STUDY OF GENETIC DIVERGENCE FOR GRAIN YIELD AND YIELD COMPONENTS IN FINGER MILLET (*Eleusine coracana* (L.) Gaertn.)

BY

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B.Sc. (Ag.)

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

MASTER OF SCIENCE IN AGRICULTURE

(GENETICS AND PLANT BREEDING)

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2013

CERTIFICATE

Mr. NISHIT DEBBARMA has satisfactorily prosecuted the course of research and that the thesis entitled “**STUDY OF GENETIC DIVERGENCE FOR GRAIN YIELD AND YIELD COMPONENTS IN FINGER MILLET [*Eleusine coracana* (L.) Gaertn]**” submitted is the result of the 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 the degree of any university.

Date:

Place:

(**Dr. P.V. RAMA KUMAR**)
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CERTIFICATE

This is to certify that the thesis entitled **“STUDY OF GENETIC DIVERGENCE FOR YIELD AND YIELD COMPONENTS IN FINGER MILLET (*Eleusine coracana* (L.) Gaertn.)”** submitted in partial fulfillment of the requirements for the degree of ‘Master of Science in Agriculture’ of the Acharya N.G. Ranga Agricultural University, Hyderabad is a record of the bonafied original research work carried out by **Mr. NISHIT DEBBARMA** under our guidance and supervision.

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

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Date:

Place: Bapatla ***(Nishit Debbarma)***

LIST OF SYMBOLS AND ABBREVIATIONS

AICSMIP	:	All India Coordinated Small Millet Improvement Project
A.M	:	Ante meridiem
ANOVA	:	Analysis of Variance
ARS	:	Agricultural Research Station
CV	:	Co-efficient of Variation
CD	:	Critical Difference
cm	:	Centimetre
GA	:	Genetic Advance
GAM	:	Genetic Advance as per cent of Mean
GCV	:	Genotypic Co-efficient of Variation
k	:	Constant based on selection intensity
log	:	Logarithm
mm	:	Millimetre
M t	:	Million tonnes
M ha	:	Million Hectares
NS	:	Non-significant
PCV	:	Phenotypic coefficient of variation
PCA	:	Principal Component Analysis
RCBD	:	Randomized complete block design
S	:	Significant
SD	:	Standard Deviation
SEm	:	Standard Error of mean
%	:	Per cent
^{0}C	:	Degree centigrade

df	:	Degrees of freedom
et al.,	:	and co-workers
h^2 (b)	:	Heritability in broad sense
ha	:	Hectare
Plant^{-1}	:	Per plant

DECLARATION

I, Mr. **NISHIT DEBBARMA** hereby declare that the thesis entitled “**STUDY OF GENETIC DIVERGENCE FOR GRAIN YEILD AND YEILD COMPONENTS IN FINGER MILLET [*Eleusine coracana* (L.) Gaertn]**” submitted to the Acharya N. G. Ranga Agricultural University for the degree of Master of Science in Agriculture in the field of **Genetics and Plant Breeding** is the result of original research work done by me. I also declare that the thesis or any part thereof has not been published earlier in any manner.

Place: (**NISHIT DEBBARMA**)

Date: **I.D. No. BAM-11-18**

ABSTRACT

Name of the author	:	**NISHIT DEBBARMA**
Title of the thesis	:	**STUDY OF GENETIC DIVERGENCE FOR GRAIN YIELD AND YIELD COMPONENTS IN FINGER MILLET (*Eleusine coracana* (L.) Gaertn)**
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University	:	**ACHARYA N. G. RANGA AGRICULTURAL UNIVERSITY**
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The present investigation was carried out during *kharif* 2012 at Agricultural College Farm, Bapatla with 60 genotypes of finger millet (*Eleusine coracana* (L.) Gaertn) to study variability, heritability, genetic advance as per cent of mean, genetic divergence, character association and the magnitude of direct and indirect effects of 10 yield component traits *viz.* days to 50% flowering, days to maturity, plant height (cm), number of productive tillers, number of fingