and shoot nitrogen. 1000 seed weight showed significant positive correlation with shoot dry weight and shoot nitrogen. Genotypic correlations between 1000 seed weight and seed protein were higher than phenotypic correlations.

Shoot dry weight was found to be positively associated with seed protein and shoot nitrogen. Whereas, seed protein had significant and positive genotypic correlation only with shoot nitrogen.

4.3.3.3 Association analysis in segregating population (F_2 generation)

Twenty F_2 populations derived from a 4 x 5 line x tester programme were utilised to study the character association in segregating populations. The seed yield was found to be significantly positively correlated with days to 50% flowering (0.3180*), plant height (0.6042*) number of clusters per plant (0.6087**), pods per plant (0.7228**), pod length (0.4447**), seeds per pod (0.6512**), 1000 seed weight (0.7461**), shoot dry weight (0.985**), and shoot nitrogen (0.8547**),

Table 4.61: Phenotypic (P) and Genotypic (G) correlation coefficients between yield and yield components in F₂ generation

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Days to 50% flowering	1.0000	0.8575**	0.3577*	-0.1421	0.0511	0.3273*	-0.0456	-0.0658	-0.0540	0.3127*	0.3213*	0.1762	0.3180*
	G	0.9714	0.4046	-0.1942	0.2104	0.6825	-0.0579	-0.1077	-0.0694	0.3545	0.3987	0.2240	0.3752
Days to maturity	1.0000	1.0000	0.2678	-0.1848	0.0393	0.3685*	-0.0837	-0.1482	-0.1527	0.2527	0.2387	0.0902	0.2659
	G	1.0000	0.2894	-0.2056	0.1053	0.6012	-0.0799	-0.1533	-0.1540	0.2746	0.4326	0.1097	0.2879
Plant height (cm)	1.0000	1.0000	1.0000	-0.5134**	0.4777**	0.4715**	0.5154**	0.4739**	0.5891**	0.5664**	0.0647	0.3444*	0.6042**
	G	1.0000	1.0000	-0.5368	0.6333	0.6915	0.5465	0.4863	0.6145	0.5746	0.1082	0.3737	0.6156
Number of branches per plant	1.0000	1.0000	1.0000	1.0000	-0.1141	-0.1669	-0.5900**	-0.8397**	-0.3726*	-0.3472*	0.1797	-0.1061	-0.3325*
	G	1.0000	1.0000	1.0000	-0.1041	-0.2012	-0.6460	-0.5718	-0.3620	-0.3643	0.3576	-0.1442	-0.3425
Number of clusters per plant	1.0000	1.0000	1.0000	1.0000	1.0000	0.6325**	0.0092	0.2660	0.3503*	0.5674**	-0.1361	0.5414**	0.6087**
	G	1.0000	1.0000	1.0000	1.0000	0.6655	0.0303	0.3500	0.4462	0.7033	0.3717	0.7357	0.7387
Number of pods per plant	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.0853	0.2680	0.3676*	0.6512**	0.1867	0.5719**	0.7228**
	G	1.0000	1.0000	1.0000	1.0000	1.0000	0.1782	0.3732	0.5048	0.9249	0.6331	0.8298	0.9548
Pod length (cm)	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.6980**	0.7925**	0.4620**	0.0180	0.1972	0.4447**
	G	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.7508	0.8409	0.4970	-0.0158	0.2346	0.4761
Seeds per pod	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.8016**	0.6685**	0.0494	0.5133**	0.6512**
	G	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.8387	0.6879	0.1430	0.5667	0.6660
1000 seed weight (g)	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.7391**	0.1527	0.5821**	0.7461**
	G	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.7778	0.3801	0.6826	0.7776
Shoot dry weight (g)	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.1570	0.8477**	0.9857**
	G	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.4567	0.9162	0.9937
Seed protein (%)	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.2173	0.1647
	G	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.5741	0.4814
Shoot nitrogen (%)	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.8547**
	G	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.9213
Grain yield per plant (g)	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
	G	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000

* = Phenotypic correlation coefficients ; G = Genotypic correlation coefficients
 ** = Significant at 5% level ; ** = Significant at 1% level

phenotypically. Whereas seed yield was found to be negatively associated with branches per plant at phenotypic (-0.3325^*) level (Table 4.61).

Among the yield components, significant positive phenotypic correlations were observed between days to 50% flowering and days to maturity, plant height, pods per plant, shoot dry weight, and seed protein; Days to maturity with pods per plant; plant height with number of clusters per plant, pods per plant, pod length, seeds per pod, 1000 seed weight, shoot dry weight and shoot nitrogen; Clusters per plant with pods per plant, 1000 seed weight, shoot dry weight and shoot nitrogen; Number of pods per plant with 1000 seed weight, shoot dry weight and shoot nitrogen; Pod length with seeds per pod, 1000 seed weight, shoot dry weight; Seeds per pod with 1000 seed weight, shoot dry weight and shoot nitrogen; 1000 seed weight with shoot dry weight and shoot nitrogen; shoot dry weight with shoot nitrogen. Genotypic correlations for days to maturity with seed protein, branches per plant with seed protein, clusters per plant with seeds per pod, pods per plant with seed protein, 1000 seed weight with seed protein, shoot dry weight with seed protein and seed protein with shoot nitrogen were higher than phenotypic correlations. Branches per plant was negatively

associated with pod length, seeds per pod, 100 seed weight and shoot dry weight.

4.3.3.4 Changes in associations between parents and F_1 s

Grain yield was found to have significantly positive association with days to 50% flowering, pod length and seed protein in F_1 s at phenotypic level which was absent among the parents.

Among the yield component traits the non-significant association in parents between the character pairs given below become significantly positive in F_1 generation. They are days to 50% flowering with shoot dry weight, seed protein and shoot nitrogen; days to maturity with seed protein and shoot nitrogen; days to maturity with seed protein; plant height with shoot nitrogen; number of branches per plant with seeds per pod and 1000 seed weight; pod length with shoot nitrogen; shoot dry weight with seed protein and seed protein with shoot nitrogen.

Plant height showed significantly negative association with branches in F_1 though it was not significant in parents.

4.3.3.5 Changes in association between parents and F_2 s

Grain yield showed significantly positive association with days to 50% flowering, and pod length

at phenotypic and genotypic level in F_2 s though it was not significant in parents. Grain yield was negatively associated with branches per plant in F_2 generation while it was not significant in parents. The non-significant association between grain yield and seed protein in parents became positively significant at genotypic level in F_2 s.

Similarly, the non-significant association in parents between days to 50% flowering and shoot dry weight, days to 50% flowering and seed protein, plant height and pod length, plant height and shoot nitrogen, branches per plant and seeds per pod, clusters per plant and seeds per pod, pod length and shoot dry weight, became significantly positive in F_2 both at genotypic and phenotypic levels. Whereas the non-significant association in parents became significantly positive only at genotypic level in F_2 between days to maturity and seed protein, clusters per plant and seeds per pod, number of pods per plant and seed protein, 1000 seed weight and seed protein, shoot dry weight and seed protein and seed protein and shoot nitrogen.

Plant height with number of branches per plant, branches per plant with seeds per pod, shoot dry weight and 1000 seed weight, showed significant negative association in F_2 generation while they were non-significant in parents. The positive and significant

association between branches per plant and the number of pods per plant among parents became non-significant in F_2 generation.

4.3.3.6 Changes in associations from F_1 s and F_2 s

Grain yield had non-significant association with the number of branches per plant in F_1 but changed to significantly negative in F_2 , whereas for days to maturity with plant height significantly positive association among F_1 s became non-significant in F_2 generation.

4.3.4 Path analysis

The direct and indirect effect of different yield component traits on yield were worked out through path analysis of genotypic and phenotypic correlations in parents, F_1 s and F_2 s separately and are presented in tables 4.62 to 4.67, respectively.

Parents

Path analysis in parents revealed that shoot dry weight (0.8930 and 0.8489) followed by number of pods per plant (0.1033 and 0.1047) and pod length (0.0965 and 0.0520) had positive direct effect on seed yield both at genotypic and phenotypic level. Number of pods per plant followed by 1000 seed weight, seeds per pod, clusters per plant, plant height and shoot nitrogen

Table 4.62: Genotypic path coefficient analysis for grain yield in parents

Character	Days to 50% flowering	Days to 50% flo- maturity	Days to Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Days to 50% flowering	0.0196	0.0098	-0.0200	0.0185	-0.0007	0.0594	-0.0117	0.0001	-0.0106	0.2825	0.0051	-0.0013	0.3113
Days to maturity	0.0191	0.0101	-0.0193	0.0176	-0.0009	0.0564	-0.0131	0.0002	-0.0091	0.2364	0.0067	-0.0003	0.3113
Plant height (cm)	0.0111	0.0055	-0.0353	0.0067	-0.0020	0.0610	0.0377	-0.0008	-0.0310	0.6293	-0.0020	0.0072	0.6813
Number of branches per plant	0.0057	0.0028	-0.0037	-0.0633	-0.0012	0.0561	0.0658	0.0006	0.0096	0.2182	0.0007	0.0118	0.2913
Number of clusters per plant	0.0040	0.0026	-0.0208	0.0234	-0.0034	0.0547	-0.0154	-0.0002	-0.0201	0.4697	0.0013	0.0146	0.5413
Number of pods per plant	0.0113	0.0055	-0.0208	0.0344	-0.0018	0.1033	-0.0188	0.0000	-0.0175	0.7561	0.0000	0.0197	0.8713
Pod length (cm)	-0.0024	-0.0014	-0.0138	-0.0431	-0.0005	-0.0201	0.0965	-0.0014	-0.0252	0.2485	-0.0014	0.0011	0.2313
Seeds per pod	-0.0013	-0.0012	-0.0179	-0.0232	-0.0003	0.0017	0.0849	-0.0016	-0.0290	0.4878	0.0009	0.0088	0.5013
1000 seed weight (g)	0.0052	0.0023	-0.0272	-0.0150	-0.0017	0.0451	0.0606	-0.0012	-0.0402	0.7340	0.0054	0.0146	0.7813
Shoot dry weight (g)	0.0062	0.0027	-0.0249	0.0155	-0.0018	0.0875	0.0268	-0.0009	-0.0330	0.8930	0.0041	0.0233	0.9913
Seed protein (%)	0.0051	0.0034	0.0035	0.0021	-0.0002	0.0000	-0.0067	-0.0001	-0.0110	0.1830	0.0198	0.0129	0.2113
Shoot nitrogen (%)	-0.0009	-0.0001	-0.0090	0.0264	-0.0017	0.0721	0.0039	-0.0005	-0.0208	0.7375	-0.0090	0.0282	0.8413

Table 4.63: Phenotypic path coefficient analysis for grain yield in parents

	Days to 50% flowering	Days to 50% flowering	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)	
Days to 50% flowering	-0.0175	0.0378	-0.0084	0.0194	-0.0015	0.0528	-0.0066	-0.0010	0.0027	0.2640	0.0055	-0.0006	0.3465
Days to maturity	-0.0169	0.0391	-0.0082	0.0188	-0.0019	0.0498	-0.0068	-0.0020	0.0025	0.2208	0.0075	-0.0004	0.3420
Plant height (cm)	-0.0098	0.0213	-0.0151	0.0074	-0.0044	0.0516	0.0182	0.0087	0.0081	0.5872	-0.0021	0.0091	0.6113
Number of branches per plant	-0.0047	0.0103	-0.0016	-0.0719	-0.0023	0.0480	-0.0321	0.0053	-0.0025	0.1735	0.0020	0.0122	0.2493
Number of clusters per plant	-0.0032	0.0091	-0.0079	0.0201	-0.0083	0.0498	0.0058	0.0012	0.0050	0.4256	0.0000	0.0176	0.5147
Number of pods per plant	-0.0088	0.0186	-0.0074	0.0329	-0.0040	0.1047	-0.0086	-0.0002	0.0041	0.6051	0.0012	0.0219	0.7195
Pod length (cm)	0.0022	-0.0052	-0.0056	-0.0445	-0.0009	-0.0172	0.0520	0.0150	0.0065	0.2219	-0.0024	0.0019	0.2240
Seeds per pod	0.0009	-0.0044	-0.0072	-0.0210	-0.0005	-0.0010	0.0431	0.0181	0.0072	0.4341	-0.0009	0.0110	0.4794
1000 seed weight (g)	-0.0045	0.0088	-0.0114	-0.0165	-0.0039	0.0402	0.0313	0.0122	0.0107	0.6883	0.0050	0.0185	0.7787
Shoot dry weight (g)	-0.0055	0.0102	-0.0104	0.0147	-0.0042	0.0746	0.0136	0.0093	0.0087	0.8489	0.0027	0.0295	0.9320
Seed protein (%)	-0.0035	0.0108	0.0012	0.0054	0.0000	0.0045	-0.0046	-0.0006	0.0020	0.0838	0.0270	0.0111	0.1371
Shoot nitrogen (%)	0.0003	-0.0004	-0.0036	0.0228	-0.0038	0.0598	0.0026	0.0052	0.0052	0.6524	0.0078	0.0383	0.7566

also exerted indirect effect on seed yield via shoot dry weight. Plant height, number of clusters per plant, seeds per pod, 1000 seed weight showed negative direct effect on grain yield (Tables 4.62 and 4.63).

F₁ generation

Genotypic path coefficient analysis in F₁ generation indicated that the grain yield in mungbean was directly influenced by the number of pods per plant (0.3412) followed by shoot dry weight (0.2429), shoot nitrogen (0.2120), pod length (0.1860), 1000 seed weight (0.1513) and seeds per pod (0.1085). Days to 50% flowering and seed protein exerted negative direct effect on seed yield. Days to maturity, plant height, branches per plant, clusters per plant, and shoot nitrogen showed indirect effects on seed yield through number of pods per plant. However, phenotypic path coefficient analysis revealed that shoot dry weight (0.3473) followed by number of pods per plant (0.2777), shoot nitrogen (0.1754), days to maturity (0.1093) and seeds per pod (0.1600) had direct effect on seed yield. Plant height, number of clusters per plant, number of pods per plant, seeds per pod, 1000 seed weight and shoot nitrogen influenced seed yield indirectly through shoot dry weight. Days to 50% flowering showed negative direct effect on grain yield (Tables 4.64 and 4.65).

Table 4.64: Genotypic path coefficient analysis for grain yield in F_1 generation

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Correlation with grain yield
Days to 50% flowering	0.0789	0.0302	0.0136	0.0505	0.0214	0.1954	-0.0251	-0.0176	0.0367	0.0375	-0.0014	-0.0097	0.3525
Days to maturity	-0.0768	0.0310	0.0131	0.0483	0.0257	0.1837	-0.0284	-0.0221	0.0318	0.0191	-0.0019	-0.0023	0.1940
Plant height (cm)	-0.0437	0.0165	0.0246	0.0192	0.0559	0.1870	0.0666	0.0396	0.1113	0.1520	0.0009	0.0476	0.6321
Number of branches per plant	-0.0340	0.0128	0.0040	-0.1170	0.0247	0.1631	1.1162	-0.0295	-0.0405	0.0133	-0.0004	0.0631	-0.3003
Number of clusters per plant	-0.0202	0.0096	0.0165	0.0346	0.0836	0.1803	0.0327	0.0198	0.0880	0.1271	-0.0006	0.1181	0.7203
Number of pods per plant	-0.0452	0.0167	0.0142	0.0559	0.0442	0.3412	-0.0359	-0.0042	0.0696	0.1656	-0.0004	0.1474	1.0000
Pod length (cm)	0.0106	-0.0047	0.0088	-0.0731	0.0147	-0.0658	0.1860	0.0945	0.0970	0.0767	0.0004	0.0094	0.5463
Seeds per pod	-0.0128	-0.0063	0.0090	-0.0318	0.0152	0.0131	0.1620	0.1085	0.0980	0.1281	-0.0003	0.0744	0.8661
1000 seed weight (g)	0.0191	0.0065	0.0181	-0.0313	0.0486	-0.1569	0.1182	0.0703	0.1513	0.2101	-0.0013	0.1132	0.8433
Shoot dry weight (g)	-0.0122	0.0024	0.0154	0.0084	0.0437	0.2326	0.0587	0.0572	0.1309	0.2429	-0.0009	0.1704	1.0000
Seed protein (%)	-0.0191	0.0101	-0.0038	0.0083	0.0083	0.0230	-0.0124	0.0059	0.0326	0.0371	-0.0059	0.0881	0.5222
Shoot nitrogen (%)	0.0036	-0.0003	0.0055	0.0349	0.0466	0.2372	0.0083	0.0381	0.0808	0.1953	-0.0025	0.2120	0.8472

Table 4.65: Phenotypic path coefficient analysis for grain yield in F₁ generation

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Correlation with grain yield
Days to 50% flowering	-0.2107	0.1608	0.0602	0.0363	0.0119	0.1401	-0.0127	-0.0250	0.0259	0.0518	0.0076	-0.0024	0.3713
Days to maturity	-0.2034	0.1666	0.0580	0.0371	0.0159	0.1350	-0.0137	-0.0321	0.0221	0.0268	0.0097	-0.0017	0.1619
Plant height (cm)	-0.1161	0.0885	0.1093	0.0140	0.0336	0.1403	0.0319	0.0582	0.0770	0.2114	-0.0045	0.0354	0.6228
Number of branches per plant	-0.1775	0.0626	0.0155	-0.0987	0.0133	0.1103	0.0528	-0.0390	-0.0268	0.0194	0.0036	0.0389	-0.2713
Number of clusters per plant	-0.0421	0.0446	0.0619	0.0221	0.0593	0.1553	0.0183	0.0169	0.0542	0.1624	-0.0005	0.0773	0.5113
Number of pods per plant	-0.1063	0.0810	0.0552	0.0392	0.0352	0.2777	-0.0164	-0.0122	0.0427	-0.2301	-0.0021	0.1005	0.7211
Pod length (cm)	0.0289	-0.0246	0.0375	-0.0561	0.0116	-0.0490	0.0930	0.1332	0.0664	0.0972	-0.0025	0.0100	0.5211
Seeds per pod	0.0329	-0.0334	0.0398	-0.0240	0.0063	-0.0212	0.0774	0.1600	0.0671	0.1737	0.0016	0.0581	0.8111
1000 seed weight (g)	-0.0514	0.0347	0.0793	-0.0249	0.0303	0.1118	0.0582	0.1011	0.1061	0.2887	0.0070	0.0882	0.7111
Shoot dry weight (g)	-0.0314	0.0129	0.0665	0.0055	0.0277	0.1840	0.0260	0.0800	0.0882	0.3473	0.0033	0.1267	0.9111
Seed protein (%)	-0.0481	0.0487	-0.0148	0.0106	-0.0009	-0.0177	-0.0071	0.0076	0.0224	0.0343	0.0333	0.0609	0.3111
Shoot nitrogen (%)	0.0029	-0.0017	0.0220	0.0219	0.0262	0.1592	0.0053	0.0529	0.0534	0.2508	0.0116	0.1754	0.7111

F₂ generation

Path analysis in F₂ indicated that shoot dry weight (0.7051) had maximum direct effect on seed yield followed by 1000 seed weight (0.1164) and shoot nitrogen (0.1042) at genotypic level, whereas shoot dry weight (0.9195) followed by plant height (0.1104) were found to have maximum direct on seed yield phenotypically (Tables 4.66 and 4.67). Days to 50% flowering (-0.026 and -0.0211) and pod length (-0.0180 and 0.0943) had negative direct effect, both genotypically and phenotypically, while, branches per plant (-0.0184), number of clusters per plant (-0.0323) and seeds per pod (-0.0358) had negative direct effect on seed yield only at phenotypic level. Shoot nitrogen, number of clusters per plant, number of pods per plant, 1000 seed weight showed indirect effects on seed yield through shoot dry weight.

...

Table 4.56: Genotypic path coefficient analysis for grain yield in F₂ generation

	Days to 50% flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Correlation with grain yield
Days to 50% flowering	-0.0226	0.0626	0.0146	-0.0005	0.0025	0.0221	0.0008	-0.0004	-0.0063	0.2205	0.0063	0.0184	0.3752	
Days to maturity	-0.0194	0.0730	0.0109	-0.0007	0.0019	0.0248	0.0015	-0.0008	-0.0178	0.1782	0.0046	0.0094	0.2879	
Plant height (cm)	-0.0081	0.0196	0.0408	-0.0019	0.0236	0.0318	-0.0093	0.0026	0.0686	0.3994	0.0013	0.0359	0.6136	
Number of branches per plant	0.0032	-0.0135	-0.0210	-0.0056	0.0036	-0.0112	0.0106	-0.0029	-0.0434	-0.2448	0.0035	-0.0111	-0.3425	
Number of clusters per plant	-0.0012	0.0029	0.0195	-0.0004	0.0494	0.0426	-0.0002	0.0014	0.0408	0.4001	-0.0026	0.0564	0.7387	
Number of pods per plant	-0.0074	0.0269	0.0193	-0.0006	0.0312	0.0674	-0.0015	0.0015	0.0428	0.4874	-0.0036	0.0596	0.9548	
Pod length (cm)	0.0010	-0.0061	0.0210	-0.0021	0.0005	0.0057	-0.0180	0.0038	0.0922	0.3257	0.0004	0.0205	0.761	
Seeds per pod	0.0015	-0.0108	0.0193	-0.0019	0.0131	0.0181	-0.0126	0.0054	0.0933	0.4714	0.0010	0.0535	0.6660	
1000 seed weight (g)	0.0012	-0.0112	0.0241	-0.0014	0.0173	0.0248	-0.0143	0.0044	0.1164	0.5211	0.0030	0.0607	0.7776	
Shoot dry weight (g)	-0.0071	0.0185	0.0231	-0.0013	0.0280	0.0466	-0.0083	0.0036	0.0860	0.7051	0.0031	0.0883	0.9937	
Seed protein (%)	-0.0073	0.0174	0.0026	0.0007	-0.0067	-0.0126	-0.0003	0.0003	0.0178	0.1107	0.0195	0.0226	0.4814	
Shoot nitrogen (%)	-0.0040	0.0066	0.0141	-0.0004	0.0267	0.0385	-0.0036	0.0028	0.0678	0.5977	0.0042	0.1042	0.9213	

Table 4.67: Phenotypic path coefficient analysis for grain yield in F₂ generation

	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Correla- tion with grain yield
Days to 50% flowering	-0.0211	0.0606	0.0447	0.0032	-0.0068	0.0030	0.0055	0.0039	-0.0051	0.3260	0.0143	0.0072	0.3180
Days to maturity	-0.0205	0.0006	0.0320	0.0034	-0.0034	0.0026	0.0075	0.0055	-0.0113	0.2525	0.0155	0.0035	0.2659
Plant height (cm)	-0.0085	0.0002	0.1104	0.0088	-0.0205	0.0030	-0.0515	-0.0174	0.0449	0.5284	0.0039	0.0119	0.6042
Number of branches per plant	0.0041	-0.0001	-0.0593	-0.0184	0.0034	-0.0009	0.0609	0.0205	-0.0279	-0.3349	0.0128	-0.0046	-0.3325
Number of clusters per plant	-0.0044	0.0001	0.0699	0.0017	-0.0323	0.0029	-0.0029	-0.0125	0.0328	0.8467	0.0133	0.0235	0.6087
Number of pods per plant	-0.0144	0.0004	0.0764	0.0033	-0.0215	0.0044	0.0168	-0.0134	0.0369	0.8504	0.0227	0.0205	0.7228
Pod length (cm)	0.0012	-0.0001	0.0603	0.0106	-0.0010	0.0008	-0.0943	-0.0269	0.0615	0.4570	-0.0006	0.0073	0.4447
Seeds per pod	0.0025	-0.0001	0.0537	0.0094	-0.0113	0.0018	-0.0708	-0.0051	0.0613	0.6325	0.0051	0.0181	0.6512
1000 seed weight (g)	0.0015	-0.0001	0.0679	0.0063	-0.0145	0.0022	-0.0793	-0.0300	0.0731	0.7152	0.0136	0.0218	0.7461
Shoot dry weight (g)	-0.0075	0.0002	0.0635	0.0060	-0.0227	0.0040	-0.0469	-0.0246	0.0569	0.9195	0.0161	0.0293	0.9857
Seed protein (%)	-0.0084	0.0003	0.0119	-0.0059	-0.0120	0.0028	0.0015	-0.0051	0.0278	0.4144	0.0358	0.0183	0.1647
Shoot nitrogen (%)	-0.0047	0.0001	0.0413	0.0024	-0.0237	0.0036	-0.0221	-0.0203	0.0499	0.8425	0.0205	0.0319	0.8547

DISCUSSION

CHAPTER V

DISCUSSION

5.1 STUDIES ON GENETIC VARIABILITY AND DIVERGENCE

5.1. Genetic variability

The success of any breeding programme depends on the quantum of genetic variability available for exploitation. Though a number of workers have reported variability for yield and yield component traits, it has not reflected in the improvement of mungbean yields.

Most of the quantitative characters are highly influenced by the environment, the phenotypic variability among genotypes does not give a true indication of the heritable and non heritable components of variation. To get an idea of genetic variability in the existing genotypes with respect to quantitative characters it becomes necessary to study them under an array of distinguishable environments.

Burton (1952) and Vishnuswarup and Chagle (1962) indicates that genetic variability together with the heritability estimates would give a better idea on the amount of advance expected from selection. The magnitude of heritable variability is the most important aspect of the genetic constitution of the breeding material, which has a close relationship on its response to selection (Panse, 1957).

The 49 lines of mungbean studied in the present investigation differed statistically for all the characters studied under all the three environments (Kharif, Rabi uplands and Rabi Rice fallows). The results obtained on variability, heritability and genetic advance in per cent of mean are discussed below.

The number of days taken to 50% flowering were less in rabi uplands and kharif compared to rabi rice fallows. The range of variation and PCV and GCV was high for this trait under kharif season, which is considered to be the best environment. In general, the coefficients of variability were low for this trait. Paramasivan and Rajasekharan (1980), Medhi et al. (1980) and Ramana and Singh (1987) also reported low variability for this trait. High heritability coupled with low genetic advance over mean was recorded for days to 50% flowering in the present study. Singh and Malhotra (1970b) and Medhi et al. (1980), Singh and Pathak (1986) and Ramana and Singh (1987) also reported high h^2 coupled with low GA over mean for this trait in Mungbean. High h^2 coupled with low genetic advance indicates the importance of non additive gene action in the inheritance of this trait.

Number of days taken to mature were less in kharif and rabi upland while it was more in rabi rice fallows. The range of variation, PCV and GCV were also

low for this trait. Low variability for days to maturity in mungbean was also reported by Bhargava et al. (1966), Veeraswamy et al. (1973), Joshi and Kabaria (1973), Medhi et al. (1980), Rosaiah et al. (1987) and Ramana and Singh (1987). High h^2 coupled with low GA over mean was recorded in all the environments. High h^2 along with low genetic advance over mean was reported in mungbean for this trait by Singh and Malhotra (1970b), Joshi and Kabaria (1973), Medhi et al. (1980) and Shah and Patel (1981). High h^2 along with low genetic advance indicates the operation of non additive gene action for this trait.

The plant height was high in the kharif and low in both the rabi uplands and rabi rice fallows. The range of variation was found to be moderately high for this trait in all the environments. High heritability coupled with moderate to high GA was recorded over the environments. Wider variability for plant height was also reported by Bhargava et al. (1966), Chowdhury et al. (1971), Giriraj (1973), Veeraswamy et al. (1973), Medhi et al. (1980), Shah and Patel (1981), Siddaraju (1987). Ramana and Singh (1987), Pandey ^{et al} (1988) and Tickoo et al. (1988). Empig et al. (1970) obtained higher heritability coupled with high genetic advance for this trait. High h^2 coupled high GA over mean indicates the operation of additive gene action for this

trait, selection is therefore useful in improving this trait.

The range of variation and the mean number of branches per plant were high in rabi uplands, while the PCV and GCV were high in kharif season. In general the coefficients of variation were high under all the environments. Bhargava et al. (1966), Gupta and Singh (1969), Krishnaswamy et al. (1973), Veeraswamy et al. (1973), Sandhu et al. (1979), Siddaraju (1987), Pandey et al. (1988) and Sandhu et al. (1988) also reported wider variability for this trait. High h^2 coupled with high GA over mean was obtained for this trait in the present study. Similar results for this trait were also reported by Krishnaswamy et al. (1973) and Siddaraju (1987) in mungbean. High h^2 coupled with high GA over mean indicates the operation of additive gene action for this trait (Johnson et al. (1957).

The number of clusters per plant and the range of variation were high in Kharif season. PCV and GCV estimates were moderate to high for this trait under all the environments. Bhargava et al. (1966), Singh and Malhotra (1970b), Veeraswamy et al. (1973), Sandhu et al. (1979), Pandey et al. (1979), Singh and Sharma (1981), Siddaraju (1987), Rosaiah et al. (1987), Ramana and Singh (1987), and Sandhu et al. (1988) reported high variability for this trait. High heritability coupled

with high genetic advance was recorded for this trait in the present study is in confirmity with the results of other workers (Bhargava et al., 1966; Veeraswamy et al., 1971; Veeraswamy et al., 1973; Medhi et al., 1980; Shah and Patel, 1981; Siddaraju, 1987; Rosaiah et al., 1987 and Ramana and Singh, 1987) in mungbean. High h^2 coupled with high GA over mean indicates the additive gene action for this trait.

The number of pods per plant and the range of variation was high in Kharif season. Moderate to higher values of PCV and GCV were recorded in all the environments. Moderate to high variability for this trait in mungbean was also reported by Bhargava et al. (1966), Gupta and Singh (1969), Singh and Malhotra (1970b), Chowdhury et al. (1971), Veeraswamy et al. (1973), Giriraj (1973), Sandhu et al. (1979), Misra and Sahu (1985), Siddaraju (1987), Rosaiah et al. (1987), Ramana and Singh (1987), Pandey et al. (1988), Sandhu et al. (1988), and Tickoo et al. (1988). High h^2 coupled with high GA over mean obtained in the present study is inconfirmity with the findings of Bhargava et al. (1966), Giriraj (1973), Paramasivan and Rajasekharan (1980), Shah and Patel (1981), Parida (1982), Chowdhury (1982), Parida and Singh (1984), Singh and Pathak (1986), Siddaraju (1987), Rosaiah et al. (1987), and Ramana and Singh (1987). High h^2 coupled with high GA

over mean indicates the operation of additive gene action for number of pods per plant.

The pod length was found to be high in Kharif whereas, the range of variation was high in rabi uplands. Phenotypic and genotypic coefficients of variation were low for this trait under all the environments. Bhargava et al. (1960), Singh and Malhotra (1970b), Chowdhury et al. (1971), and Rosaiah et al. (1987) also observed low variability for this trait. High h^2 coupled with low GA over mean was recorded for this trait under all the environments studied, indicates the operation of non additive gene action. Similar results in Mungbean were also reported by Gupta and Singh (1969), Giriraj (1973), Veeraswamy et al. (1973), Pokle and Nomulwar (1975) and Chowdhury et al. (1982).

The number of seeds per pod and the range of variation were found to be high in Kharif followed by rabi rice follows. Both PCV and GCV were low in all the environments. Low variability for pod length in mungbean was also reported by Singh and Malhotra (1970b), Giriraj (1973), Joshi and Kabaria (1973), Chowdhury et al. (1982), Rosaiah et al. (1987) and Ramana and Singh (1987). High heritability along with low genetic advance over mean was recorded under all the environments indicating that this trait is controlled by

non additive gene action. Similar results were also reported by Giriraj (1973), Chowdhury et al. (1982) and Parida (1982).

Seed weight was found to be high in kharif and rabi uplands. Whereas, the range of variation for this trait was high in rabi under uplands and rice fallows. PCV and GCV were low for this trait under all the environments. Bhargava et al. (1966), Chowdhury et al. (1982) and Ramana and Singh (1987) also reported low coefficients of variability for 1000 seed weight. High h^2 coupled with low GA over mean was recorded for this trait under all the environments. Gupta and Singh (1969), Chowdhury et al. (1982), Ramana and Singh (1987) also reported high h^2 along with low GA over mean, indicating the operation of non-additive gene action.

Mean shoot dry weight and the range of variation was high in kharif compared to other two seasons. Estimates of PCV, GCV, h^2 and GA in per cent over mean were high in all the environments revealing the importance of additive gene action governing this trait.

Seed protein content was found to be high in rabi uplands and kharif seasons, whereas, the range of variation was high under kharif and rabi rice fallows.

Coefficients of variability were low in all the environments. Low range of variability for this trait in mungbean was also reported by Yohe and Poehlman (1972), Tsou and Hsu (1978), Rosaiah *et al.* (1987) and Sandhu *et al.* (1988). High h^2 coupled with low GA over mean were recorded for this trait in all the environments indicating that seed protein content is under the control of non additive gene action. Relatively low degree of genetic variance observed in this study for this trait suggests the need for introgression of favourable genes from wider genetic resources or from related species.

Shoot nitrogen content was found to be high in the rabi uplands and kharif seasons, while the range of variation was high in rabi rice fallows. Estimates of PCV and GCV were low for shoot nitrogen under all the environments. Similar results were also reported by Rosaiah (1987) in Mungbean. High h^2 coupled with moderate to high estimates of GA over mean was recorded for this trait in all the environments indicating predominance of additive genes responsible for the inheritance of shoot nitrogen content.

Grain yield was found to be high in kharif season followed by rabi uplands. The range of variation for this trait was high in kharif and rabi rice fallows. Estimates of PCV and GCV were high under

all the environments. High variability for seed yield was also reported by Bhargava et al. (1966), Singh and Malhotra (1970b), Chowdhury et al. (1971), Giriraj (1973), Veeraswamy et al. (1973), Sandhu et al. (1979), Virmani et al. (1983), Siddaraju (1987), Pandey et al. (1988), Ramana and Singh (1988) and Tickoo et al. (1988). High h^2 along with high GA over mean recorded for this trait under all environments indicates the predominance of additive gene action. High h^2 coupled with high GA as per cent of mean for this trait was also reported by Giriraj (1973), Rosaiah et al. (1987) and Ramana and Singh (1987) in Mungbean.

High h^2 estimates obtained for all the morphological as well as yield attributes in the present investigation indicates that not much selection pressure has been applied on this crop. In the present study, plant height, number of branches per plant, shoot dry weight and grain yield per plant showed high variability, whereas moderately high variability was recorded for number of clusters per plant and number of pods per plant. Low variability was recorded for days to 50% flowering, days to maturity, pod length, number of seeds per pod,, 1000 seed weight, seed protein and shoot nitrogen.

Broad sense h^2 estimates include dominance, epistasis as well as additive genetic variance and the

estimates so obtained should be considered as maximum heritabilities (Paul, 1978). If the h^2 is mainly due to the additive gene effects, then only it is associated with high genetic gain as in case of plant height, number of branches per plant, number of clusters per plant, number of pods per plant, shoot dry weight, shoot nitrogen and grain yield per plant. Whereas, if the h^2 is mainly due to non additive effects (dominance, epistasis) the genetic advance will be low as in the case of days to 50% flowering, days to maturity, pod length, number of seeds per pod, 1000 seed weight and seed protein. Traits with high h^2 estimates together with high genetic gain can be improved through selection.

5.1.2 Genetic Divergence

Genetic variability, is the basic requirement for making progress in crop breeding. Therefore, in any breeding programme inclusion of genetically diverse parents is essential in order to create new reservoirs of variability which, in turn would help in recombining genes from diverse sources. The multivariate analysis using Mahalanobis D^2 statistic provides a useful statistical method for measuring the amount of genetic diversity in a given population in respect of characters considered together and to classify the genotypes on the basis of genetic diversity.

The magnitude of genotype environment interactions is a linear function of environments. Any genetical investigation on the quantitative characters become complicated when more than one environment is considered because of the change in the environments. Hence, it is essential to repeat the experiment in more than one environment.

Forty nine cultivars of Mungbean consisting of advanced breeding lines derived from selection, hybridization (single, double and multiple crosses) and mutation breeding along with the released and the lines of coordinated varietal trials were studied under three environments, viz., kharif (E1), rabi uplands (E2) and rabi Rice fallows (E3). The data collected on 13 quantitative traits were subjected to multivariate analysis and the genetic diversity was estimated. The magnitude of D^2 values suggested that there was considerable diversity in the material studied. Gupta and Singh (1969), Ramanujam et al. (1974), Malhotra et al. (1974), and Tawar et al. (1988) also estimated wide genetic diversity in the material studied by them on Mungbean. Maximum D^2 values were estimated under E2 Rabi upland (E2) followed by kharif (E1) and Rabi Rice Fallows (E3).

The lowest D^2 values between LGG 417 and LGG 418; LGG 418 and LGG 422 and LGG 127 and LGG 402 were

recorded under kharif, Rabi uplands and Rabi Rice Fallows, respectively, indicating that these genotypes are very close to each other. While maximum D^2 values were recorded between LGG 421 and LGG 434 in kharif, LGG 402 and LGG 424 in rabi uplands and LGG 426 and Pusa 111 in rabi rice fallows suggesting that these genotypes are genetically divergent.

Intra cluster distance values were low in cluster III under kharif (E1). Cluster I under Rabi uplands (E2) and Cluster I in Rabi rice fallows (E3) indicating that the genotypes included in these clusters were genetically identical. Inter cluster distances were minimum between cluster IX and XII (E1), cluster X and XI (E2) and cluster II and V (E3) indicating a close relationship and similar magnitude for most of the characters of the genotypes in these clusters. Maximum inter cluster distances observed between cluster VIII and X (E1); cluster I and VIII (E2); cluster V and VII (E3) indicating wider genetic diversity between the genotypes included in these groups. Clusters showing maximum intercluster distance were also considerably diverse for the various traits studied including yield. Selecting parents from such clusters for hybridization programmes would help to achieve novel recombinants.

Inter cluster distances were low under E1 between clusters I and XIV; I and II; II and IV and I

and IV which comprises the genotypes developed from Andhra Pradesh (LGG series), Punjab (ML 267, ML 26-10-3), Delhi (Pusa 103 and Pusa 111) and from Uttar Pradesh (UPM 79-3-4). Similarly under E2 between cluster I and II; I and III; II and III; I and V and II and IV and under E3 between cluster I and VII, I and VIII the inter cluster distances were low.

The 49 genotypes studied were grouped into 14, 11 and 8 different clusters under E1, E2 and E3, respectively. The genotypes varied in clustering pattern in different environments, thereby emphasizing the importance of multienvironment studies for quantitative assessment of genetic diversity. High magnitudes of genotype x environment interactions were observed for all the characters studied as evident from differential clustering pattern of genotypes in different environments. Variation in clustering pattern in different environments was also indicated in Mungbean by Rao and Suryawanshi (1988).

Seven genotypes in E1 (LGG 426, LGG 429, LGG 434, LGG 443, $DC_1 \times DC_2 - 4$ SB - SB, $DC_1 \times DC_2 - 1$ SB - SB and ML 26-10-3) three genotypes in E2 (LGG 441, LGG 450 and Pusa 103) and five genotypes in E3 (LGG 441, LGG 446, LGG 449, Pusa 111 and Pusa 103) could not be clubbed with any other clusters as they maintained separate identity from others. The genotypes

constituting single cluster possessed either high or low mean performance for one or more characters. Clusters which consisted of more number of genotypes showed average performance, as none of the characters occupied extreme positions, viz., cluster II in E1, cluster III in E2 and cluster I in E3.

Genotypes did not show any tendency to cluster with their parents under E1 and E2 where they were randomly distributed, while under E3 both parents (LGG 127, ML 26-10-3, Pusa 105, ML 267, ML 33 and UPM 79-3-4) and their derivatives (LGG 402, LGG 403, LGG 410, LGG 419, LGG 421 etc.) were included in the same cluster (I). Gupta and Singh (1969) reported that parentage had definite effect on clustering pattern in Mungbean. Deviations in the present study (kharif and rabi) may be attributed to the differences in environmental conditions and to the extent of genetic recombinations created through breeding programmes.

The results of the present study did not establish any relationship between geographical diversity and genetic diversity. The explanation for grouping of genotypes from the same geographical origin into different groups was due to the wide genetic divergence in features which might have resulted on account of genetic drift and selection in different environments. Murty et al. (1965) in Brassica; Murty

and Anand (1966) in Linseed; Arunachalam and Jawahar Ram (1969) in Sorghum; Singh and Bains (1968) in Cotton; Gupta and Singh (1969) and Malhotra et al. (1974) in Mungbean; Jaya Prakash et al. (1974) in Cowpea and Shanmugam (1983) in Urdbean also indicated that geographic diversity need not be associated with genetic diversity and the direction of selection practiced in different geographical locations determines the genetic divergence.

Information regarding the factors responsible for differentiation at intra and inter cluster levels can be obtained by comparing the cluster means of the characters studied. Cluster XII, IX, VII and II in E1; cluster IX, VI, XI and III under E2; cluster V, II, VI and III in E3 recorded higher means for most of the characters studied. There appears to be some overlapping between constituents of clusters and for character means. Selection of the parents based on genetic diversity in any hybridization programme, yield potential of the cluster should also be considered. Based on per se performance and inter cluster distances five genotypes viz. LGG 421, LGG 429, LGG 442, LGG 487-3 and $DC_1 \times DC_2 - 4SB - SB$ in E1 (kharif), six genotypes viz. LGG 410, LGG 418, LGG 424, LGG 437, LGG 441 and LGG 442 in E2 (Rabi uplands) and three genotypes viz. LGG 424, LGG 446 and LGG 449 were found to be genetically

diverse from others. Crossing among these genotypes based on combining ability studies may provide better chances for getting transgressive segregants.

5.2 GENOTYPE X ENVIRONMENT INTERACTION STUDIES

Mungbean is cultivated alround the year under different cropping systems in Andhra Pradesh. Though, mainly a kharif season crop, it is also cultivated in Rabi (both uplands and rice fallows) and in summer seasons. It is a short day plant and is sensitive to the environmental factors such as, day length, temperature, soil moisture regimes, soil structure and soil fertility and cropping system under which it is grown.

A desirable variety should possess stability in performance besides high yield. Stability, depends on the ability of a genotype to hold certain morphological and physiological attributes steadily or allowing them to vary, resulting in a predictable genotype x environment interaction for yield.

A population which can adjust its phenotypic state in response to environmental fluctuations and gives high and stable economic return can be termed well buffered (Singh and Singh, 1980). Grafius (1956) emphasized the need to study the individual yield components, rather than yield per se to understand the

stability and to predict the effects of the environments. Testing of genotypes under different environments differing in unpredictable variations is an accepted approach for selecting stable genotypes (Eberhart and Russell, 1966).

The yielding ability and response to environmental changes are the two independent attributes of a genotype and are governed by separate gene systems (Finlay and Wilkinson, 1963; Bucio Alanis et al., 1969; Bains, 1976; Verma et al., 1978 and Gupta, 1984). Mungbean breeders are interested in developing varieties that are stable in performance in different environments. A precise knowledge on the nature and magnitude of genotype x environment interactions is important in understanding the stability in yield of a particular variety before it is recommended for general cultivation. High genotype x environment interactions are likely to restrict a variety's adaptability.

In the present investigation, 20 diverse mungbean genotypes were studied under six environments (in three seasons viz., kharif, rabi uplands and rabi rice fallows over two years) to understand the stability of yield components in relation to the stability of yield; nature and magnitude of genotype x environment interactions; to identify the genotypes of wider

adaptability and specific adaptability and to study character associations and the direct and indirect affects of yield components on grain yield under different environments. The results obtained are discussed under the following sections taking the objectives into consideration.

1. Performance of mungbean genotypes under different environments
2. Genotype x environment interactions
3. Stability in performance of mungbean genotypes and
4. Character associations and path coefficient analysis under different environments.

5.2.1 Mean performance of mungbean genotypes under different environments

The results indicated that none of the genotype was consistently superior for all the characters under all the environments. A linear relation existed between mean performance and environmental index for the characters studied. Kharif, 1988 (E4) was found to be the most favourable high yielding environment, which is characterised by uniformly good rainfall throughout the crop period. Most of the yield component traits viz., plant height, number of clusters per plant, number of

Pods per plant, shoot dry weight and grain yield recorded better values under this environment. Kharif, 1987 (E1) characterised by intermittent moisture stress resulted in low mean values for all the characters.

The environment, Rabi uplands 1987-88 (E2) was characterised by receding soil moisture conditions and shorter day length favoured early flowering and early maturity of the genotypes. Rabi uplands 1988-89 (E5) though similar to Rabi uplands 1987-88 (E2), a supplementary irrigation was provided to save the crop was found superior for number of pods per plant, 1000 seed weight and seed protein per cent.

Rabi rice fallows 1987-88 and 1988-89 were observed to be poor environments. Cultivation in rice fallows is characterised by zero tillage, high soil moisture in the initial stages of establishment, no fertilizer application and weed management is given which ultimately resulted in low mean values for plant height, number of branches, number of pods, number of clusters, shoot dry weight, shoot nitrogen, seed protein and grain yield.

Mungbean genotypes flowered and matured early under rabi uplands (E2 and E5) condition compared to rabi rice uplands (E3 and E6) or kharif (E1 and E4). The low temperatures during the crop period and high

soil moisture in the initial stages were responsible for slow initial growth which ultimately took longer time to reach maturity under rice fallows. Two genotypes viz., D12/333 and MH 309 were early to flower and mature under all the environments.

Plant height, number of branches, number of clusters, number of pods per plant, number of seeds per pod, shoot dry weight and grain yield were superior under the favourable environment Kharif, 1988 while they were low under poor environments Rabi rice fallows, 1987-88 and 88-89. Whereas, pod length, 1000 seed weight, shoot nitrogen, and seed protein were high under rabi uplands. Gopal Singh and Singh (1982) also reported higher seed weight, shoot nitrogen and seed protein during rabi season. Higher temperatures at pod development stage might have favoured translocation of vegetative nitrogen to reproductive parts and accumulation of soluble nitrogen and thereby resulting in increased protein content of the seed. Amirshahi and Tavakoli (1970) in mungbean and Yadav and Tomer (1985) in urdbean also reported variation of protein content due to environment (sowing dates).

Though, the expression of the yield component traits in general, was superior during kharif seasons, the genotypes, appears to be specific in their adaptation to different environments. Genotypes LGG

407, LGG 410, PDM 84-145, PDM 54 and ML 267 were found to be superior for grain yield in kharif and rabi uplands (E1, E2, E4 and E5). While LGG 450 and Pusa 105 were superior in rabi rice fallows (E3 and E6).

Cultivation of pulses in rice fallows is an unique system in Krishna-Godavari deltas of Andhra Pradesh. In this system the mungbean seed is sown in the standing rice crop, 2-3 days before its harvest. There is no land preparation, intercultivation, weeding, manuring and irrigation. The crop, thus sown survives entirely on residual moisture and fertility. The varietal adaptability to this system are highly location specific and the varieties developed elsewhere are not suitable. In the present study two varieties LGG 450 and Pusa 105 appears to be suitable for rice fallows by virtue of their better performance over other genotypes in respect of plant height, number of pods per plant, shoot dry weight and finally grain yield.

The genotypes which recorded consistantly superior performance over environments for various characters are summarised below.

S.No.	Character	Genotype
1.	Days to 50% flowering	D12/333, MH 309, K 851
2.	Days to maturity	D12/333, MH 309
3.	Plant height (cm)	LGG 407, LGG 410, ML 131
4.	Number of branches per plant	None
5.	Number of clusters per plant	LGG 407, LGG 410, LGG 450 Pusa 84-145, Pusa 105
6.	Number of pods per plant	LGG 407, LGG 410, LGG 450
7.	Pod length (cm)	LGG 426, K 851
8.	Number of seeds per pod	K 851
9.	1000 seed weight (g)	LGG 407, LGG 410, PDM 84-145 Pusa 105, K 851, PDM 54
10.	Shoot dry weight (g)	LGG 407, LGG 410
11.	Seed protein (%)	None
12.	Shoot nitrogen (%)	LGG 407, LGG 410, LGG 450
11.	Grain yield (g)	LGG 407, LGG 410, LGG 450 PDM 84-145, K 851, Pusa 105

5.2.2 Genotype x environment interactions

Genotype x environment interactions are known to interfere with the evaluation of genotypes and thus reduce the progress of selection in plant breeding programmes as the genetic nature of a genotype is masked (Comstock and Moll, 1964; Singh et al., 1943b). Therefore, estimation of the nature and magnitude of genotype x environment interaction has been emphasized

in a variety of crops. Stable genotypes interact less with the environment in which they are grown. Stable genotypes helps to achieve predictable stable production through the wider or specific adaptability of the genotypes (Allard and Bradshaw, 1964).

Joint regression analysis is commonly followed for studying genotype x environment interactions (Yates and Cochran, 1938). In different analyses, either the regression coefficient (Finlay and Wilkinson, 1963) or the regression coefficient along with the deviation from regression (Eberhart and Russell, 1966) are used as parameters of stability.

Environment wise analysis of variance revealed that significant differences existed among the genotypes under each environment for all the characters. The pooled analysis also revealed significant differences among the genotypes for all the characters indicating that real differences existed. The environmental (linear) effects were also significant for all the traits suggesting that the environments selected differed in influencing the performance of genotypes. Most of the variance was due to environment for all the characters. Such profound influence of environment on the grain yield of mungbean was also reported by Imrie and Shanmugasundaram (1987) and Ramana and Singh (1987).

Highly significant genotype x environment interactions were recorded for all the characters indicating that the genotypes had divergent linear response to environmental changes. Significant G x E interactions in mungbean were also reported by Joshi (1969 and 1972), Tomar et al. (1972), Ramanujan (1975), Chowdhury and Haque (1977), Verma et al. (1978), Imrie et al. (1981), Imrie and Butleer (1982), Reddy and Sreeramulu (1984) and Naresh Mehrotra and Chowdhury (1986).

Partitioning of genotype x environment interactions indicated that a substantial portion of variation was linear for all the characters except for days to 50 per cent flowering and days to maturity. Similar significant genotypes x environment (linear) interaction in mungbean were reported for number of pods per plant and 1000 seed weight by Ramanujam (1975); for plant height, Imrie et al. (1982), for pods per plant and grain yield by Reddy and Sreeramulu (1984); for number of seeds per pod and grain yield by Pandey et al. (1988); for plant height, number of clusters per plant, number of pods per plant, number of seeds per pod, 1000 seed weight and grain yield by Ramana and Singh (1987).

Pooled deviations were significant when tested against pooled error for all the characters suggesting that deviation from linear regression also contributed

substantially towards the differences in stability of genotypes. A major portion of genotype x environment interactions was attributable to linear component (predictable) except for days to 50% flowering and days to maturity, where pooled deviations (unpredictable) contributed more to the total interaction for days to flowering and maturity. The prediction of $g \times e$ interactions has become possible based on the relative magnitudes of linear and non linear components using linear regression analysis. The non linear component of genotype x environment interaction was predominant in case of days to 50 per cent flowering and days to maturity. Hence, prediction for these traits can be made by taking the stability parameters of individual genotypes into consideration.

5.2.3 Stability performance of mungbean genotypes

Both linear regression (b_i) and deviations from regression ($S^2 d_i$) components of genotype x environment interaction should be considered along with mean while judging the phenotypic stability of a genotype (Eberhart and Russell, 1966). Linear regression(b_i) is a measure of response of a variety, while deviations around regressions measures the stability of genotypes, with the lowest standard deviations being the most stable and vice versa. Therefore, a stable genotypes should have desired mean performance, unit regression coefficient

and low deviations from regressions. Taking these parameters into consideration the results obtained are discussed.

Two genotypes viz., D12/333 and K 851 are considered to be stable genotypes for days to 50 per cent flowering as they recorded average response ($b_i=1$) and non significant deviations from linear regressions over environments along with desired mean (Low mean). Pusa 105 with high mean and average response also showed predictable performance and hence it is considered to be stable variety for late flowering. MUG 125 with mean value around general mean, below average response ($b_i < 1$) and non significant deviations is considered to be stable under unfavourable environments. Whereas PDM 84-155 with above average value for days to 50 per cent flowering showed below average response but its performance is predictable for late flowering under poor environments. Four genotypes viz., MH 309, ML 267, LGG 127 and PDM 54 with desired mean, showed average response but unpredictable in their performance, LGG 407, LGG 410, ML 26-10-3 and UPM 79-4-12 with high mean and average response are unpredictable. Five genotypes LGG 403, PS 16, ML 131, LGG 426 and UPM 83-10 with average mean showed below average response and unpredictable performance. Two genotypes PDM 84-145 and

LGG 450 with mean value around general mean and average response also unstable.

Only one genotype PS 16 with high mean and average response showed predictable performance and hence, is considered to be stable for late maturity. Four genotypes LGG 407, LGG 410, PDM 84-145, Pusa 105, ML 26-10-3 and UPM79-4-12 with high mean and above average response were found to be unpredictable. LGG 403 and ML 131 with high mean and below average response were found to be unstable. Three genotypes, MUG 125, LGG 127 and LGG 426 with mean value around general mean showed unpredictable and below average response. PDM 54, K 851 and ML 267 which are early in maturity and average response while PDM 84-155, UPM 83-10, LGG 450 with average response and high mean were unpredictable in their behaviour. Two genotypes MH 309 and D12/333 with low mean and below average response showed unpredictable performance.

One genotype UPM 79-4-12 with high mean and average response was found to be stable for plant height over environments. Six genotypes viz., LGG 407, LGG 410, LGG 450, Pusa 105, ML 26-103 and PS 16 with high mean recorded above average response but unpredictable in behaviour and hence may be suitable to better environments. Eight genotypes MUG 125, LGG 426, PDM 84-145, PDM 84--155, D12/333, MH 309, LGG 127 and ML 267

with low mean, below average response showed unpredictable performance. K 851 and UPM 83-10 with low mean and above average response were considered to be unstable. PDM 54 with low plant height showed average response but unstable. LGG 403 with average plant height and ML 131 with higher plant height showed below average response have predictable performance under poor environments.

PS 16 has recorded mean value around general mean and average response with predictable performance was considered to be a stable genotype for the number of branches per plant. Eight genotypes LGG 403, LGG 407, LGG 410, MH 309, LGG 127, PDM 54, K 851 and UPM 79-4-12 with low number of branches per plant and below average response showed unpredictable behaviour. MUG 125, LGG 426, D12/333 and ML 267 with desirable mean and above average response were unstable. Three genotypes PDM 84-145, PDM 84-155 and Pusa 105 with high mean showed average response and LGG 450 with high mean and below average response were found to be unpredictable. Whereas, ML 26-10-3 and ML 131 with low mean and average response were unstable in performance over environments. The genotype UPM 83-10 with low mean and above average response was found to be unstable.

The genotype ML 267 with more number of clusters and average response showed predictable

performance. Hence, it is considered as a stable genotype for number of clusters per plant. The genotypes LGG 407, LGG 410, Pusa 105 with more number of clusters showed below average response and predictable performance. Hence, they are expected to perform better under poor environments for this trait. MUG 125 with high mean, above average response and predictable performance is considered suitable under favourable environments. Whereas, LGG 403 with high mean and below average performance was found to be unpredictable in performance. PDM 54, PDM 84-145, PDM 84-155, D 12/333, MH 309 and PS 16 with low mean, below average response were unstable. K 851, PDM 84-155 and UPM 83-10 with low mean showed above average response were also unstable. LGG 450 with high mean and average response showed unpredictable performance. ML 26-10-3, UPM 79-4-12 and ML 131 with low mean, average response and LGG 426 with low mean and below average response showed predictable behaviour.

Two genotypes, MUG 125 and PDM 84-145 with mean value around general mean, unit regression coefficient average response showed predictable performance for number of pods over environments and hence, they may be considered as stable genotypes. Five genotypes LGG 407, LGG 410, LGG 426, PDM 54 and ML 267 with high mean for number of pods per plant showed above average response

and predictable performance may be expected to perform better under favourable environments. LGG 450 and Pusa 105 with high mean, below average response showed predictable performance and hence, they were considered to be stable and suitable under unfavourable environments. LGG 403 with high mean and average response was found unstable.

Two genotypes ML 131 and K 851 recorded high mean and average response with predictable performance for pod length. Hence these two genotypes were considered to be stable genotypes for pod length. LGG 426, PDM 84-145, PDM 84-155 and Pusa 105 with high mean showed below average response and unstable. PS 16 with high mean and above average response was also unstable. Four genotypes viz., ML 26-10-3, PDM 54, ML 267 and UPM 79-4-12 with low mean and high response showed unpredictable performance. Whereas, LGG 407, LGG 410, D 12/333, MH 309 and LGG 127 with low mean and low response showed instability for pod length over environments. Three genotypes viz., MUG 125, LGG 450 and LGG 403 with low mean and unpredictable performance showed average response.

PDM 84-145 and K 851 with high mean for number of seeds per pod showed average response and predictable behaviour under different environments. Hence, these genotypes were considered to be stable for this trait.

ML 131 with high mean and stability in performance showed high response indicating its suitability to favourable environments. Genotypes, UPM 83-10, PS 16, LGG 407 and LGG 426 with high mean recorded above average response but their performance over environments was unpredictable. Whereas, LGG 127 with high mean and low response was unstable. Two genotypes, MH 309 and PDM 54 with low mean and high response were also unpredictable. The genotypes viz., UPM 79-4-12, ML 267, ML 26-10-3, MUG 125, LGG 403 and PDM 84-155 have recorded low mean and below average response were unpredictable in performance. Whereas, LGG 410, Pusa 105 and LGG 450 with low mean and low response showed predictable performance.

The genotypes, LGG 410, LGG 450 and PDM 54 with high mean showed average response ($b_i=1$) and predictable performance ($S^2_d = 0$) over a range of environments for 1000 seed weight. Hence, they may be considered as stable genotypes for this trait. K 851, LGG 407 and Pusa 105 with high mean and above average response ($b_i > 1$) were unstable. Two genotypes, PDM 84-155 and PDM 84-1 with high mean, low response ($b_i < 1$) and predictable performance were suitable to poor environments. Four genotypes viz., MH 309, ML 131, ML 26-10-3 and ML 267 with low mean and low response were also stable under poor environments. While, MUG 125, LGG 426, LGG 403, D

12/333 and UPM 79-4-12 with low mean, high response were found suitable for favourable environments. The genotypes, LGG 127 and PS 16 with low mean showed above average response were unpredictable, while UPM 83-10 with low mean and below average response was unstable.

Four genotypes K 851, ML 267, PDM 54 and PDM 84-145 with high mean showed average response and predictable performance for shoot dry weight indicating their adaptability to all the environments. Two genotypes LGG 407 and LGG 426 with high mean and high response were predictable in their behaviour for shoot dry weight and hence were suitable for favourable environments. LGG 450 and Pusa 105 with high mean value showed low response and were stable in their performance under rice fallows. The genotype, LGG 410 had high mean above average response was found to be unpredictable. LGG 127 and UPM 79-4-12 with low mean showed below average response and predictable performance. PDM 84-155 and ML 131 showed above average response with low mean and predictable behaviour. Whereas, MUG 125, PS 16, LGG 403, MH 309, D 12/333, UPM 83-10 and ML 26-10-3 with low response and low mean were found to be predictable in their performance.

Four genotypes LGG 403, LGG 407, LGG 426, LGG 410 and ML 267 with high mean showed above average response for shoot nitrogen and their performance was predictable. Hence, these genotypes are suitable to favourable environments. LGG 450, Pusa 105 and PDM 84-145 with high mean and low response were unpredictable. PS 16, UPM 83-10, UPM 79-4-12, D 12/333, LGG 127, PDM 54 and ML 26-10-3 with high response and predictable behaviour recorded low mean performance. The genotype MUG 125 recorded low mean, average response and unpredictable performance. MH 309 with low mean showed above average response but its performance was unpredictable. Two genotypes, viz., PDM 84-155 and ML 131 with low mean showed below average response and unpredictable performance. K 851 with high mean, above average response was unpredictable in its performance.

Four genotypes, LGG 426, LGG 403, LGG 407 and LGG 410 with high mean showed low response and predictable performance for seed protein content indicating their suitability to low yielding environments. MUG 125, D 12/333 and Pusa 105 with high mean and average response were found to be predictable and hence they may be considered stable over the environments. PDM 84-145 had low mean and below average response and unpredictable behaviour. While UPM 83-10 and UPM 79-4-12 with low mean had high response and

unpredictable behaviour. Genotypes, ML 131, LGG 127, PDM 84-155, PS 16 and ML 267 with low mean and above average response showed predictable behaviour. Whereas, LGG 450, K 851 and ML 26-10-3 with low mean and low response showed predictable behaviour. PDM 54 and MH 309 with low mean and average response showed predictable behaviour over environments.

Four genotypes viz., PDM 84-145, ML 267, K 851 and PDM 54 with high mean yield showed average response for yield were also predictable in their performance, hence they may be considered as stable high yielding genotypes. LGG 410 and ML 131 showed high mean and above average response with predictable performance, hence they were suitable for better environments. LGG 403 and Pusa 105 with high mean performance showed low response and predictable behaviour, hence they may be considered suitable for unfavourable environments. LGG 407 and LGG 426 recorded high yield and better response were however, unpredictable in their performance. The genotype, LGG 450 with high mean and below average response was found to be unpredictable. However, PS 16, UPM 83-10 and ML 26-10-3 expressed low response and predictable performance but with low yield levels. Whereas, PDM 84-155 with low mean under favourable environment was also predictable in its performance. LGG 127 and UPM 79-4-12 with low mean and below average response were unpredictable genotypes.

5.2.3 Association among the stability parameters

The relationship between mean and stability parameters of yield and yield components will help to select a trait phenotypically stable in performance. A positive correlation of mean values of plant height, number of branches per plant, number of pods per plant, number of seeds per pod, shoot dry weight and grain yield with linear regression (bi) in the present investigation suggests that genotypes with high mean performance for these characters were responsive to favourable environments. Therefore, mean values for the above characters may be used in order to judge the stability of the genotypes. In the present study LGG 407, LGG 410, LGG 403 and LGG 426 which recorded high mean values for yield and yield components were all unstable. Similar indications were reported by Finlay and Wilkinson (1963), Perkins and Jinks (1963 and 1968), Fripp and Caten (1973), Ramanujam and Gupta (1974), Sanghi and Kandalakar (1983) and Jain and Pandya (1988).

Non significant association between deviations from linear regression with mean performance and linear regression coefficients in case of days to 50% flowering, days to maturity, plant height, number of branches, number of clusters, number of pods per plant, seeds per pod, 1000 seed weight, shoot dry weight and grain yield indicated that non-linear component of genotype x environment interactions are independent of the mean performance and linear regression coefficients for these characters. It was also suggested the involvement of different genetic systems in the control of stability parameters. Similar observations of the non-association of deviations from regressions with mean and regression coefficients were also reported by Eberhart and Russell (1966), Westernman (1971), Paroda and Hayes (1971), and Yadav and Kumar (1985). Significant correlation between non sensitivity coefficients (deviations from regression) and mean performance in case of pod length; deviations from regression and linear regression in case of shoot nitrogen and seed protein indicates the possible presence of linkage among stability of these characters.

Stability of grain yield of genotype is determined to a considerable extent by the relative stabilities of different component characters (Luthra et al., 1977). Grafius (1956) also suggested that selection

for stable genotypes could be augmented through selection for stability in yield components.

In the present study four genotypes, PDM 54, K 851, PDM 84-145 and ML 267 were identified as stable genotypes for grain yield. In addition to stability for grain yield PDM-54 also possessed stability for 1000 seed weight and shoot dry weight; K 851 for days to 50% flowering, pod length, number of seeds per pod, shoot dry weight; PDM 84-145 for number of pods per plant, number of seeds per pod and shoot dry weight and ML 267 for number of clusters per plant and shoot dry weight. Thus, stable genotypes for grain yield were always found to be associated with stable performance of shoot dry weight in the present study. The mungbean genotypes evaluated under six environments for environmental sensitivity in the present study could be grouped into three categories for grain yield.

Group-1. High yielding and stable under all environments-K 851, PDM 54, PDM 84-145 and ML 267.

Group-2 High yielding and suitable to favourable environments-LGG 407, LGG 410, LGG 426 and ML 131.

Group-3 High yielding and suitable under unfavourable environments LGG-403, LGG 450, Pusa 105.

5.3 COMBINING ABILITY STUDIES

Mungbean improvement in the past has been through selection and most of the present day cultivars are pureline selections from local strains. Recently the attention has been given to develop high yielding varieties through hybridization. However, the technique used is far from satisfactory, as most of the hybridization is between random parents and chance selections are made among the segregating populations. Breeding programmes based on the sound knowledge, on the genetic nature of yield and yield component traits, only can help to achieve the target quickly and reliably.

Combining ability analysis helps the Mungbean breeder in selecting the parents and the breeding method to be employed to improve a particular trait, as it provides the information on the genetic nature of the characters.

General combining ability refers to the average performance of a line in a series of hybrid combinations and is attributable to additive (fixable) gene action, while the specific combining ability refers to the deviation in the performance of a cross than what would be expected on the basis of the average performance of the lines involved and is attributable primarily to dominant, over-dominant and epistatic effects of genes

(non additive). The non additive gene action is mostly non fixable and often brings about in phenotypes that are not attainable under normal additive gene action.

The sum of the additive gene effects produced by the genes lacking dominance (additive genes) and by the additive contribution of genes along with dominance or epistatic effects is the additive component of genetic variance. Additive gene action tends to produce a normal phenotypic distribution. The non additive gene actions results from dominance, epistasis and various other interactions effects which are non fixable. The ratio of 'gca' variance and 'sca' variance provides an estimate of the predominance of additive gene effects or the non additive effects.

Heterosis is defined as the increased vigour of F_1 over parental mean and is a genetic expression of beneficial effects of hybridization. Heterosis could be used as an indicative of the crosses which are likely to throw productive transgressive segregants (Singh and Jain, 1979). The extent of heterosis and inbreeding depression would also give an idea of the genetic control of a particular character.

In the present study, line x tester analysis was employed using four lines (Pusa 105, ML 267, K 851 and D 12/333) and five testers (PDM 54, MH 309, LGG

410, LGG 450 and UPM 79-4-12). The resulted 20 F_1 s and F_2 s along with their parents were studied during kharif 1988-89 with the following objectives.

1. To identify parents with high 'gca' and crosses with good 'sca' effects for grain yield and yield components.
2. To understand the nature of gene action governing the yield and yield component traits of Mungbean.
3. To study the extent of heterosis and inbreeding depression for various characters studied.
4. To study character association and path analysis for yield and yield components in segregating and non-segregating populations.

The mean squares due to lines and testers were significant for all the characters both in F_1 and F_2 generations indicating wider variability among the lines and testers used. Mean squares due to lines were greater than testers for plant height, number of branches per plant, pod length, number of seeds per pod, and 1000 seed weight while for the other traits the mean squares in testers were greater than the lines indicating the wider variability for the respective characters among the lines and testers.

Line x tester interaction mean sum of squares were significant for days to 50% flowering, branches per plant, pod length, number of seeds per pod and grain yield in F_1 generation while they were significant for plant height, number of branches per plant, pod length, number of seeds per pod, shoot dry weight, shoot nitrogen and grain yield in F_2 generation suggesting that 'gca' of parents was largely responsible for the performance of the hybrids for other traits, namely, days to maturity, number of clusters, number of pods per plant, 1000 seed weight and seed protein (%). This indicated the importance of utilising good general combiners for these characters in a breeding programme designed to raise yield levels (Hormuzdi and More, 1989). The heterosis, degree of dominance, heritability and estimates of combining ability variance components for yield and yield components are discussed character wise.

5.3.1 Days to 50% flowering

Heterosis for days to 50% flowering in the crosses was in the desirable direction over mid parent. The average heterosis for this trait was -3.03 over mid parent and 0.77 over better parent. Highest heterosis (-2.26%) was recorded by K 851/PDM-54. Significant heterosis for days to 50% flowering was reported in mungbean by Singh and Jain (1970), Swindell and Poehlman

(1976) and Ramanujam (1978) in desirable direction only ³¹⁶
over the mid parent.

Estimates of 'sca' variance were greater than 'gca' variance in F_1 while the variances due to 'gca' were greater than 'sca' variance in F_2 generation. The change in the estimates of variances from F_1 and F_2 generation indicates the importance of both additive and non additive gene action governing this trait. Higher variance due to 'gca' in F_2 may be more reliable due to the availability of large number of recombinants indicating predominance of additive gene action over non additive genes. Predominance of additive gene action in the inheritance of days to 50% flowering was reported in mungbean by Singh and Singh (1974 b), Tiwari and Ramanujam (1974), Yohe and Poehlman (1975), Godhani et al. (1978), Ramanujam (1978), Raghuram Reddy (1980), Nagaraja Rao and Mahaboaob Ali (1983), Patel (1983), Rao et al. (1984) and Patel (1989).

The importance of non-additive gene action for this trait was also reported by Murty et al. (1976). Swindell and Poehlman (1978) and Deshmukh and Manjare (1980). However, there was no indication of the importance of both the types of gene action governing this trait.

Higher magnitudes of the degree of dominance both in F_1 (0.774) and F_2 (0.670) also indicated the importance of both additive as well as non-additive gene action (dominant) in the present study.

The heritability estimates were found to be moderate in F_1 (40.96) and F_2 (33.81) which is in agreement with the results of other workers for this trait.

Among the lines D 12/333 and K 851 and testers PDM 54, MH 309 and LGG 450 recorded significant 'gca' effects and per se performance in desirable direction and thus are good general combiners. The crosses which recorded significant negative 'sca' effects in F_1 (ML 267 x UPM 79-4-12 and Pusa 105 x LGG 410) and in F_2 (Pusa 105 x LGG 450) involved High x Low, Low x Low and Low x High general combiners indicating the importance of both additive and non additive gene actions governing this trait. Negative and significant 'sca' effects for days to 50% flowering in the crosses indicates the possibility of improvement for earliness. This trait can be improved by using a breeding method which mop up both additive and non additive gene effects. Recurrent selection and diallel selective mating which provides opportunity for selection, recombination and accumulation of the desired genes, may help in the exploitation of fixable as well as non fixable types of

gene effects. In fact, a judicious approach of integrating classical approach of pedigree and bulk method with recurrent selection or diallel selective mating may be fruitful to develop novel types.

5.3.2 Days to maturity

The cross Pusa 105 x LGG 410 recorded negative heterosis over mid parent (-3.50) and better parent (-2.05). The average heterosis over mid and better parent for this trait was low (-1.52 and 0.57). Significant negative heterosis for days to maturity was also reported by Singh and Jain (1970), Swindell and Poehlman (1976) and Ramanjuam (1978).

Variances due to 'gca' were higher than 'sca' for this trait both in F_1 and F_2 generations indicating predominantly additive gene action governing this trait. This finding is further confirmed by the higher estimates of heritability (62.17 and 59.55) and low degree of dominance in F_1 and F_2 generations respectively. Predominance of additive gene action for this trait was also reported by Murty et al. (1976), Gupta et al. (1978); Ramanujam (1978); Raghuram Reddy (1980); Patel (1983); Rao et al. (1984) and Malik and Singh (1986) and Patel (1988) in mungbean.

Among the lines, D 12/333 and K 851 and testers PDM 54, MH 309 and LGG 450 were found to be good general combiners for early maturity. Two crosses in F_1 generation, Pusa 105 x LGG 410 (L x L) and K 851 x UPM 79-4-12 (H x L) and two crosses in F_2 generation, K 851 x LGG 450 (H x H) and ML 267 x MH 309 (L x H) recorded significant 'sca' effects for early maturity. The cross D 12/333 x LGG 450 (H x H) with early in maturity recorded significant 'sca' effects in F_1 and F_2 , indicating the predominance of additive gene effects. Therefore, the crosses K 851 x LGG 450 and D 12/333 x LGG 450 may be handled through pedigree selection for isolation of early maturing lines.

5.3.3 Plant height (cm)

Positive heterosis for plant height was recorded in five crosses over mid parent. The cross D 12/333 x LGG 450 recorded maximum heterosis of 4.84 per cent over mid parent. The average heterosis was low (0.25 per cent) over mid parent indicating the absence of heterosis in general, for plant height in the present study. This was further confirmed by the non significant parent versus crosses interactions. Positive heterosis for plant height over mid parent only was also reported in mungbean by Bhatnagar and Singh (1964), Swindell and Poehlman (1976), and Reddy and Sree Ramulu (1982).

Variance due to 'gca' was greater than 'sca' variance both in F_1 and F_2 generations indicating predominance of additive gene action for this trait. High heritability (84.26 and 85.91) estimates and low degree of dominance (0.116 and 0.295) in F_1 and F_2 generations respectively also supports the importance of additive gene action. The mean plant height of the crosses was close to the mid parent values, also indicating the absence of dominance. Yohe and Poehlman (1975), Gupta et al. (1978), Deshmukh and Manjare (1980), Nagaraja Rao and Mahaboob Ali (1983), Singh (1984) and Malik and Singh (1986) reported the importance of additive gene action for this trait. However, the importance of non-additive gene action for this trait was also reported by Ahuja (1980), Lal et al. (1982), Raghu Ram Reddy and Sree Ramulu (1982), Ahuja and Chowdhury (1984) and Patel (1989). The importance of both additive and non additive gene action for this character was reported by Swindell and Poehlman (1978), Malik and Singh (1983) and Rao et al. (1984) in Mungbean.

Lines, Pusa 105 and K 851, and testers LGG 410 and LGG 450 were found to be the good general combiners for this trait. In F_1 generation D12/333 x MH 309 (L x L) recorded significant 'sca' effects but recorded low mean for plant height. The discrepancy between the

performance and its respective 'sca' effects may be explained on the basis of the two estimates is a comparison of an absolute value and a relative value. Absolute value (Performance of the crosses) being similar, the relative values ('sca' effects) would increase with a decrease in the performance (Mean of the two parents) of the population. Three crosses viz. ML 267 x MH 309, K 851 x LGG 410 and D 12/333 x PDM 54 showed significant negative 'sca' effects in F_2 generation. This may be due to the presence of unfavourable gene combinations.

5.3.4 Number of branches per plant

Maximum heterosis of 98.2 and 94.69 per cent was recorded over mid and better parent, respectively for this character by ML 267 x PDM 54. The average heterosis over mid and better parent was 18.89 and 9.42 per cent, indicating the operation of non additive gene action governing this trait. Seven crosses recorded significant and positive heterosis over better parent while 13 crosses showed significant positive heterosis over mid parent. Heterosis for the number of branches over mid parent was also reported by Bhatnagar and Singh (1964), Singh and Singh (1972), Singh and Singh (1974), Swindell and Poehlman (1976), Malhotra et al. (1983) and Ilyas Ahmad Malik et al. (1988) while over

better parent only Misra et al. (1970) reported positive heterosis.

Estimates of 'sca' variance were greater than 'gca' variance both in F_1 and F_2 generations, also indicated the predominance of non additive gene action for this character. Low values of heritability (8.95 and 6.25) and high degree of dominance (3.00 and 3.67) in F_1 and F_2 respectively, supports the predominance of non additive gene action governing this trait.

Importance of non additive gene action in the inheritance of the number of branches obtained in the present study in conformity with the results of Sen and Murty (1960), Swindell and Poehlman (1976), Murty et al. (1976), Godhani et al. (1978), Singh (1980) and Patel (1988) in mungbean. However, importance of additive gene action (Nagaraja Rao and Mahboob Ali ,1983; and Malik and Singh ,1986) and additive and non additive gene action (Singh and Singh, 1972 and Singh 1972) was also reported for number of branches in mungbean.

Among the female parents D 12/333 and testers PDM 54 were found to be good general combiners for the number of branches. Five crosses viz. ML 267 x PDM 54 (L x H), D 12/333 x UPM 79-4-12 (H x L), ML 267 x MH 309 (L x L), K 851 x LGG 410 (L x L) and Pusa 105 x LGG 450 (L x L) showed significant 'sca' effects both in F_1 and F_2 .

Of the five, ML 267 x PDM 54 and D 12/333 x UPM 79-4-12 recorded significant 'sca' effects coupled with high mean and positive heterosis over better parent. Since, non-additive gene action was found predominant, breeding method involving selection, inter mating the selections and reselection may help to improve this trait.

5.3.5 Number of Clusters per plant

The cross combination, Pusa 105 x LGG 410 recorded maximum heterosis over the better parent. The average heterosis however, was low over better parent indicating predominance of additive gene action. Four crosses over mid parent and two crosses over better parent recorded significant positive heterosis for this trait. Heterosis for the number of clusters over mid parent was reported by Singh and Jain (1970), Gupta et al. (1978), Raghu Ram Reddy (1980). Malhotra et al. (1983) while, Ilyas Ahmad Malik et al. (1988) reported heterosis for the this trait over better parent.

Estimates of 'gca' variances were higher than 'sca' variances in both the generations for the number of clusters per plant also indicating the predominance of additive gene action for this trait. Singh (1974), Raghuram Reddy (1980) and Malik and Singh (1986) reported the importance of additive gene action in the inheritance of this trait while the importance of non

additive gene action (Sen and Murty, 1960; Singh and Singh, 1972; Singh and Singh 1974 b; Murthy et al. 1976; Godhani et al., 1978 and Natarajan et al., 1978) and additive as well as non additive gene action (Deshmukh and Manjare, 1980 and Malhotra et al., 1980) was also reported in mungbean for the number of clusters per plant. Low heritability estimates in both the generations suggests that this character is highly influenced by the environment and evident from the estimation of high error variance. The degree of dominance was medium to low in F_1 and F_2 generations, respectively.

The lines Pusa 105 and ML 267 and testers LGG 410 and LGG 450 with high mean performance were the good general combiners for this trait. The crosses, pusa 105 x LGG 410 (H x H) and Pusa 105 x LGG 450 (H x H) with higher mean and significant positive values of the heterosis showed significant 'sca' effects indicating operation of additive gene action. Simple selection through pedigree breeding may lead to the improvement of the number of clusters.

5.3.6 Number of pods per plant

The cross combinations, K 851 x LGG 410 (21.20 per cent) and K 851 x UPM 79-4-12 (14.76 per cent) showed heterosis over the mid parent for number of

Pods. The average heterosis over mid and better parent were 10.4 and 1.09 per cent, respectively. Though, six crosses recorded positive heterosis over mid parent, only three crosses viz., K 851 x LGG 410, K 851 x LGG 450 and D12/333 x LGG 450 recorded significant positive heterosis over the better parent. Heterosis for the number of pods over mid parent, was also reported by Singh and Jain (1970), Misra et al. (1970), Singh and Singh (1974a), Swindell and Poehlman (1976), Gupta et al. (1978), Raghu Ram Reddy (1980) and Malhotra et al. (1983), while over better parent Bhatnagar and Singh (1964) and Ilyas Ahmad Malik et al. (1988) reported positive heterosis in Mungbean.

Estimates of variance due to 'gca' were higher than 'sca' variance both in F_1 and F_2 generations indicating the predominance of additive gene action for this trait. Heritability was low for this trait in both F_1 and F_2 generations. The low estimates of degree of dominance in both the generations (0.707 and 0.680) also supports the predominance of additive gene action for the trait. Importance of additive gene action for the number of pods was also reported by Singh and Singh (1971 a, b); Singh and Singh (1974); Raghuram Reddy (1980) and Malik and Singh (1986), Whereas, Singh (1972); Singh and Singh (1974 a), Singh et al. (1975); Gupta et al. (1978); Deshmukh and Manjare (1980) and

Nagaraja Rao and Mahboob Ali (1983) reported the importance of non additive gene actions, while, Malhotra et al. (1980) and Rao et al. (1984) reported both additive and non additive gene actions governing this trait.

Female parent Pusa 105 and male parents PDM 54, LGG 410 and LGG 450 were found to be good general combiners with high mean performance. Five crosses viz: Pusa 105 x LGG 410 (H x H), Pusa 105 x LGG 450 (H x H), ML 267 x LGG 450 (L x H), K 851 x LGG 410 (H x H), K 851 x LGG 450 (H x H) both in F_1 and F_2 generations, D 12/333 x LGG 450 (L x H) and Pusa 105 x MH 309 (H x L) in F_2 only recorded significantly higher number of pods and 'sca' effects. The crosses Pusa 105 x LGG 410, Pusa 105 x LGG 450, K 851 x LGG 410, K 851 x LGG 450, involved (H x H) general combiners and therefore may be handled through pedigree breeding for increasing the number of pods. In general, hybridization followed by selection may lead to the improvement of this trait as the additive gene action is predominant.

5.3.7 Pod length (cm)

Maximum heterosis over mid and better parent was recorded by the cross Pusa 105 x PDM 54 for pod length. Seventeen crosses recorded positive heterosis over mid parent, however, only nine crosses showed

heterosis over the better parent. The average heterosis was low over mid parent indicating that the superiority of the crosses for pod length was mainly due to additive gene action. Heterosis for pod length over mid parent (Singh and Jain, 1970) while over better parent (Bhatnagar and Singh, 1964) was reported in mungbean.

Variances due to 'gca' were greater than 'sca' variances indicating the predominance of additive gene action governing this trait. Singh and Jain (1971 b); Chowdhary et al. (1971), Raghuram Reddy (1980), Patel (1983) and Patel et al. (1988) also reported the predominance of additive gene action for pod length. However, both additive and non additive gene actions (Singh et al., 1972; Singh and Singh, 1974a; Murty et al., 1976; Godhani et al., 1978; Luthra et al., 1979; and Malhotra et al., (1983) and non additive gene actions (Pokle and Nomulwar, 1975; Gupta et al., 1978; Nagaraja Rao and Mahboob Ali, 1983 and Lal et al., 1982) were also reported in Mungbean.

High heritability estimates (66.66 and 44.44%) in F_1 and F_2 generations, were recorded. The degree of dominance (0.517 and 0.707) was moderate in both F_1 and F_2 generations indicating the importance of dominant effects also.

Among the lines, K 851 and testers, PDM 54 were found to be good general combiners for pod length. Only the cross, D12/333 x MH 309 (L x L) in F_1 generation recorded significant 'sca' effects however, showed lower pod length, which might be due to unfavourable gene combinations. Improvement in pod length can be achieved through pedigree breeding, as additive gene effects are predominant in governing this trait.

5.3.8 Number of seeds per pod

ML 267 x PDM 54 showed maximum heterosis over mid parent. The average heterosis over mid and better parent was low indicating the additive gene action. Though, 11 crosses showed heterosis over mid parent, none of the crosses recorded heterosis over the better parent. Heterosis for the number of seeds per pod over mid parent was reported by Singh and Singh (1972), Singh and Singh (1974), Swindell and Poehlman (1976), Ramanujam (1978) and Ilyas Ahmad Malik *et al.* (1988) in mungbean. Heterosis over better parent was also reported by Bhatnagar and Singh (1964) and Singh and Jain (1970).

Estimates of variances due to 'gca' were higher than 'sca' variance for number of seeds per pod both in F_1 and F_2 generations indicating the predominance of additive gene action. Heritability estimates were high

in both F_1 (63.64) and F_2 (58.46) generations coupled with moderate levels of degree of dominance in F_1 (0.617) and F_2 (0.688) suggests the importance of dominant or epistatic effects of gene action to a certain extent.

The results obtained in the present study on the inheritance of seeds per pod is in agreement with the result of by Singh and Singh (1971a; 1974b); Tiwari and Ramanujam (1974); Luthra et al. (1977) and Malhotra et al. (1986) in mungbean. Singh et al. (1970); Singh and Singh (1975a); Yohe and Poehlman (1975); Swindell and Poehlman (1976); Ramanujam (1978) and Raghuram Reddy (1980) reported importance of additive gene action whereas, Sen and Murty (1960); Murty et al. (1976); Godhani et al. (1978); Gupta et al. (1978); Deshmukh and Manjare (1980), Nagaraja Rao and Mahboob Ali (1983), Patel (1983) and Patel et al. (1988) reported predominance of non additive gene actions for number of seeds per pod in Mungbean.

Line K 851, and testers LGG 410 and LGG 450, with high per se performance were found to be good general combiners for the number of seeds per pod. Two crosses viz. ML 267 x UPM 79-4-12 (L x L) and K 851 x MH 309 (H x L) in F_1 and three crosses viz. ML 267 x LGG 450 (L x H), K 851 x PDM 54 (H x L) and D 12/333 x MH 309 (L x L) showed significant 'sca' effects in F_2

generation. All the crosses showing good 'sca' effect involved H x L or L x L general combiners, indicates the operation of predominantly non additive gene action for this trait. The inconsistency of 'sca' effects in F_1 and F_2 generations may be due to the presence of complementary epistatic interactions or dominance x dominance interactions (Gupta and Ramanujam, 1974) governing this trait.

The number of seeds per pod can be improved by choosing breeding methods such as Diallel selective mating or Biparental matings and advancing through pedigree method later as both additive and non-additive gene actions operate in the inheritance of this trait.

5.3.9 1000 seed weight (g)

A maximum heterosis for 1000 seed weight was recorded by Pusa 105 x LGG 410 over the better parent. The average heterosis over mid parent and better parent indicated that the influence of non additive gene action is less for this trait. Heterosis for 1000 seed weight in mungbean with varying degrees was also reported by Bhatnagar and Singh (1964) and Misra et al. (1970) over mid and better parent, respectively.

Estimates of variances due to 'gca' were higher than 'sca' in both F_1 and F_2 generations, indicating the predominance of additive gene action in the inheritance

of this trait. These are in agreement with Singh and Jain (1971 a); Singh and Singh (1972); Singh and Singh (1974 a); Yohe and Poehlman (1975); Ramanujam (1978); Raghuram Reddy (1980); Deshmukh and Manjare (1980); Singh (1984), Malik and Singh (1986), Patel (1983) and Patel et al. (1988). Predominance of non additive (Sen and Murty, 1960; Tiwari and Ramanujam, 1974; Murty et al., 1976; Godhani et al., 1978 and Malik and Singh, 1986) and both additive and non additive gene actions (Singh and Singh, 1974 and 1974 b and Imrie et al., 1988) was also reported for seed weight in mungbean.

Heritability estimates for this trait were high both in F_1 and F_2 while, the degree of dominance estimates were moderate in F_1 to low in F_2 also supports the importance of additive gene actions.

The lines, Pusa 105 and K 851 and testers PDM 54, LGG 410 and LGG 450 were found to be good general combiners coupled with high per se performance both in F_1 and F_2 . Four crosses in F_1 and three in F_2 recorded significant 'sca' effects. The crosses which recorded significant 'sca' effects for the trait involved H x H (K 851 x LGG 450, Pusa 105 x LGG 450 in F_1 and K 851 x PDM 54 in F_2) or H x L or L x H (Pusa 105 x UPM 79-4-12 ML 267 x PDM 54 in F_1 and F_2 or even L x L (D 12/333 x MH 309 in F_2) general combiners indicating the operation of additive, as well as non additive gene actions. The

significant 'sca' combination which involved H x H general combiners viz. K 851 x PDM 54, Pusa 105 x LGG 450 and K 851 x LGG 450 may be advanced through pedigree breeding for selecting superior lines for higher seed weight. However, from the over all analysis of 1000 seed weight it is evident that the additive gene actions though predominant, non-additive gene actions also play an important role. Hence, the breeding method should be judiciously planned by intermating F_2 's (biparental crosses) followed by single plant selections for improving the seed size in Mungbean.

The higher 'sca' effects recorded in F_2 compared to F_1 generation in the present study may be due to the genetic diversity present among the parents or due to presence of repulsion phase linkage and linkage disequilibrium in early generations (Gill et al., 1974).

5.3.10 Shoot dry weight (g)

Maximum heterosis over mid parent and over better parent was recorded in K 851 x LGG 450 for shoot dry weight. Eight crosses recorded heterosis over better parent, whereas, 14 crosses recorded positive heterosis over mid parent.

Variances due to 'gca' were higher than 'sca' variances indicating the predominance of additive gene

action in the inheritance of shoot dry weight. High heritability (64.73 and 67.56) and low degree of dominance (0.355 and 0.549) in F_1 and F_2 generations recorded also indicates the predominance of additive gene action in the inheritance of this trait.

Among the female parents, Pusa 105 and K 851, and male parents, LGG 410 and LGG 450 were found to be good general combiners. Five crosses in F_1 viz., ML 267 x MH 309 (L x L), ML 267 x LGG 410 (L x H), K 851 x PDM 54 (H x L), D 12/333 x PDM 54 (L x L) and D 12/333 x LGG 410 (L x H) and five crosses in F_2 viz., Pusa 105 x PDM 54 (H x H), Pusa 105 x MH 309 (H x L), Pusa 105 x LGG 450 (H x H), ML 267 x LGG 450 (L x H) and D 12/333 x UPM 79-4-12 (L x L) have recorded significant 'sca' effects. Crosses involving L x L general combiners with significant 'sca' effects did not record high mean for shoot dry weight whereas, crosses involving H x H or L x H combinations with significant 'sca' effects recorded higher mean values for shoot dry weight.

Shoot dry weight can be improved through pedigree method or bulk method of breeding utilizing Pusa 105 x LGG 450 and Pusa 105 x PAM 54 crosses. While other combinations with high 'sca' effects involve H x L or L x L combinations, indicates the importance of both additive and non-additive gene action. Hence,

biparental crosses followed by single plant selection may help to improve this trait.

5.3.11 Seed Protein (%)

Average heterosis for seed protein over mid parent was low indicating the absence of over dominance or epistatic gene actions governing this trait. Maximum heterosis over mid parent was recorded by K 851 x MH 309, whereas, D 12/333 x LGG 410 recorded maximum heterosis over better parent.

Estimates of variance due to 'gca' were higher than 'sca' variance both in F_1 and F_2 generations indicating the predominance of additive gene action. Tiwari and Ramanujam (1976) and Raghuram Reddy (1980) also recorded the importance of additive gene action. However, predominance of non additive gene action (Singh 1973; Wilson et al., 1985 and Tawar and Sudhanshu Jain, 1988) and both additive and non additive gene actions (Singh and Singh 1973 b; Luthra et al., 1977 and Singh, 1984) was also reported in the inheritance of seed protein in Mungbean. Heritability estimates for this trait were low in F_1 and F_2 generations. The degree of dominance was also low both in F_1 and F_2 supports the importance of additive gene action for this character.

Two testers, PDM 54 and LGG 410 were found to be good general combiners for seed protein with high

mean performance. None of the crosses recorded significant 'sca' effects for this trait also indicates the predominance of additive gene action. This trait could be improved through pedigree or bulk method of breeding. However, proper selection methods need to be developed as this trait was found to be highly influenced by environment.

5.3.12 Shoot Nitrogen (%)

The cross K 851 x UPM 79-4-12 recorded maximum heterosis over mid parent and ML 267 x PDM 54 over better parent. Only one cross ML 267 x PDM 54 recorded significant heterosis over better parent though 10 crosses have recorded significant positive heterosis over mid parent. Average heterosis for shoot nitrogen over mid and better parents was low for this trait.

Estimates of both 'gca' and 'sca' variances were equal both in F_1 and F_2 generations for this trait indicating the importance of both additive and non additive gene action. The heritability estimates were low and the degree of dominance was high both in F_1 and F_2 also supports the importance of both additive and non-additive gene actions.

The test crosses LGG 410 both in F_1 and F_2 , whereas, Pusa 105 and LGG 450 in F_1 generation only, were found to be good general combiners. Two crosses viz., ML 267

x LGG 450 and K 851 x MH 309 recorded significant 'sca' effects involving L x H and L x L general combiners indicated the predominance of non additive gene action in these combinations for this trait. Hence, breeding methods involving cyclic hybridizations (Recurrent selection or diallel selective mating) may be employed to improve this trait.

5.3.13 Grain yield per plant (g)

Maximum heterosis for grain yield per plant over mid parent and over better parent was recorded by K 851 x LGG 450. Only six crosses showed positive heterosis for grain yield over better parent, though 17 crosses showed heterosis over mid parent. Heterosis for grain yield over mid parent in mungbean was reported by Singh and Singh (1972); Singh (1974a); Singh and Singh (1974a); Gupta et al. (1978); Sree Kumar and Abraham (1978); Raghu Ram Reddy (1980); Malhotra et al. (1980) and Quah et al. (1983) whereas Bhatnagar and Singh (1964); Singh and Singh (1970); Misra et al. (1970); Krishna Rao and Nagur (1979); Imrie et al. (1988) and Ilyas Ahmad Malik et al. (1988) reported heterosis over the better parent. The crosses, pusa 105 x PDM 54, pusa 105 x LGG 410, pusa 105 x LGG 450, K 851 x LGG 410, K 851 x LGG 450 recorded significant heterosis for grain yield coupled with high mean values. These crosses also recorded heterosis for important yield component traits

like the number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, 1000 seed weight and shoot dry weight.

Estimates of 'gca' variance were greater than 'sca' variance for this trait both in F_1 and F_2 generations indicating the predominance of additive gene action. High heritability estimates and the low degree of dominance recorded both in F_1 and F_2 also favoured the predominance of additive gene action. This is in agreement with the results of Yohe and Poehlman (1975), Tiwari and Ramanujam (1976), Ahuja (1980), Raghu Ram Reddy (1980), Singh (1984) and Malik and Singh (1986). However, predominance of non additive gene action (Singh and Singh, 1972; Singh and Singh, 1974; Tiwari and Ramanujam, 1974; Singh et al., 1975; Murty et al., 1976; Gupta et al., 1978; Krishna Rao and Nagur, 1979; Deshmukh and Manjare, 1980 and Basaeeruddin and Nagur, 1981) and both additive and non additive gene actions (Singh and Jain, 1971; Singh and Singh, 1974b; Luthra et al., 1977; Rao et al., 1984; Ahuja and Chowdhury, 1984; Patel et al., 1988; and Tawar and Sudanshu Jain, 1989) were also reported for grain yield in mungbean.

Among the female parents, pusa 105 and K 851 and male parents LGG 410, PDM 54 and LGG 450 were found to be good general combiners in both the generations. Seven crosses viz., pusa 105 x PDM 54 (HxH), pusa 105 x

LGG 410 (HxH), pusa 105 x LGG 450 (HxH), ML 267 x LGG 450 (LxH), K 851 x LGG 410 and K 851 x LGG 450 recorded significant 'sca' effects along with high mean. The significant sca combinations which involved H x H general combiners may be advanced through pedigree method of breeding for improving yield per se. While the crosses ML 267 x LGG 450, ML 267 x LGG 410 which involved L x H combinations may be studied through biparental or diallel selective mating or any other form of recurrent selection in the early generations followed by single plant selections, so as to exploit both additive as well non additive gene actions. Desirable and stable performing transgressive segregants may be realised in these crosses if additive gene system present in the good general combiner and complementary epistatic effect present in the other act in the same direction.

An over view of the results obtained from combining ability analysis reveal that different types of gene actions governing the expression of yield and yield components. These are summarised below :

S.No.	Character	Nature of gene action	Degree of dominance
1.	Days to 50% flowering	Additive and Non-additive	High
2.	Days to maturity	Additive	Low
3.	Plant height (cm)	Additive	Low
4.	Number of branches per plant.	Non-additive	High
5.	Number of clusters per plant	Additive	Low
6.	Number of pods per plant	Additive	Low
7.	Pod length (cm)	Additive and Non-additive	High
8.	Number of seeds per pod	Additive and Non-additive	Moderate
9.	1000 seed weight (g)	Additive	Low
10.	Shoot dry weight (g)	Additive	Low
11.	Seed protein (%)	Additive	Low
12.	Shoot nitrogen (%)	Additive and Non-additive	High
13.	Grain yield (g)	Additive	Low

Grafius (1959) suggested that there cannot be any one gene system for yield per se and that yield is an end product of multiplicative interaction between yield and yield components. Heterosis manifestation for grain yield in the present investigation in pusa 105 x PDM 54, pusa 105 x LGG 410, pusa 105 x LGG 450, ML 267 x LGG 450, K 851 x LGG 410, K 851 x LGG 450, D12/333 x LGG

450 and D12/333 x UPM 79-4-12 is primarily due to complementary combination of two or more of the following component traits viz., number of clusters per plant, number of pods per plant, number of seeds per pod, 1000 seed weight and shoot dry weight; therefore, selections should be made taking these yield components into consideration.

An over all evaluation of 'gca' effects of parents for various characters indicate that among the lines K 851 and pusa 105 and among testers LGG 410, PDM 54 and LGG 450 were found to be good general combiners for most of the yield components including yield. It is also suggestive that parents showing high 'gca' effects for grain yield also showed high 'gca' effects for yield components, whereas, a parent showing high 'gca' effect for component traits is not necessarily be a good general combiner for grain yield. The good general combiners for various traits are given in Table 5-1

5.4 ASSOCIATION ANALYSIS

Yield component characters show associations among themselves and also with yield. Unfavourable associations between the desired attributes under selection may limit genetic advance. Hence, a knowledge on the associations between the yield and yield

Table 5.1: Good general combiners for yield and yield components in mungbean

Parents/ Character	Days to 50% flo- wering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of clusters per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	1000 seed weight (g)	Shoot dry weight (g)	Seed protein (%)	Shoot nitrogen (%)	Grain yield per plant (g)
Lines													

Pusa 105			+		+	+			+	+			+
ML 267					+								
K 851	+	+	+				+	+	+	+			+
D12/333	+	+		+									
Testers													

PDM 54	+	+		+		+	+		+		+		+
MH 309	+	+											
LGG 410			+		+	+		+	+	+	+	+	+
LGG 450			+		+	+		+	+	+			+

+ indicates good general combiner													

components is essential for efficient selection in any crop improvement programme.

Yield is a complex quantitatively inherited character, highly influenced by the environment, hence if the selection is based on yield as a single trait alone improvement will be slow. Whereas, the yield components are less complex in inheritance and influenced by the environment to a lesser extent. Thus, effective improvement in yield may be brought about through selections in yield components (Srivastava et al., 1972). Correlation studies have been reported in mungbean by several workers, but the results reported were conflicting. A more reliable information can be derived by studying the association analysis simultaneously in different environments to identify reliable associations and also by using non segregating (parents and F_1 s) and segregating (F_2 s) populations to understand the changes in association due to recombinants as a result of hybridization.

In the present study, correlation coefficients have been worked out from two experiments, one using 20 genotypes of mungbean grown under six environments and the other, with nine parents, 20 F_1 and 20 F_2 populations of a line x tester programme.

Genotypic correlations, in general were higher than phenotypic correlations. The high genotypic correlations may be due to relative stability of genotypes as majority of them have been subjected to certain amount of selection (Johnson et al., 1959). This also indicates the joint responses in the effects of characters are unidirectional and basically genetic in nature (Acharya et al., 1984).

5.4 ASSOCIATION ANALYSIS UNDER DIFFERENT ENVIRONMENTS

An overall perusal of the genotypic and phenotypic correlations indicated that yield was found to be consistantly positively associated with the number of clusters, number of pods, 1000 seed weight, shoot nitrogen and shoot dry weight under all the environments. These are in broad agreement with the results reported on the association between number of clusters and yield (Singh and Singh, 1970 b; Singh and Malhotra, 1970a; Malhotra et al., 1973 and 1974; Krishnaswamy et al., 1973; Raghuram Reddy, 1980; Boomikumaran and Rathinam, 1980; Thandapani and Sakharam Rao, 1984; Ramana and Singh, 1987 and Raut et al., 1987).

Almost all the workers have indicated that the number of pods per plant had positive association with

grain yield of mungbean. The positive associations of 1000 seed weight with grain yield obtained in the present study is in conformity with results of Malhotra et al., 1968; Gupta and Singh, 1969; Bhaumik and Jha, 1976; Parida, 1982; Chowdhury et al., 1982; Kumari and George, 1985; Rosaiah, 1987; Sandhu et al., 1988 and Xianghuai He et al., 1988 in Mungbean.

Positive association of shoot dry weight with grain yield obtained in the present study is in conformity with the results reported by Arwooth ~~at~~ Lampang et al. (1988) and Natarajan and Palaniswamy (1988). Positive association of shoot dry weight with grain yield suggests that a genotype with fast initial growth to attain a good canopy by anthesis stage may help to achieve higher yields by improving the total dry matter production. Positive association of shoot nitrogen with grain yield was also reported by Thandapani (1985) and Rosaiah (1985) in Mungbean.

Pod length and number of seeds per pod were found to have no association with grain yield under all the environments studied. Similar associations were also reported by Tomar et al. (1973); Shakoor et al. (1979) and Raghuram Reddy (1980) in Mungbean.

Consistently positive correlations recorded between the number of clusters, number of pods, 1000

seed weight, shoot dry weight and shoot nitrogen with grain yield and non significant associations of the pod length and number of seeds per pod with grain yield under all the environments indicated that these associations are consistant and can be relied upon for selection.

Days to 50% flowering and grain yield showed positive correlations with yield only in rabi uplands and were not significant in other environments. Chandel et al. (1973); Joshi and Kabaria, (1973); Malhotra et al. (1973); Giriraj and Vijaya Kumar (1974); Raghuram Reddy (1980) and Liu et al. (1988) have reported positive and significant associations of days to 50% flowering with grain yield. Positive association of days to maturity with grain yield was recorded only in rabi uplands. Singh et al. (1968); Joshi and Kabaria (1973); Gupta et al. (1982) recorded positive association between days to maturity and grain yield whereas, Singh and Malhotra (1970) and Shah and Patel (1981) observed no associations.

Plant height showed significant positive association with grain yield only in rabi uplands (E2) and rabi rice fallows (E3) and no association in other environments, positive association of plant height with grain yield was reported by Giriraj and Vijaya Kumar (1974); Yohe and Pehlman (1975); Upadhya et al. (1980);

Raghuram Reddy (1980); Boomi Kumaran and Rathinam (1981); Liu et al. (1984); Misra and Sahu (1985); Rosaiah (1985) and Sandhu et al., (1988).

Number of branches showed positive correlation with grain yield only in rabi rice fallows (E3) in the present study. Malhotra et al. (1974), Pokle and Patil, (1975), Upadhya et al. (1980), Nagaraja Rao (1981), Shamsuzzaman et al. (1983) have reported positive correlations between branches and grain yield, while, Singh et al. (1975), Singh et al. (1976) and Raut et al. (1988) observed no associations.

Seed protein content showed non significant association with yield in all the environments. Non significant associations of seed protein with grain yield were reported by Raghuram Reddy (1980), Thandapani and Sakharam Rao (1984), Rosaiah (1985), Bhadra et al., (1987) and Sandhu et al. (1988). This has indicated that the independent genetic control of protein content and that improvement in yield coupled with high protein content can be made simultaneously.

The diverse associations recorded in different environments between days to 50% flowering, days to maturity and number of branches with grain yield indicates that their associations are influenced by the

environments and therefore they may not be better/reliable indicators.

Associations among the yield component traits also, some associations were consistent over all the environments, while the others varied with the environment. The details of the consistent and non consistent associations over environments are discussed. Only consistent associations may be taken as better indices in breeding programme.

Days to 50% flowering showed inconsistent associations with days to maturity, plant height, number of branches, number of clusters, number of pods per plant, pod length, number of seeds per pod, 1000 seed weight, shoot nitrogen, shoot dry weight and seed protein over the environments. Days to maturity showed consistently positive associations only with plant height under all the environments, while it showed inconsistent associations with number of pods, number of clusters, number of branches per plant, pod length, seeds per pod, 1000 seed weight, shoot dry weight, seed protein and shoot nitrogen over the environments.

Plant height showed inconsistent associations with branches, number of clusters, number of pods per plant, pod length, number of seeds per pod, 1000 seed

weight, shoot dry weight, seed protein and shoot nitrogen over the environments. Number of branches per plant recorded inconsistant association with number of clusters, number of pods per plant, pod length, number of seeds per pod, 1000 seed weight, shoot dry weight, seed protein and shoot nitrogen over the environments.

Number of clusters per plant showed consistantly positive association with shoot dry weight over environments, while it showed inconsistant associations with number of pods per plant, pod length, number of seeds per pod, 1000 seed weight, seed protein and shoot nitrogen.

Number of pods per plant recorded consistantly positive correlation with shoot dry weight over environments, while it recorded inconsistant associations with pod length, number of seeds per pod, 1000 seed weight, seed protein and shoot nitrogen. Pod length showed consistantly positive associations with number of seeds per pod over environments, while it showed inconsistant associations with 1000 seed weight, shoot dry weight, seed protein and shoot nitrogen. The positive correlation of pod length with number of seeds per pod was reported by Malhotra et al., 1974; Bhaumik and Jha, 1976; Singh et al., 1981; Nagaraja Rao, 1981; Parida and Singh, 1984; Ramana and Singh, 1987 and Sandhu et al., 1988 in mungbean.

1000 seed weight recorded consistantly positive correlations with shoot dry weight and shoot nitrogen over environments, but inconsistant associations with seed protein. Shoot dry weight showed consistantly positive and significant association with seed protein and shoot nitrogen, while seed protein showed the consistantly positive correlation with shoot nitrogen over environments.

5.4.2 Association analysis using different populations

Correlation coefficients of parents, F_1 hybrids and F_2 populations derived from a line x tester programme indicated that plant height, number of clusters, number of pods per plant, number of seeds per pod, 1000 seed weight, shoot dry weight and shoot nitrogen showed positive associations with yield in parents F_1 s and F_2 s.

Days to 50% flowering, pod length and seed protein showed no association with grain yield among the parents and were found to have significant positive associations in F_1 generation. This may be due to the complementation of the favourable gene complexes. Grain yield showed positive association with days to 50% flowering and pod length in F_2 's though it was not significant in parents, indicating that the changed

associations formed between these characters could be due to recombination. Grain yield was found to have a non significant negative correlation with number of branches per plant both in parents and F_1 s and was changed to significantly negative association in F_2 generation may be due new recombinants in the segregating populations.

Among the yield component traits the non-significant association in parents between the character pairs given below became significantly positive in F_1 generation. They are, days to 50% flowering with shoot dry weight, seed protein and shoot nitrogen; days to maturity with seed protein; plant height with shoot nitrogen; number of branches per plant with seeds per pod and 1000 seed weight; number of clusters per plant with seeds per pod and seed protein; number of pods per plant with seeds per pod and 1000 seed weight; pod length with shoot nitrogen; shoot dry weight with seed protein and seed protein with shoot nitrogen may be due to the complementation of favourable genes in F_1 . Similarly, plant height showed significantly negative association with branches in F_1 though it was not significant in parents.

The non significant association in parents between days to 50% flowering and shoot dry weight, days to 50% flowering and seed protein, plant height and pod

length, plant height and shoot nitrogen, branches and number of seeds per pod, clusters per plant and number of seeds per pod, pod length and shoot dry weight, became significantly positive in F_2 . Plant height with number of branches, branches with seeds per pod, shoot dry weight and 1000 seed weight, showed negative association in F_2 generation while they were non significant in parents. Branches showed positive association with the number of pods among parents while it became non significant in F_2 generation. The changes in F_2 compared to the parents might have resulted due to new recombinants in the segregating populations. The undesirable correlations if any, in F_2 may be broken by appropriate biparental matings or mutation breeding or diallel selective matings (Jenson, 1970).

Days to maturity and plant height which showed positive association in F_1 s became non significant in F_2 generation. This change in association may be attributed to the modifications in the linkages as a result of recombination.

5.5 PATH COEFFICIENT ANALYSIS

Correlation simply measures mutual associations without regard to causation, while path coefficient analysis provides an effective means of untangling

direct and indirect causes of association and permits a critical examination of the specific forces acting to produce a given correlation and measures the relative importance of each causal factor.

5.5.1 Path analysis under different environments

Shoot dry weight was found to have maximum direct positive effect on grain yield under all the environments studied. In addition to shoot dry weight; shoot nitrogen and number of pods per plant also exerted direct positive effect to a certain extent under all the environments. Number of seeds per pod exerted direct positive effect on yield in E4, E5 and E6. Shoot dry weight, pods per plant and shoot nitrogen also showed significant positive correlations under all the environments with grain yield.

The direct positive effect of number of pods per plant on grain yield was reported by several workers, in Mungbean Singh et al., 1970; Singh and Malhotra, 1970; Chandel et al., 1973; Malhotra et al., 1974; Pokle and Patil, 1975; Reddy and Krishnaiah, 1977; Rathnaswamy, et al., 1978; Saraswathy et al., 1979; Shakoor et al., 1979; Sandhu et al., 1980; Upadhyia and Singh, 1981; Malik et al., 1982; Guptaa et al., 1982; Khalid et al., 1984; Thulasidas and Rao, 1984; Kumari and George, 1985; Misra and Sahu, 1985; Santhisree, 1985; Khan, 1987; Raju, 1987; and Raut et

al., 1988 ; While Singh et al., 1970; Singh and Malhotra, 1970b; Pokle and Patil, 1975; Reddy and Krishnaiah, 1977; Rathnaswamy et al., 1978; Saraswathy et al., 1979; Sandhu et al., 1980; Gupta et al., 1982; Malik et al., 1982; Vidhyadhar et al., 1984, Chema et al., 1984, Khan, 1987 and Raut et al., 1988 reported direct effect of number of seeds perpod in grain yield.

Number of pods per plant, 1000 seed weight and shoot nitrogen also exerted positive indirect effect on grain yield through shoot dry weight under all the environments in the present study. Number of branches per plant had negative direct effect on yield in all the environments except in rabi rice fallows 1987-88. Therefore shoot dry weight, number of pods per plant, 1000 seed weight and shoot nitrogen may be considered in the selection processes aimed at the improvement of mungbean.

5.6 PATH ANALYSIS WITH DIFFERENT POPULATIONS

Path analysis indicated that shoot dry weight had maximum positive direct effect on grain yield in parents and F_2 populations at genotypic and phenotypic path whereas number of pods per plant showed positive direct effect on grain yield at genotypic level in F_1 s. Number of pods per plant, shoot nitrogen, 1000 seed weight, number of clusters per plant also influenced grain yield indirectly through shoot dry weight in

parents, F_1 's and F_2 's. Plant height, number of clusters per plant, number of seeds per pod and 1000 seed weight had negative direct effect in parents whereas days to 50% flowering in F_1 s and F_2 s and pod length in F_2 showed negative direct effect on yield.

Association analysis in Mungbean indicated that the number of clusters, number of pods, 1000 seed weight, shoot dry weight and shoot nitrogen were found to have positive correlations with grain yield and were consistent over the environments. These yield components also possessed same desirable associations among themselves. Association analysis in different populations (parents, F_1 's and F_2 's) under single environment also indicated the significant and positive associations of number of clusters per plant, number of pods per plant, 1000 seed weight, shoot dry weight, shoot nitrogen with grain yield. Path analysis indicated that shoot dry weight had maximum direct effect on grain yield whereas, number of clusters per plant, number of pods per plant, 1000 seed weight and shoot nitrogen were observed to have considerable indirect positive effect through shoot dry weight on grain yield. Hence, a plant type with tall habit, more number of clusters, more number of pods, higher seed weight, higher shoot dry weight and shoot nitrogen with limited number of branches is expected to give higher yield in Mungbean.

SUMMARY

CHAPTER VI

SUMMARY

Mungbean (Vigna radiata (L.) Wilczek) is an important pulse crop of India and is used as an excellent source of high quality vegetable protein in our diets. With the development of early maturing, photoinensitive varieties in recent years, it has become an important component in many cropping systems and its area and production are on the increase. However, the problem of low and uncertainty in productivity potentials still persists in mungbean. Among the various factors, limiting the productivity, lack of variability for yield potential is one of the concern to the plant breeders. However, the research carried out on this crop revealed wider genetic variability by majority of the workers in the material handled. However, this variability could not be translated into higher productivity, probably because the variability present in the crop was not fully understood or the variability was not easily usable. Hence, an attempt has been made in the present investigation to understand the genetic nature of the yield and its stability through multipronged approach involving studies on (i) the nature of genetic diversity (ii) the genotype x environment interactions (iii) the gene actions governing the yield and yield

component traits through combining ability analysis with the help of a line x tester analysis and (iv) character associations from a number of experiments including the studies of different environments and populations. The investigations were carried out at the Regional Agricultural Research Station, APAU, Lam and its satellite experimental centre for Rice Fallow Pulses at Munipalle during 1987 to 1989 kharif, rabi and rice fallows.

Forty nine mungbean genotypes, comprising of released varieties, promising cultures under pre-release testing, advanced breeding lines generated through hybridization and mutation, were studied in three seasons to understand the genetic variability and diversity present in this crop. Wider genetic variability was recorded for number of branches per plant, number of clusters per plant, number of pods per plant, shoot dry weight and grain yield. Higher variability and heritability coupled with higher genetic advance over mean was observed for the number of branches, plant height, number of clusters, number of pods per plant, shoot dry weight at maturity and grain yield per plant.

Multivariate analysis using D^2 statistic on the 49 genotypes studied over three seasons indicated the presence of considerable genetic diversity in

mungbean crop. Clustering pattern of the genotypes was influenced by the environments. The genotypes studied formed into maximum number of clusters 14 during kharif 1988 followed by 11 in rabi uplands 1987-88 and 8 in rabi rice fallows, 1987-88. The pattern of distribution of the genotypes into clusters was random irrespective of the parents except under E_3 (rabi rice fallows) where both the parents and their derivatives were included in the same cluster. Genotypes derived through multiple crossing programme formed separate clusters indicating the formation of novel or high degree recombinants which made them distinct from others. Further no relation between geographic diversity and genetic diversity was observed indicating that the direction of selection practiced in different geographical locations determines the genetic divergence. The traits like, plant height, number of pods per plant, shoot dry weight, nitrogen content of the plant at flowering and grain yield per plant influenced to a maximum extent the clustering pattern. Based on the yield performance and inter cluster distances the following genotypes were found genetically diverse from others viz., LGG 421, LGG 429, LGG 442, LGG 487-3 and $DC_1 \times DC_2$ -4SB-SB in E_1 (kharif), LGG 410, LGG 418, LGG 424, LGG 437, LGG 441 and LGG 442 in E_2 (rabi uplands) and LGG 424, LGG 446 and LGG 449 in E_3 (rabi rice fallows). Selection of these lines as parents in hybridization

programme will result in rare recombinants and transgressive segregants.

Twenty diverse genotypes consisting of released and pre release cultures were studied under six environments during 1987-88 and 1988-89 to study the stability parameters for yield and yield components of mungbean. The genotypes and the environments were significant for all the characters studied. A substantial portion of the genotype x environment interaction was linear for plant height, number of branches, number of clusters, number of pods per plant, pod length, number of seeds per pod, 1000 seed weight, shoot dry weight, shoot nitrogen and grain yield per plant, whereas, non-linear portion of interaction was predominant for days to 50% flowering and days to maturity. The relationship between mean performance and the environmental index was linear. Kharif 1988, was found to be favourable environment for the expression of the traits, whereas, rabi rice fallows, 1987-88 and 88-89 were unfavourable environments. The genotypes studied are classified into three groups based on the stability analysis (Eberhart and Russel, 1966). (i) High yielding and stable under all the environments - K 851, PDM 54, PDM 84-145 and ML 267 (ii) High yielding and better suitable for favourable environments - LGG 407, LGG 410, ML 131 and LGG 426 (iii) High yielding

and suitable only for unfavourable environments - Pusa 105, LGG 450 and LGG 403.

Positive association between the mean performance and linear regression coefficient of grain yield, indicated that the high yielding lines (LGG 403, LGG 407, LGG 410 and LGG 426) were unstable. Associations of deviations from regression with mean performance and linear regression were non-significant for days to 50% flowering, days to maturity, plant height, number of branches, number of clusters number of pods per plant, number seeds per pod, 1000 seed weight, shoot dry weight, shoot nitrogen and grain yield which indicates the presence of independent genetic system in the control of stability parameters for these traits. Correlation between deviation from regressions and mean performance in case of pod length and deviations from linear regression with linear regression coefficient in shoot nitrogen and seed protein indicates the possible presence of linkage among stability parameters of these characters.

The response to selection of any trait depends on the nature of its inheritance and the breeding method employed. Hence, the knowledge on the gene actions governing a trait in mungbean is essential. In the present study combining ability analysis using a line x tester programme was carried out both in F_1 and

F₂ generations. In general the variance due to 'gca' was greater than 'sca' for all the traits studied except for the number of branches per plant and days to 50% flowering indicating the predominance of additive gene action governing these traits. The heritability (narrow sense) estimates were high for days to maturity, plant height, pod length, number of seeds per pod, 1000 seed weight, shoot dry weight and grain yield per plant.

The degree of dominance was high or moderately high for days to 50% flowering, number of branches, pod length, number of seeds per pod and shoot nitrogen indicating the importance of non-additive gene action governing these traits.

An overall view of the variance components ('gca' and 'sca'), degree of dominance and heritability, the gene actions governing the various traits, it was found that days to maturity, plant height, number of clusters, number of pods per plant, 1000 seed weight, shoot dry weight, seed protein and grain yield were governed by additive gene action. These traits can be improved through breeding methods involving selection of single plants or bulk selection. Number of branches per plant was found to be governed by non-additive gene action. Improvement in such a character can be made by following cyclic hybridization

methods (Recurrent selection, diallel selective mating and biparental mating). Days to 50% flowering, pod length, number of seeds per pod and shoot nitrogen were found to be governed by both additive and non additive gene action. Recurrent selection and diallel selective mating in the early stages followed by selection may leads to their improvement.

Among the lines, pusa 105 and K 851 and among the testers PDM 54, LGG 410 and LGG 450 were found to be the good general combiners for most of the yield contributing traits and yield.

Seven crosses viz., pusa 105 x PDM 54 (HxH), pusa 105 x LGG 410 (HxH), pusa 105 x LGG 450 (HxH), ML 267 x LGG 410 (LxH), ML 267 x LGG 450 (LxH), K 851 x LGG 410 (HxH) and K 851 x LGG 450 (HxH) recorded significant 'sca' effects with high mean yield. The significant sca combinations which involved HxH general combiners may be advanced through pedigree method of breeding for improving yield per se. While ML 267 x LGG 410 and ML 267 x LGG 450 which involved LxH combinations may be studied through biparental or diallel selective mating or any other form of recurrent selection so as to combine additive as well as non additive gene actions.

Association analysis of yield and yield components over six environments with 20 genotypes indicated that number of clusters per plant, number of pods per plant, 1000 seed weight, shoot dry weight and shoot nitrogen were found to have consistent positive and significant correlation with grain yield while number of branches per plant was found to have negative associations with grain yield under all environments except in rabi rice fallows (E3). Pod length and number of seeds per pod had consistent non-significant correlations with grain yield over environments. Other component traits showed inconsistent associations with grain yield.

Association analysis studies with different populations viz., parents, F_1 's and F_2 's under single environment also indicated significant positive associations of number of clusters, number of pods, 1000 seed weight, shoot dry weight, shoot nitrogen, pod length and number of seeds per pod with grain yield in mungbean.

Changes in the association of days to 50% flowering and shoot dry weight; days to 50% flowering and seed protein; plant height and pod length; plant height and shoot nitrogen; number of branches per plant and number of seeds per pod; clusters per plant and seeds per pod, pod length and shoot dry weight from

parents to F_2 were observed. This may be due to breakage of linkages.

Path coefficient analysis carried out under six different environments with a set of 20 genotypes and with different populations (Parents, F_1 's and F_2 's) under one single environment indicated that shoot dry weight was found to have maximum positive direct effect on grain yield followed by the number of pods per plant. Number of pods per plant, 1000 seed weight and shoot nitrogen also exerted positive indirect effect on grain yield through shoot dry weight. Number of branches per plant showed negative direct effect on grain yield.

From the present investigations it is evident that wider genetic variability is present in the mungbean. Higher estimates of heritability coupled with high genetic advance were recorded for number of clusters number of pods per plant, shoot dry weight and grain yield per plant. Combining ability analysis revealed that all the important traits such as the number of clusters per plant, number of pods per plant, 1000 seed weight, shoot dry weight and grain yield per plant are governed by additive genes. Whereas, number of branches per plant is governed by non additive gene action. The breeding methods involving cyclic hybridizations in the initial stages (Recurrent

selection, diallel selective mating or biparental matings) followed by single plant selections for the first order yield component traits or yield per se may lead to improvement in yield potential of mungbean.

Number of clusters per plant, number of pods per plant, 1000 seed weight, shoot dry weight and shoot nitrogen showed consistently positive and significant association whereas, number of branches per plant had negative association with grain yield in all the environments. Shoot dry weight followed by number of pods per plant and shoot nitrogen recorded high positive direct effect while number of branches per plant had consistent negative direct effect on grain yield. Taking these into consideration a plant type with less branching, tall, with higher number of bearing nodes and pods per clusters was suggested to achieve quantum jumps in yield potential of mungbean.

LITERATURE CITED

LITERATURE CITED

- Acharya D, Chatopadhyaya P and Dana S 1984 Correlations and inheritance of primary leaf size in mungbean. Indian Journal of Genetics and Plant Breeding 44: 121-126.
- Adams M W and Shank D B 1959 The relationship of heterozygosity to homeostasis in maize hybrids. Genetics 44: 777-786.
- Ahn C S, Chen J H and Chen H K 1985 Performance of the ninth and tenth International Mungbean Nursery Trial. Asian Vegetable and Research and Development Centre Shanhua Tainan 868.
- Ahuja S L 1980 Diallel analysis in F_2 generation of greengram (Vigna radiata (L) Wilczek). Thesis Abstracts 6: 110-111.
- Ahuja S L and Chowdhury R K 1984 Graphical and component analysis of mungbean. Indian Journal of Heredity 16: 4-10.
- Allard R W 1960 Principles of plant breeding. John Willey and Sons Inc. New York pp 485.
- Allard R W 1961 Relationship between genetic diversity and consistency of performance in different environments. Crop Science 1: 127-133.
- Allard R W and Bradshaw A D 1964 Implications of genotype environment interaction in applied plant breeding. Crop Science 4: 503-508.
- Allard R W and Workman P L 1963 Population studies in Predominantly self - pollinated species. IV seasonal fluctuations in estimated values of genetic parameters in Lima bean populations. Evolution 17: 470-80.

- Amirshahi M C and Tanakoli M 1970 Protein content of different varieties of five species of pulse crops. Improving plant protein by nuclear techniques proceedings of symposium jointly organised by the IAEA and FAO 331-35 Vienna Austria 8-12 June 1970
- Anand I J and Murty B R 1968 Genetic divergence and hybrid performance in Linseed. Indian Journal of Genetics and Plant Breeding 28: 178-185.
- AOAC 1970 Official methods of analysis. The Association of Official Agricultural Chemists Washington DC.
- Arora P K, Chandel K P and Joshi B S 1973 Morphological diversity in Phaseolus sublobatus Roxb. Current Science 42: 359-361.
- Arunachalam V 1981 Genetic distance in plant breeding. Indian Journal of Genetics and Plant Breeding 41: 226-36.
- Aruachalam V and Jawahar Ram 1967 Geographical diversity in relation to genetic divergence in cultivated sorghum. Indian Journal of Genetics and Plant Breeding 27: 369-80.
- Arwooth Na Lampang S, Pichitparn S, Singh and Vanakojimongki 1988 Mungbean growth pattern in relation to yield. In Proceedings Second International Symposium on Mungbean, Bangkok Thailand pp 104-168.
- AVRDC 1974 Asian Vegetable Research and Development Centre Annual Report for 1972-73 Shanhua Tainan pp 210
- AVRDC 1977 Asian Vegetable Research and Development Centre Annual Report for 1976 Shanhua Tainan pp 47.
- AVRDC 1979 Asian Vegetable Research and Development Centre Annual Report for 1978 Shanhua Tainan pp 173.

- AVRDC 1984 AVRDC Organisation and Plans. Asian Vegetable Research and Development Centre, Shanhua, Tainan pp 405.
- AVRDC 1988 Asian Vegetable Research and Development Centre. Annual Report 1987, Shanhua, Tainan pp 215.
- Bains K S and Gupta V P 1972 Stability of yield and yield components in bread wheat. Indian Journal of Genetics and Plant Breeding 32 : 306-12.
- Basaeruddin Md and Nagur T 1981 Combining ability for grain yield in Greengram (Vigna radiata (L) Wilczek). Madras Agricultural Journal 68 : 582-87.
- Becker H C and Leon J 1988 A Review. Stability analysis in plant breeding. Plant Breeding 101 : 1-23.
- Bhadra S L, Akhtan M I, Shill M and Osman K T 1987 Variation in seed protein of Mungbean and its relation to seed yield and size. TVIS Niews, Taiwan 2 : 2-3.
- Bhargava P D, Johri J N, Sharma S K and Bhatt B N 1966 Morphological and genetic variability in greengram. Indian Journal of Genetics and Plant Breeding 26 : 370-373.
- Bhatnagar C P and Singh B 1964 Heterosis in mungbean. Indian Journal of Genetics and Plant Breeding 24 : 89-91.
- Bhaumik P K and Jha A R 1976 Estimation of physiological relationship through path coefficient analysis in Mungbean (Phaseolus aureus (Roxb.)). Indian Agriculturist 20 : 1-10.
- Bliss F A, Barker L N, Franckowiak J D and Hall T C 1975 Genetic and environmental variations of seed yield, yield components and seed protein quality of Cowpea. Crop Science 13 : 656-680.
- Boomikumaran P and Rathinam M 1981 Correlation and path analysis in Greengram. Madras Agricultural Journal 68 : 643-647.
- Borlaug N E 1973 Building a protein revolution on grain legumes. In Nutritional Improvement of Food Legumes by Breeding. Protein Advisory Group of United Nations pp 7-11.

- Breese E L 1969 The measurement and significance of G.E interactions in grasses. *Heredity* 24: 27-44.
- Breese E L 1972 Biometrical genetics and its applications. *Proceedings of VI Eucaroia Congress*. Cambridge pp 135-146.
- Bucio Alanis, Perkins Jean H and Jinks J L 1968 Environmental and Genotype - Environmental components of variability. IV Segregating Generations. *Heredity* 24: 115-127.
- Burton G W 1952 Quantitative inheritance in grasses. *Proceedings of the Sixth International Congress* pp 277-83.
- Chandel K P S 1981 Wild Vigna species in the Himalayas. *Plant Genetics Resources News Letter* 45: 17-19.
- Chandal K P S, Joshi B S and Pant K C 1973 Yield in mungbean and its components. *Indian Journal of Genetics and Plant Breeding* 33: 271-76.
- Chandra S 1988 Problems and prospects of mungbean improvement in India. *Proceedings of the Second International Symposium on Mungbean held at Bangkok Thailand Nov 16-20, 1987*.
- Chowdhury J B, Chowdhury R K and Kakar S N 1971 Studies on the genetic variability in mung (Phaseolus aureus Roxb). *Journal of Research Punjab Agricultural University, Ludhiana* 8: 169-172.
- Chowdhury S K and Haque M N 1977 Stability performance of some greengram varieties. *Indian Journal of Agricultural Sciences* 47: 303-304.
- Chowdhury R K, Singh R K and Kakar S K 1982 Correlation coefficients and selection indices in Mungbean (Vigna radiata (L) Wilczek). *Pulse Crops News Letter* 2: 22-24.

- Comstock R E and Robinson H F 1948 The component of genetic variance of populations of biparental progenies and their use in estimating the average degree of dominance. *Biometrics* 4: 254-66.
- Comstock R E and Moll R H 1963 Genotype - environment interactions; In *Statistical Genetics and Plant Breeding* NAS-NRC Publication 982 pp 164-196.
- Comstock R E and Robinson H F 1952 Estimation of average dominance of genes. In *Heterosis* (ed. ~~G. M. M. M.~~ ^{G. M. M. M.}). Iowa State College Press Ames pp 494-516.
- Cowell R (ed) 1978 Proceedings of the first International Mungbean Symposium, Tainan.
- Dahiya B S and Jeswani L H 1974 Phenotypic adaptability and stability of characters related to productivity in Khesari Dal Lathyrus sativus (L.) *Israel Journal of Agricultural Research* 23: 95-101.
- Dahiya B N, Singh V P and Dahiya B S 1984 Relative efficiency of mass selection for seed size pedigree selection for yield per se in Greengram. *Legume Research* 7: 77-81.
- Dana S 1966a The cross between Phaseolus aureus Roxb. and Phaseolus mungo (L.). *Genetica* 37: 259-74.
- Das P K and Gupta T Das 1984 Multivariate analysis in Blackgram. *Indian Journal of Genetic and Plant Breeding* 44: 243-47.
- De D N and Krishnan R 1966 Cytological studies of the hybrid Phaseolus aureus x Phaseolus mungo. *Genetica* 37: 588-600.
- De Candolle A 1884 Origin of cultivated plants New York. Hafner Publishing Reprinted in 1959 Bailey I H 1949. In *Manual of Cultivated Plants* New York. MacMillan.

- Deshmukh R B and Manjare M R 1980 Combining ability in Mungbean (Vigna radiata (L.) Wilczek). Legume Research 3: 97-101.
- Dewey D R and Lu K H 1959 A correlation and path coefficient analysis of components of crested wheat grass seed production. Agronomy Journal 51: 515-518.
- Dickerson G E 1955 Genetic slippage in response to selection for multiple objectives. Cold Spring Harbour Symposia on Quantitative Biology 20: 213-24.
- Directorate of Pulses Research 1986 All India Coordinated pulses Improvement Project, Kanpur. Improved varieties of pulse crops in India pp. 68.
- Directorate of Pulses Research 1988 Technology of increasing pulse production in India. Directorate of Pulse Research. Indian Council of Agricultural Research pp 10.
- Eberhart S A and Russell W A 1966 Stability parameters for comparing varieties. Crop Science 6: 36-40.
- Empig L T, Lantican R M and Escuro P B 1970 Heritability estimates of quantitative characters in mungbean (Phaseolus aureus Rox) Crop Science 10: 240-41.
- Erskine W 1977 Adaptation and competition in mixtures of cowpea (Vigna unguiculata (L.) Walp). Euphytica 26: 93-202.
- Esh G C, De T S and Basu U P 1960 Influence of genetic strain and environment on protein content in pulses. Science 129: 48-49.
- Erskine W and Khan T N 1977 Genotype, Genotype x environmental and environmental effects on grain yield and related characters of Cowpea (Vigna umguiculata (L.) Walp). Australian Journal of Agricultural Research 28: 609-617.

- Falconer D S 1964 Introduction to quantitative genetics. Second Edition. Oliver and Boyd Edinburgh pp 340.
- Fernandez G C J and Miller J C Jr. 1985 Estimation of heritability by parent - offspring regression. Theoretical Applied Genetics 70 : 650-654.
- Fernandez G C J and Shanmugasundaram 1988 The AVRDC mungbean improvement program : The past, present and future. In Mungbean Proceedings of the second international symposium held at Bangkok, Thailand pp 58-70.
- Finlay R W and Wilkinson 1963 The analysis and adaptation in a plant breeding programme. Australian Journal of Agricultural Research 14 : 742-54.
- Fisher R A and Yates F 1963 Statistical tables for biological agricultural and medical research. Oliver and Boyd London pp 46-63.
- Francis T R and Kannenberg L W 1978 Yield stability studies in short-season Maize 1. A descriptive method for grouping genotypes. Canadian Journal of Plant Science 58 : 1029-1034.
- Fripp Y and Caten C E 1973 Genotype environmental interactions in Schizophyllum commune III. The relationship between mean expression and sensitivity to change in environment. Heredity 30 : 341-349.
- Gill A S, Verma M M, Dhaliwal H S and Sandhu T S 1983 Interspecific transfer of resistance to mungbean yellow mosaic virus from Vigna mungo to Vigna radiata. Current Science 52 : 31-33.
- Gill K S, Sandhu T S, Singh K and Brar J S 1975 Evaluation of mungbean (Vigna radiata (L.) Wilczek) germplasm. Crop Improvement 2 : 99-104.
- Giriraj K 1973 Natural variability in greengram (Phaseolus aureus Roxb.). Mysore Journal of Agricultural Science 7 : 184-187.
- Giriraj K and Vijayakumar S 1974 Path Coefficient analysis for yield attributes in mungbean. Indian Journal of Genetics and Plant Breeding 34 : 27-30.

- Godhani P R, Jaisani B G and Patel G J 1978 Epistasis and other genetic variances in greengram varieties. Research Journal of Gujarat Agricultural University 4: 16.
- Gopalsingh B and Singh K N 1982 Effect of climatic factors on growth attributes of Mungbean. The Andhra Agricultural Journal 29:114-119.
- Government of Andhra Pradesh 1988 Area and production of principal crops in Andhra Pradesh Economic and Statistical Bulletin January-December 1988. Bureau of Economic and Statistics.
- Grafius J E 1956 Components of yield in Oats. A geometric interpretation. Agronomy Journal 48: 419-423.
- Griffing 1956 Concept of general and specific combining ability in relations to diallel crossing system. Australian Journal of Biological Sciences 9: 963-93.
- Griffing B and Lambridge J 1963 Phenotypic stability of growth in self fertilized species Arabidopsis thaliana. In Statistical Genetics and Plant Breeding NAS-NRC Publications 982: 369-394.
- Gupta S N, Arora N D, Singh R K and Chowdhury B D 1978 Combining ability and gene action in mungbean. Indian Journal of Heredity 10: 59-66.
- Gupta M P and Singh R B 1969 Variability and correlation studies in Greengram (Phaseolus aureus Roxb.). Indian Journal of Agricultural Sciences 39: 482-93.
- Gupta M P and Singh R B 1970 Genetic divergence and its components in Greengram. Indian Journal of Genetics and Plant Breeding 30: 212-21.

- Gupta V P 1971 Studies on adaptability combining ability and gene action in Bengalgram Cicer arietinum (L.). Ph.D Thesis submitted to P.G. School IARI, New Delhi.
- Gupta S N, Lal S, Arora K and Jatasara D S 1980 Heterosis for yield and yield components in mungbean. Indian Journal of Heridity 12: 49-55.
- Gupta S N, Lal S and Rai L 1982 Correlations and path analysis in mungbean (Vigna radiata (L.) Wilczek). Haryana Agricultural University. Journal of Research 12: 281-291.
- Gupta V P, Ramanujam S and Kaul A K 1974 Stability analysis in respect of protein, sulphur and protein value index of seed and its implication in adaptation of chickpea (Cicer arietinum (L.). Genetica 6: 247-61.
- Hanson W D 1970 Genotypic stability. Theoretical Applied Genetics 40: 226-231.
- Hormuzdi S G and More T A 1989 Studies on combining ability in cucumber (Cucumis sativus L.). Indian Journal of Genetics and Plant Breeding 49: 161-166.
- Huhn M 1979 Beitrage zur Erfassung der phanotypischen stabilitat. Medizin und Biologie 70: 112-117 (cf. Plant Breeding 101: 1-25).
- Hymowitz T, Collins F I and Poehlman J M 1975 Relationship between the content of oil, protein and sugar in mungbean seed. Tropical Agriculture 52: 47-51.
- Ilyas Ahmad Malik, Yousaf Ali and Mohammad Saleem 1988 Incorporation of tolerance to Mungbean yellow mosaic virus from local germplasm into exotic large seeded mungbean. In Proceedings of Second International Symposium on Mungbean held at Bangkok Thailand pp 297-307.

- Imrie B C and Bulter K L 1982 An analysis of variability and genotype x environment interaction in mungbean (Vigna radiata (L.) Wilczek) in South Eastern Queensland. Australian Journal of Agricultural Research 33: 523-30.
- Imrie B C, Drake D W, Delacy I H and Byth D E 1981 Analysis of genotypic and environmental variation in international mungbean trials. Euphytica 30: 301-11.
- Imrie B C and Shanmugasundaram 1987 Source of variation in yield in international mungbean trials. Field Crop Research 16: 197-208.
- Imrie B C, Ratcliff D and Eerens J P J 1988 Analysis of gene action in crosses between early and late maturing mungbeans. Proceedings of the Second International Symposium on Mungbean, Bangkok Thailand pp 146-151.
- Jain H K 1981 Evolving a new production technology of pulses. Pulse Crops News Letter 1: 1-2.
- Jain H K and Mehra K L 1980 In Summerfield R J and Bunting A H (eds) Advances in Legume Science London HMSO 456-68.
- Jain K C and Pandya B P 1984 Relationship between genetic divergence and phenotypic stability in chickpea. Indian Journal of Genetics and Plant Breeding 44: 276-79.
- Jain K C and Pandya B P 1988 Relationship between mean performance and stability parameters in chickpea (Cicer arietinum (L.)). Legume Research 11: 103-108.
- Jain K C, Pandya B P and Punde K 1981 Genetic divergence in chickpea 41: 220-225.
- Jain K C, Pandya B P and Pande K 1984 Stability of yield components of chickpea genotypes. Indian Journal of Genetics and Plant Breeding 44: 159-163.

- Jebaraj S and Marappan P V 1981. Mutagenic effectiveness and efficiency of gamma rays and ethyl methane sulphonate in greengram (Vigna radiata (L.) Wilczek). Madras Agricultural Journal 68: 631-637.
- Jensen N F 1970 A diallel selective mating system for cereal breeding. Crop Science 10: 629-635.
- Jinks J L and Mather K 1955 Stability in development of heterozygotes and homozygotes. Proceeding of Royal Society of Botany 143: 561-578.
- Jeswani 1986 Breeding strategies for the improvement of pulse crops. Indian Journal of Genetics and Plant Breeding 46: 267-280.
- Johanson W 1908 Elements derexakton, Erblchkeits lahre 1st eds. Jena Gustov Fisher pp 515.
- Johnson V A and Frey C L 1974 Genetic improvement of protein. Journal of Agricultural Food Chemistry 22: 558-566.
- Johnson H W, Robinson H F and Comstock R E 1955 Estimates of genetic and environmental variability in soyabean. Agronomy Journal 47: 314-18.
- Joshi S N 1972 Stability parameters for comparing greengram (Phaseolus aureus Roxb.) Varieties. Madras Agricultural Journal 59: 195-197.
- Joshi S N 1969 Variety x environment interaction in varietal tests of greengram (Phaseolus aureus Roxb). Indian Journal of Agricultural Sciences 39: 1010-12.
- Joshi S N and Kabaria M M 1973 Inter relationship between yield and yield componetns in (Phaseolus aureus Roxb). Madras Agricultural Journal 60: 1331-1334.

- Kaltisikes P J and Larter E N 1970 The interaction of genotype and environment in Durum Wheat. *Euphytica* 19: 236-42.
- Kasthuri R, Jayapragasam M, Sree Rangaswamy S R, Gowri G and Sadasivam S 1987 *TVIS News, Taiwan* 2: 7-8.
- Katiyar R P 1988 Component compensation for stability of yield in urdbean at high altitudes. *Indian Journal of Genetics and Plant Breeding* 48: 225-233.
- Kempthorne O 1957 *An Introduction to genetic statistics*. John Wiley and Sons, INC. New York.
- Khan I A 1987 Path coefficient analysis of yield attributes in mutants of Mungbean. *TVIS News Taiwan* 2: 15-16.
- Krishnaswamy S, Fazlullah Khan A K and Sreerangaswamy SR 1973 Association of Metric Traits in mutants of *phaseolus aureus* Roxb. *Madras Agricultural Journal* 60: 1323-26.
- Krishna Rao K V and Nagur T 1979 Line x Tester analysis of combining ability for seed yield in greengram. *Madras Agricultural Journal* 66: 639-642.
- Krober O A 1970 Effects of variety and locations on the protein content of pulses. *Indian Journal of Agricultural Sciences* 40: 1025-30.
- Kumari K T P and George M K 1985 Correlation and path analysis in greengram. *Agricultural Research Journal of Kerala* 20: 82-85.
- Lackey J A 1977 A synopsis of *phaseolus Leguminosae - papilionodeae*). Ph.D Dissertation Iowa State University Ames pp 293.
- Lal S, Gupta S N and Tomer Y S 1982 Line x tester analysis in mungbean. *Haryana Agricultural University. Journal of Research* 12: 438-43.

- Lamprecht H 1959 Investigation on the heterosis in peas. Dehrecen Mezozađ Akad Tudocany E.V.K. 185-194.
- Lawn R J 1979a Agronomic studies on Vigna Spp. in South Eastern Queensland I. Phenological response of cultivars to sowing date. Australian Journal of Agricultural Research 30 : 855-70.
- Lawn R J and Ahn C S 1985 Mungbean (Vigna radiata (L.) Wilczek)/Urdbean Vigna mungo (L.) Hepper) in Grain Legumes (eds) Summerfield R J and Roberts E H Collins London pp 584-623.
- Leon J and Becker H C 1988 Repeatability of some statistical measures of phenotypic stability correlations between single year results and multi year results. Plant Breeding 100 : 137-42.
- Lewis D 1954 Gene-environment interaction. A relationship between dominance heterosis, phenotypic stability and variability. Heredity 8 : 333-356.
- Lill D J, Gao H F and Zheny K P 1984 Studies on local cultivars of (Vigna radiata (L.) Wilczek) in Fujian I. yield correlations and regressions analysis. Journal of Fujian Agricultural College 13 : 135-40 (C F : PBA 1985. 5987).
- Lin C S, Binns M R and Lebkovitch L P 1986 Stability analysis. Where do we stand? Crop Science 26 : 894-90.
- Lukoki L, Marechal R and Otoul E 1980 Les ancetres sangages des haricots cultives : Vigna radiata (L.) Wilczek and Vigna mungo (L.) Hepper Bell. Jard. Bot. Nat. Belgique 50 : 385-391.
- Lush J L 1940 Intra-sire correlation on regression of offspring on dams as a method of estimating heritability of characters. Proceedings of American Society of Animal Production 33 : 292-301.
- Luthra O P, Kakar S N and Singh R K 1977 Combining ability studies of yield and quality characters in greengram (Vigna radiata (L.) Wilczek). Haryana Agricultural University. Journal of Research 7 : 200-205.
- Luthra O P, Arora N P, Singh R K and Chowdhary 1979 Genetic analysis in metric traits in mungbean (Vigna radiata (L.) Wilczek). Haryana Agricultural University. Journal of Research 9 : 19-24.

- Mahalanobis P C 1936 On the generalized distance in statistics. Proceedings of National Institute of Sciences (Indian) 2 : 49-55.
- Malhotra V V 1970 Studies on genetic variability, correlation and multivariate analysis for yield, protein and some quantitative characters in mungbean (Phaseolus aureus (Roxb). M.Sc.thesis, Punjab Agricultural University, Ludhiana.
- Malhotra R S 1983 Genetics of pod length, seeds per pod, and seed size in mungbean (Vigna radiata (L.) Wilczek). Genetica Agraria 37 : 345-53.
- Malhotra R S and Singh K B 1971 Multivariate analysis in Blackgram (Phaseolus mungo (L.) Hepper). Indian Journal of Agricultural Sciences 44 : 212-14.
- Malhotra R S and Singh K B 1973 Genetic variability and path coefficient analysis for protein in greengram (Phaseolus aureus Roxb). Egyptian Journal of Genetics and Cytology 5 : 170-73.
- Malhotra R S, Singh K B and Dodni J S 1973 Discriminant function in Phaseolus aureus Roxb. Madras Agricultural Journal 60 : 1327-1330.
- Malhotra V V, Sukhdev Singh and Singh K B 1974 Relation between geographic diversity and genetic divergence and the relative role of each character towards maximising divergence in greengram. Indian Journal of Agricultural Sciences 44 : 811-815.
- Malhotra V V, Sukhdev Singh and Singh K B 1974a Yield components in greengram (Phaseolus aureus Roxb). Indian Journal of Agricultural Sciences 44 : 136-46.
- Malhotra R S, Gupta P K and Arora N D 1980 Diallel analysis over environments in mungbean. Indian Journal of Genetics and Plant Breeding 40 : 64-66.

- Malik J S, Paroda R S and Arora N D 1973 Genotype - environment interactions for green fodder yield in cowpea (Vigna sinensis). Plazucht 69: 333-39.
- Malik B P S, Singh V P, Chowdhury B D and Chowdhury R K 1982 Path coefficients and selection indices in greengram. Indian Journal of Agricultural Sciences 52: 288-91.
- Malik B P S and Singh 1983 Genetics of some metric traits in greengram. Indian Journal of Agricultural Sciences 53: 1002-5.
- Malik B P S and Singh V P 1986 Detection of epistatic, additive and dominance variation in greengram (Vigna radiata (L.) Wilczek). Genetica Iberica 38: 119-127.
- Marechal R 1970 Donnees Cytologiques Surles especes dela sous. tribudes Phaseolinae. Deuxieme Serie. Bull. Jard. Bot Nat. Belgique 40: 307-348.
- Marechal R, Mascherpa J M and Stainer F 1981 Taxonometric study of the phaseolus - Vigna complex and related genera. In Advances in Legume Systematics (eds). Polhill R M and Raven P H. Royal Botanical Gardens, Kew.
- Marechal R 1982 Arguments for global conception of the genus vigna. Taxon 31: 280-283.
- Medhi B N, Nazarika M H and Chowdhury P K 1980 Genetic variability and heritability for seed yield components in greengram (Vigna radiata (L.) Wilczek). Tropical Grain Legume Bulletin 17/18: 32-34.
- Mehra R B and Ramanujam S 1979 Adaptation in bengalgram. Indian Journal Genetics and Plant Breeding 39: 492-500.
- Misra R C, Sahu R C and Tripathy D 1970 A note on Heterosis in greengram (Phaseolus aureus Roxb). curent Science 39: 190-91.

- Misra R C and Sahu B C 1985 Genetic parameters, correlation and path coefficient analysis in greengram (Vigna radiata (L.) Wilczek). The Andhra Agricultural Journal 32 : 87-91.
- Mungomery V E, Byth D E and Williams R J 1972 Environmental effects and varietal performance of cowpeas (Vigna sinensis) and mungbean (Phaseolus species) accessions in South Eastern Queensland. Australian Journal of Experimental Agriculture and Animal Husbandary 12 : 523-27.
- Muntzing A 1945 Hybrid vigour in crosses between purelines of Galeopsis tetrahit. Hereditas Lund. 31 : 391-98.
- Muralidharan V, Rangaswamy S R S and Rathnaswamy R 1988 Inheritance of small leaf and wrinkled leaf nature in Blackgram (Vigna mungo (L.) Hepper). Current Science 57 : 438-39.
- Murthy B R 1975 Biology of adaptation in chickpea. International Workshop on Grain legumes. ICRISAT 239-51.
- Murthy B R and Anand I J 1966 Combining ability and genetic diversity in some varieties of Linum usitatissimum. Indian Journal of Genetics and Plant Breeding 26 : 21-36.
- Murthy B R, Mathur J B L and Arunachalam V 1965 Self incompatibility and genetic divergence in Brassica campestris var. brown Sarson. Sankhya Series B 27 : 271-78.
- Murthy B K, Patel G J and Jaisani B G 1976 Gene action and heritability estimates of some quantitative traits in mungbean. Gujarat Agricultural University Research Journal 2 : 1-4.
- Murugesan R, Dhamu K P and Rathnaswamy R 1986 Simultaneous selection model for plant selection in Greengram. Madras Agricultural Journal 73 : 457-465.
- Nagaraja Rao B 1981 Heterosis and combining ability studies in Greengram (Vigna radiata (L.) Wilczek) M.Sc.(Ag.) thesis submitted to Andhra Pradesh Agricultural University, Hyderabad.

- Nagaraja Rao B and Mahboob Ali S 1983 Combining ability in greengram (Vigna radiata (L.) Wilczek). The Andhra Agricultural Journal 31 : 42-44.
- Narasimham M 1929 A note on the pollination of blackgram and greengram in the Godavari district. Agronomy Journal India 24 : 397-401.
- Naresh Mehrotra and Chowdhury B D 1986 Evolving phenotypically stable mungbean varieties for rainfed conditions. Pulse Crops News Letter 6 : 18-19.
- Nassar R and Huhn M 1987 Studies on the estimation of phenotypic stability. Test of significance for non parametric measures of phenotypic stability. Biometrics 43 : 45-53.
- Natarajan M and Palaniswamy 1988 Association between yield and dry matter components in mungbean. Indian Journal of Pulses Research 1 : 23-26.
- Natarajan C, Thiyagarajan K and Ayyamperumal A 1989 Combining ability in Mungbean. Indian Journal of Pulses Research 2 : 15-19.
- Ong M S 1978 Effects of seed size and colour on protein and starch contents of mungbean (Vigna radiata (L.) Wilczek). Unpublished BS thesis, University of Phillipines at Las Banos College, Laguna pp 76.
- Otoul E, Marechal R, Dardenne G and Desmedt F 1975 Des dipeptides soufres differentient nettement Vigna radiata de Vigna mungo. Phytochemistry 14 : 173-179.
- Pal B P and Singh H 1946 Studies in Hybrid vigour. II. Notes on manifestation of hybrid vigour in the Brinjal and Bittergourd. Ibid 6 : 19-33.
- Pandey K, Raghuvarshi S S and Singh S P 1988 Selection of parameters for different traits in mungbean (Vigna radiata (L.) Wilczek). Narendra Deva Journal of Agricultural Research 3 : 69-72.

- Pandya B P, Singh D P and Sharma B L 1978 Evaluation of mungbean (Vigna radiata (L.) Wilczek) Geermplasm. Pantnagar Journal of Research 3: 15-20.
- Panse V G 1957 Genetics of quantitative characters in relation to plant breeding. Indian Journal of Genetics and plant Breeding 17: 318-28.
- Panse V G and Sukhatme P V 1978 Statistical methods for agricultural workers, 3rd Edition. ICAR New Delhi pp 347.
- Paramasivam J and Rajasekharan S 1980 Genetic variability in greengram (Vigna radiata (L.) Wilczek). Madras Agricultural Journal 67: 421-24.
- Parida S 1982 The evaluation of varietal and wide crosses in Greengram. M.Sc Thesis. Govinda Vallabha Pantnagar University of Agriculture and Technology Pantnagar India pp 83.
- Parida D and Singh D P 1984 Association, Heritability and Genetic advance in the F_2 generation of wide and varietal cross of Greengram. Madras Agricultural Journal 71: 351-56.
- Paroda R S and Hayes J D 1971 An investigation of genotype environment interactions for rate of ear emergence in spring barley. Heredity 26: 157-175.
- Paroda R S and Thomas T A 1988 Genetic Resources of Mungbean (Vigna radiata (L.) Wilczek) in India. Proceedings of the Second International Symposium AVRDC held at Bangkok Thailand pp 19-27.
- Patel I D 1983 Genetic analysis of yield and its components in greengram (Vigna radiata (L.) Wilczek). Ph.D Thesis, Sukhadia University Udaipur.
- Patel J A, Patel S A, Zawri P P and Pathak A R 1988 Combinning ability analysis in Mungbean. Indian Journal of Pulses Research 1: 105-110.

- Paul N K 1978 Genetic architecture of yield and components of yield in mustard (Brassica juncea L.). Theoretical Applied Genetics 53 : 233-37.
- Pawar S E and Bhatia C R 1980 The basis of grain yield differences in Mungbean cultivars and identification of yield limiting factors. Theoretical Applied Genetics 57 : 171-175.
- Pawar S E, Thakare R G and Bhatia C R 1986 Genetic improvement of pulse crops. Induced mutations and their use in cross breeding. In Proceedings of a workshop on the Grain Legume Production using Induced mutations FAO/IAEA Division pp 235-249.
- Perkins J M and Jinks J L 1968a Environmental and genotype - environmental components of variability III. Multiple lines and crosses. Heredity 23 : 339-356.
- Perkins J M and Jinks J L 1968 Environmental and genotype - environmental components of variability IV non-linear interaction for multiple inbred lines. Heredity 23 : 525-35.
- Perkins J M and Jinks J L 1973 The assessment and specificity of environmental and genotype environmental components of variability. Heredity 30 : 111-26.
- Pinthus M J 1973 Estimate of genotypic value. A proposed method. Euphytica 22 : 121-123.
- Piper C V and Marse W J 1974 Five oriental species of beans. United States Department of Agriculture Bulletin 119 : 16-25.
- Pokle V S and Patel V N 1974 Path coefficient analysis in Greengram (Phaseolus aureus Roxb). Science and Culture 41 : 265-66.
- Pokle Y S and Nomulwar M T 1975 Variability studies in some quantitative characters of mung (Phaseolus aureus Roxb). Punjabrao Krishi Vidyapeta Journal of Research 3 : 129-132.
- Purseglove J W 1968 Tropical Crops. Dicotyledons John Wiley and Sons, New York.

- Quah S C, Sidek M S M and Mat C H C 1983 Variation in grain yield, protein content and other agronomic characters in mungbean (Vigna radiata (L.) Wilczek). In crop improvement Research (eds) Yap T C, Graham K M and Sukaimi J, Bangi, Selangor, Malaya pp 289-294.
- Raghu Ram Reddy 1980 Combining ability and genotype - environment interactions in greengram (Vigna radiata (L.) Wilczek). Ph.D Thesis submitted to Andhra Pradesh Agricultural University Hyderabad.
- Ramana M V and Singh D P 1987 Genetic parameters and character association in greengram. Indian Journal of Agricultural Sciences 57: 661-663.
- Ramanujam S 1975 Genetic diversity, stability and plant type in pulse crops. International Workshop on grain legumes held at ICRISAT during 13-16 January 1975 pp 167-76.
- Ramanujam S 1978 Biometrical basis for yield improvement in mungbean. In R Cowell (ed) The First International Mungbean Symposium Proceedings AVRDC Tainan pp 210.
- Ramanujam S 1987 Genetical Research in pulses and oilseeds. In Genetical Research in India pp 139-151.
- Ramanujam S and Gupta V P 1974 Stability of yield and its components in bengalgram and its bearing on plant type. Indian Journal of Genetics and Plant Breeding 34A: 757-763.
- Ramanumam S and Mehra R B 1983 Biometrical studies in pulses. In recent researches in pulse crops of India. Oxford Delhi (in Press).
- Ramanujam S, Mehra S B and Makin B K 1973 Stability analysis for kharif pulses. Proceedings of ninth Workshop (kharif pulses) IARI New Delhi.

- Ramanujam S, Tiwari A S and Mehra R B 1974 Genetic divergence and hybrid performance in mungbean. *Theoretical Applied Genetics* 45 : 211-14.
- Ramanujam S, Rohewal S S and Singh S P 1984 Potentialities of heterosis breeding in Cicer. *Indian Journal of Genetics and Plant Breeding* 24 : 122-129.
- Ramussen D C and Lambert J W 1961 Variety x environment interactions in barley variety tests. *Crop Science* 1 : 261-262.
- Rao C R 1952 Advanced statistical methods in Biometrical Research. John Wiley and Sons, New York pp 236-272.
- Rao M R G, Viswanatha S R and Shivashankar G 1978 Possibility of exploiting heterosis in Soybean (Glycine max (L.) Merrill). *Current Research UAS Bangalore* 7 : 149-50.
- Rao A V, Prasad A S R, Krishna S T, Seshu D V and Srinivasan T E 1981 Genetic divergence among some brown plant hopper rice varieties. *Indian Journal of Genetics and Plant Breeding* 41 : 179-185.
- Rao S S, Singh S P and Rao S K 1984 Estimation of Additive, Dominance, Digenic Epistatic interaction effects for yield and its components in Mungbean (Vigna radiata (L.) Wilczek). *Legume Research* 7 : 6-12.
- Rao S K and Suryawanshi 1988 Genotype x environment interactions in the genetic diversity of urd germplasm collections. *Legume Research* 11 : 15-20.
- RAPA 1988 Regional office for Asia and Pacific Food and Agriculture Organisation of the United States. In pulses in Asia-Pacific Region, Bangkok, Thailand No.13.
- Rathnaswamy R, Krishnaswamy S, Iyem Perumal S and Marappan P 1978 Estimates of variability correlation coefficient and path coefficient analysis in early maturing greengram (Vigna radiata (L.) Wilczek). *Madras Agricultural Journal* 65-188-190.

- Rathnaswamy R, Thangaraj M, Shanmugam A S and Sree Rangaswamy 1986 Characters limiting productivity in Vigna radiata L. Wilczek. Madras Agricultural Journal 73 : 433-38.
- Raut S K, Chaudhari M S and Khorgade P W 1988 Character association and path analysis in Greengram (Vigna radiata (L.) Wilczek). Annals of Plant Physiology 2 : 37-42.
- Reddy K N 1980 Combining ability studies for yield and its components in mungbean (Vigna radiata (L.) Wilczek). M.Sc.(Ag.) thesis, Jawaharlal Nehru Krishi Viswa Vidhyalaya, Jabalpur.
- Reddy S R and Krishnaiah V V 1977 Study of yield components and their inter-relationships in greengram. The Andhra Agricultural Journal 24 : 69-73.
- Reddy P R K and Sreeramulu C 1984 Genotype - environment interaction and stability of performance in Greengram (Vigna radiata (L.) Wilczek). Genetica Iberica 36 : 105-116.
- Roemer T 1970 Sind die errags reichen sorten erragssicherer mitt DLG 32 : 87-89.
- Rosaiah G 1985 Genetic parameters of Morphological and physiological traits of Greengram (Vigna radiata (L.) Wilczek) mutants. M.Phil. Thesis submitted to the Nagarjuna University, Guntur, A.P.
- Rosaiah G, Santhakumari D, Satyanarayana A and Rao Y K 1987 Estimates of genetic parameters of greengram (Vigna radiata (L.) Wilczek). Indian Journal of Botany 10 : 1-6.
- Samolo B N, Sinha S K and Singh J M 1979 Adaptability of some EMS - induced greengram mutants. Indian Journal of Agricultural Sciences 49 : 776-781.
- Sandhu T S, Bhullar B S, Cheema H S and Brar J S 1978 Grain protein, yield and its components in urdbean. Indian Journal of Genetics and Plant Breeding 38 : 410-15.
- Sandhu T S, Bhullar B S, Cheema H S and Gill A S 1979 Variability and inter relationships among grain protein, yield and yield components in mungbean. Indian Journal of Genetics and Plant Breeding 39 : 480-84.

- Sandhu T S, Bhullar B S, Cheema H S and Brar J S 1980 Path coefficient analysis for grain yield and its attributes in greengram. Indian Journal Agricultural Sciences 50: 541-544.
- Sandhu T S, Singh K and Singh B 1988 Mungbean germplasm resources - evaluation and utilization. In Proceedings of the Second International Symposium on Mungbean held at Bangkok Thailand.
- Sagar P and Chandra S 1977 Heterosis and combining ability in Urdbean. Indian Journal of Genetics and Plant Breeding 37: 420-424.
- Sanghi A K and Kandalkar V S 1983 Phenotypic stability of seed yield and its components in Fodder Cowpea. Indian Journal of Genetics and Plant Breeding 43: 164-67.
- Santhisree O 1985 Genetic divergence for some quantitative characters in greengram. M.Sc (Ag) Thesis submitted to Andhra Pradesh Agricultural Univeristy Hyderabad.
- Sarbhoy R K 1977 Cytogenetical studies in the genus phaseolus L. III Evolution in the genus phaseolus - Cytologia 42: 401-413.
- Sarbhoy R K 1978 Cytogenetical studies in genus phaseolus L. I and II Sc matic and meiotic studies in fifteen species of phaseolus. Cytologia 43: 161-70.
- Satiya D R, Bedi C K and Gupta V P 1988 Quality improvement in Mungbean. A new approach. Proceedings of the Second International Symposium held at Bangkok November 16-20 1987 pp 152-158.
- Satyan B A, Ranganatha A R G and Aswathappa N 1981 Genetic variability in greengram. Pulse Crops News Letter 1: 15.

- Sen N K and Ghosh A K 1960 Interspecific hybridization between , Phaseolus aureus Roxb (Greengram) and Phaseolus mungo (L.) (Blackgram). Bulletin of Botanical Society, Bengal 14 : 1-4.
- Sen N K and Murthy A S N 1960 Inheritance of seed weight in greengram (Phaseolus aureus Roxb). Genetics 45 : 1559-1562.
- Shah R M and Patel J D 1981 Heritability of grain yield and its components in greengram (Vigna radiata (L.) Wilczek). Pulse crops News Letter 1 : 26.
- Shaik M A Q, Ahmed Z U and Oram R N 1988 Winter and Summer Mungbean Breeding for improving disease resistance and yield. Proceedings of the Second International Mungbean Symposium held at Bangkok, November 16-20 1987 pp 124-129.
- Shakoor A, Ahsaulhag and Sadiq M 1978 Induced variation in mungbean (Vigna radiata (L.) Wilczek). Environmental Experimental Biology 18 : 169-175.
- Shamsuzzaman K M, Khan M R H and Shaikh M A Q 1983 Genetic variability and character association in mungbean (Vigna radiata (L.) Wilczek). Bangladesh Journal of Agricultural Research 8 : 1-5 (cf: PBA 1985 55 : 1386).
- ✓Shanmugam A S and Sree Rangaswamy S R 1983 Variability and association studies for seedling characters in Blackgram (Vigna mungo (L.) Hepper). Madras Agricultural Journal 70 : 222-227.
- Shanmugasundaram S 1988 A catalog of Mungbean cultivars released around the World. Asian Vegetable Research and Development Centre. Tropical Vegetable Information Service, Shanhua, Tainan pp 6-8.
- Shanmugasundaram S and Poehlman J M 1988 In Genetics, Cytoogenetics and Breeding of crops (Eds) by Mandal A K (in Press).

Shanmugam AS and Sree Rangaswamy S R 1982a Multivariate analysis of genetic divergence in blackgram (Vigna mungo L.). Madras Agricultural Journal 69 : 701-706.

Shanmugam A S and Sree Rangaswamy S R 1982b Genetic diversity for quantitative characters in greengram Vigna radiata (L.) Wilczek). Madras Agricultural Journal 69 : 631-636.

Shanmugam A S and Sree Rangaswamy S R 1982c Genetic differentiation between greengram and blackgram. Genetica Agraria 38 : 149-160.

Sharma D and Bhadourai S S, Laxman Singh and Sharma H K 1984 Genetic analysis of protein content in pigeonpea. Indian Journal of Genetics and Plant Breeding 34 : 230-35.

Shukla G E 1972 Some statistical aspects of partitioning genotype - environment components of variability. Heredity 29 : 237-45.

Shull G H 1914 Methods of plant breeding by Hayes H K, Immer F R and D C Smith 1955 Mc Graw hill book Company, New York 53.

Siddaraju I G 1987 Studies on variability, correlation and genetic advance in greengram (Vigna radiata (L.) Wilczek. M.Sc.thesis submitted to University of Agricultural Science, Bangalore.

Singh T P 1970 Combining ability and genetic parameters in greengram (Phaseolus aureus Roxb.). Unpublished Ph.D.thesis, Punjab Agricultural University, Ludhiana.

Singh T P 1974a Epistatic bias and gene action for protein content in greengram (Phaseolus aureus Roxb.) Euphytica, 23 : 459-65.

- Singh K B 1974b Exploitation of heterosis in pulse crops. Proceedings of the second General Congress of the Society for Advancement of Breeding Researches in Asia and Oceania. Session XII. Improvement of grain legumes, New Delhi. Indian Society of Genetics and Plant Breeding 34 : 752-756.
- Singh M 1980 Genetic and Immunochemical analysis of heterosis in greengram (Vigna radiata (L.) Wilczek. Thesis abstracts 6 : 305-306.
- Singh D P 1982 Genetics and breeding of blackgram and greengram. Research Bulletin No.109 G B Pant University of Agriculture and Technology, Pantnagar 1-68.
- Singh R P 1984 Diallel analysis in Greengram. Journal of Research, Assam Agricultural University, 5 : 143-146.
- Singh S P 1988 Clustering of Isoresponsive genotypes in Mungbean (Vigna radiata (L.) Wilczek) using parametric and Non-parametric approaches in Mungbean. Proceedings of the Mungbean Second Inter-national Symposium held at Bangkok, Thailand pp 169-173.
- Singh B and Bhatnagar P S 1965 Correlation studies in mungbean. Indian Journal of Genetics and Plant Breeding. 25 : 105-107.
- Singh R B and Bains S S 1968 Genetic divergence for ginning outturn and its components in upland cotton (Gossypium hirsutum (L)) Varieties obtained from different geographic locations. Indian Journal of Genetics and Plant Breeding. 28 : 262-68.
- Singh R B and Gupta M P 1968 Multivariate analysis of divergence in upland cotton (Gossypium hirsutum (L)). Indian Journal of Genetics and Plant Breeding. 28 : 151-57.

Singh K B and Jain R P 1970 Heterosis in mungbean. Indian Journal of Genetics and Plant Breeding. 30: 244-50.

Singh K B and Malhotra R S 1970a Inter relationship between yield and yield components in mungbean. Indian Journal of Genetics and Plant Breeding 30:244-50

Singh K B and Malhotra R S 1970b Estimates of genetic and environmental variability in mung (Phaseolus aureus Roxb.). Madras Agricultural Journal 57 : 157-59.

Singh T P and Singh K B 1970a Heterosis in Field pea. Indian Journal of Genetics and Plant Breeding 30 : 619-624.

Singh T P and Singh K B 1970b Inheritance of clusters per noode in Mungbean (Phaseolus aureus Roxb.). Current Science 39 : 265.

Singh K B and Jain R P 1971a Combining ability for pod length and seed size in mungbean. Indian Journal of Genetics and Plant Breeding 31 : 145-48.

Singh K B and Jain R P 1971b Analysis of diallel cross in Phaseolus aureus Roxb. Theoretical and Applied Genetics 41:279-81

Singh K B and Singh J K 1971 Heterosis and combining ability in Blackgram. Indian Journal of Genetics and Plant Breeding 31 : 491-498.

Singh T P and Singh K B 1972 Combining ability in mungbean. Indian Journal of Genetics and Plant Breeding. 32 : 67-72.

Singh T P and Singh K B 1972 Moode of inheritance and gene action for yield and its components in Phaseolus aureus. Canadian Journal of Genetics and Cytology. 14 : 517-25.

- Singh T P and Singh K B 1973a Association of grain yield and its components in segregating populations of greengram. *Indian Journal of Genetics and Plant Breeding*. 33 : 112-17.
- Singh T P and Singh K B 1973b Combining ability for protein content in Mungbean. *Indian Journal of Genetics and Plant Breeding*. 33 : 430-35.
- Singh T P and Singh K B 1974a Heterosis and combining ability in Phaseolus aureus Roxb.. *Theoretical Applied Genetics* 44 : 12-16.
- Singh T P and Singh K B 1974b Components of genetic variance and dominance pattern for some quantitative traits in mungbean (Phaseolus aureus Roxb.). *Zeitschrift für Pflanzenzüchtung*. 71 : 233-42.
- Singh S P, Singh H B, Misra S N and Singh A B 1968 Genotypic and phenotypic correlations among some quantitative characters in mungbean. *Madras Agricultural Journal* 55 : 233-37.
- Singh K B, Bhullar G S, Malhotra R S and Singh J K 1972 Estimates of genetic variability, correlation and path coefficients in urd and their importance in selection. *Journal of Research, Punjab Agricultural University, Ludhiana* 9 : 41-46.
- Singh U P, Singh V and Singh P 1975 Estimates of variability, heritability and correlations for yield and its components in urd (Phaseolus mungo (L.)). *Madras Agricultural Journal* 62 : 71-72.
- Singh R K and Chaudhury B D 1979 Biometrical methods in quantitative genetic analysis. Kalyani Publishers, Ludhiana. pp 304.
- Singh S P and Ramanujam S 1981 Genetic divergence and hybrid performance in Cicer arietinum. *Indian Journal of Genetics and Plant Breeding*. 41 : 268-276.

- Singh V P and Malik B P S 1985 Studies on harvest index and related characters in greengram (Vigna radiata (L.) Wilczek. Legume Research 8 : 107-108.
- Singh R P and Pathak M M 1986 Variability studies in mungbean. Pulse Crops Newsletter 6 - 26 27.
- Singh D P and Sharma B L 1981 Evaluation of Mungbean Germplasm. Madras Agricultural Journal 68 : 289-95.
- Singh H B, Joshi B S and Thomas T A 1970 The phaseolus group. In pulse crops of India, ICAR, New Delhi.
- Singh H B, Joshi B S, Chandel K P S, Pant K C and Sarena R K 1974 Genetic diversity in some Asiatic Phaseolus species and its conservation. Indian Journal of Genetics and Plant Breeding. 34 A : 52-57.
- Singh K K, Hasan W, Singh S P and Prasad R 1976 Correlation and regression in greengram (Phaseolus aureus Roxb.). Proceedings of Bihar Academy of Agricultural Sciences. 24 : 40-43.
- Singh D P, Vaidya K R and Bhatt D D 1979 Gamma rays induced variability in Moong following two methods of handling M² poplations. Tropical grain legume Bulletin. 19 : 30-34.
- Singh S P, Yadav B S and Narsinghani V G 1984 Stability of yield components in pea. Indian Journal of Agricultural Sciences 54 : 608-12.

- Singh K N, Singh Santoshi V and Singh H G 1984 Genetic analysis of yield and yield components and protein content in pea. Analysis of general and specific combining ability. Indian Journal of Genetics and Plant Breeding. 44 : 515-91.
- Singh V P, Tomer Y S and Malik B P S 1987 Stability analysis for seed yield in pigeonpea Agricultural Science Digest. 7 : 203-207.
- Singh K P, Tyagi C S and Choudhary B D 1988 Stability analysis for phenological traits in chickpea. (Cicer arietinum) L.). Indian Journal of Agricultural Sciences. 139-40.
- Sohoo M S, Arora N D, Lodhi G P and Chandra S 1971 Genotypic and phenotypic variability in cowpeas (Vigna sinensis under different environmental conditions. Journal of Research. Punjab Agricultural University. 8 : 159-64.
- Solomon S, Argikar G P, Solanki M S and Morbad I R 1957 A study of heterosis in Cajanus Cajan (L) Mill SP. Indian Journal of Genetics and Plant Breeding. 17 : 90-95.
- Sprague G F 1976 Quantitative genetics in plant breeding. In Plant Breeding (eds) Frey K J IOWA State University IOWA.
- Sprague G F and Tatum L A 1942 General and specific combining ability in single crosses of corn. Agronomy Journal. 34 : 923-32.
- Sprague G F and Federar W T 1951 A comparison of various components in corn yield trials II. Error, year x variety, location x year and variety components. Agronomy Journal 43: 535-41.
- Sreekumar S G and Abraham A T 1978 Heterosis in greengram. Agricultural Research Journal Kerala 16: 142-147.

- Sreekumar C J A, Hill J, Breese E L and Davies A 1970 Assessing and predicting environmental response in Lolium Perenne. Journal of Agricultural Sciences (Camb). 75 : 1-9.
- Sree Ranga Swamy, Muralidharam V and Rathnaswamy R 1988 Breeding Behaviour of Vigna radiata - Vigna mungo hybrid progenies for crop improvement in mungbean. In mungbean proceedings of the second international symposium on mungbean held at Bangkok, Thailand. 187-194.
- Subramanian D 1979 Morphological studies in Vigna Savi and its related genera. Journal of Indian Botanical Society. 58 : 247-256.
- Suman Sahai and Rana R S 1980 Homology and differentiation in Phaseolus. Indian Journal of Genetics and Plant Breeding. 40 : 311-15.
- Swindell R E and Poehlman J M 1976 Heterosis in Mungbean (Vigna radiata (L.) Wilczek). Tropical Agriculture 53: 25-30.
- Swindell R E and Poehlman J M 1978 Inheritance of photoperiod response in mungbean (Vigna radiata (L.) Wilczek). Euphytica 27:325-333.
- Tai G C C 1971 Genotypic stability analysis and its application to potato regional trials. Crop Science 11: 684-90.
- Tawar M L and Shdhanshu Jain 1988 Combining ability and heterosis analysis for yield and its components in Mungbean (Vigna radiata (L.) wilczek). Narendra Deva. Journal of Agricultural Research. 3 : 141-146.
- Tawar M L, Misra A K, Rao S K and Verma S M 1988 Genetic divergence in Mungbean. Legume Research. 11 : 109-113.

- Thandapani V and Rao J S 1984 Yield parameters and their significance in greengram (Vigna radiata (L) wilczek) genotypes in relation to yield. Madras Agricultural Journal. 71 : 232-36.
- Thandapani V and Rao J S 1984 Partitioning of nutrient elements and assimilates in relation to productivity of greengram. (Vigna radiata (L) wilczek). Madras Agricultural Journal. 71 : 321-27.
- Thandapani V 1985 Nutrient content of Nitrogen, phosphorus, potassium, calcium and magnesium in Greengram (Vigna radiata (L) wilczek) at different growth stages in relation to yield. Madras Agricultural Journal. 72 : 303-310.
- Tickoo J L, Ahn C S, Chen H K and Shanmugasundaram S 1988 Utilization of the genetic variability from AVRDC Mungbean germplasm. Proceedings of the Second International Symposium on Mungbean Bangkok, Thailand. pp.103-110.
- Tiwari A S and Ramanujam S 1974 Partial diallel analysis of combining ability in Mungbean. Zits Chrifts Plazenzu Chtung 31: 103-11.
- Tiwari A S and Ramanujam S 1976 Combining ability, heterosis for protein and methionine contents in mungbean. Indian Journal of Genetics and Plant Breeding. 36 : 353-57.
- Tomar G S, Laxman Singh, Misra R K and Sharma D 1972 Effect of environment on character correlation and heritability in greengram. Society for Advancement of Breeding Researches in Asia and Oceania Newsletter. 4 : 49-52.
- Tomar G S, Laxman Singh, Misra R K 1973 Correlation and path coefficient analysis of yield characters in Mungbean. Society for Advancement of Breeding Researches in Asia and Oceania Newsletter. 5 : 125-127.

- Tsou C S, Hsu M S, Tan S T and Park H G 1979 The protein quality of Mungbean and its improvement. *Acta Horticulture*. 93 : 279-287.
- Upadhyia L P and Singh R B 1981 Path coefficient analysis in greengram populations of different maturity groups. *Journal of Research Assam Agricultural University* 2: 132-140.
- Upadhyia L P, Singh R B and Agarwal R K 1980 Character Association in Greengram populations of different maturity groups. *Indian Journal of Agricultural Sciences*. 50 : 473-76.
- Van Rheenen H A 1964 Preliminary study of natural cross fertilization in mungbean. *Netherlands Journal of Agricultural Sciences*. 12 : 260-62.
- Vavilov N I 1926 The origin, variation, immunity and breeding of cultivated plants. Translation by Chester K S, *Chromica Botanica*. 13. 1951.
- Veeraswamy R, Rathnaswamy and G A Palaniswamy 1973 Genetic variability in some quantitative characters of Phaseolus aureus Roxb. *Madras Agricultural Journal*. 60 : 1320-22.
- Verdcourt B 1970 Studies in the Leguminosae papilionoideae for the Flora of tropical East Africa 'IV' *Kew Bulletin*. 24 : 407-63.
- Verma M M, B R Murthy and H B Singh 1973 Adoption and genetic diversity in soybean II. Genetic diversity and relationship with adaptation. *Indian Journal of Genetics and Plant Breeding*. 33 : 326-33.
- Verma M M, Chahat G S and Murty B R 1978 Limitations of conventional regression analysis. A proposed modification. *Theoretical Applied Genetics*. 53 : 89-91.

- Verma M M, Gill K S and Virk D S 1987 Genotype - Environment interaction - Its measurement and significance in plant breeding. Punjab Agricultural University Ludhiana p 101.
- Verma M M and Sandhu S S 1988 Development of Mungbean varieties for favourable environments. A new selection methodology. Proceedings of the Second International Symposium on Mungbean Bangkok, Thailand. pp. 159-63.
- Vidhadhar, Sharma G S and Gupta S C 1984 Path analysis in greengram. Indian Journal of Agricultural Sciences. 544 : 144-45.
- Virmani S S, Singh K B, Kuldip Singh and Malhotra R S 1983 Evaluation of Mungbean germplasm. Indian Journal of Genetics and Plant Breeding. 43 : 54-58.
- Vishnuswarup and Chagle D S 1962 Studies on the genetic variability in Sorghum. Phenotypic variation and its heritable component in some important quantitative characters contributing towards yield. Indian Journal Genetics and Plant Breeding 23: 31-36.
- Watt E E and Marechal R 1977 The difference between mung and urd beans. Tropical Grain Legume Bulletin. 7 : 31-33.
- Westerman J M and Lawrence M J 1970 Genotype - environment interaction and developmental regulation in Arabidopsis thaliana L. Inbred lines, description. Heredity 25: 609-27.
- Whaley W G 1952 In Heterosis (ed' John W Groven). Iowa State College Press, Ames.
- Whigham D K, Minor H C and Carmer S G 1978 Effects of environmental and management on soybean performance in the tropics. Agronomy Journal. 70 : 587-92.
- Wilczek R 1954 In Flora congo Belge at Ruanda Urunde Vol. VI, Brussels.

- Williams W and Gilbert N 1960 Heterosis and inheritance of yield in the Tomato. *Heredity*. 15 : 133-50.
- Wilson D, Mercy S T and Nayar N K 1985 Combining ability in greengram. *Indian Journal of Agricultural Sciences*. 55 : 665-70.
- Wricke G 1962 Uber eine methode zur erfassung der okologischen streubreite in Feldversuchen. *Z. pflanzen zuchtg* 47: 92-96.
- Wright S 1921 Correlation and Causation. *Journal of Agricultural Research*. 20 : 557-585.
- Xianghuai He, Tsoyuanhe, Youneng Xiang and Chauenhai Jiao 1988 Research and use of Mungbean germplasm resources in Hubei China. In the Proceedings of the Second International Symposium on Mungbean, Bangkok Thailand.
- Yadhav I S and Kumar D 1985 Association between stability parameters of productive traits in Blackgram. *Madras Agricultural Journal*. 70 : 331-333.
- Yadava I S and Tommer R P S 1986 Genotype x environment interaction for plant height in urdbean. *Pulse Crop News Letter* 6: 13-14.
- Yadav I S and Tomer R P S 1985 Protein content and its stability in Blackgram. *Indian Journal of Agricultural Sciences*. 55 : 510-512.
- Yadava H S and Rao S K 1986 Genetics of yield and its components in Mungbean (*Vigna radiata* (L) wilczek). *Egyptian Journal of Genetics and Cytology*. 15 : 119-124.
- Yadavendra S P and Dixit S K 1987 Stability for seed protein in Chickpea. *Indian Journal of Agricultural Sciences*. 57 : 876-9.

Yates F and Cochran W G 1938 The analysis of group of experiments. Journal of Agricultural Sciences 28: 556-80.

Yohe J M and Poehlman J M 1972 Genetic variability in the mungbean (Vigna radiata (L) wilczek). Crop Science. 12 : 461-64.

Yohe J M and Poehlman J M 1975 Regressions, correlations and combining ability in Mungbean (Vigna radiata (L.) Wilczek). Tropical Agriculture 34: 343-52.

...

VITA

I, Nagubudi Varadarajulu Naidu, was born on 1st July, 1957 to Smt.N.Sheshamma and Sri N.Durvasulu Naidu alias Ramaiah Naidu at Muttukurupalle village, Chittoor District.

I have completed my S.S.C. from Zilla Parishad High School, Naraharipet, Gudipala Mandal, in 1973 and Intermediate from P.C.R. Government Junior College, in Chittoor district during 1975. I completed B.Sc. (Ag.) from S.V.Agricultural College, Tirupati in 1979 and M.Sc. (Ag.) at the College of Agriculture, Rajendranagar, A.P. Agricultural University, Hyderabad during 1979-1981.

I took admission into Ph.D. programme majoring Genetics and Plant Breeding at the College of Agriculture, Rajendranagar, Andhra Pradesh Agricultural University in the year 1981. Later I joined in A.P. Agricultural University in 1983 as Research Assistant and worked at ARS, Perumallapalle and as Assistant Research Officer at RARS, Tirupathi during 1983-87. Presently I am working as Asst.Research Officer in Pulse Breeding at RARS Lam, Guntur. I worked on greengram for my Ph.D. thesis work under the guidance of

Dr.A.Satyanarayana, Senior Scientist Pulses, RARS, Lam,

Guntur.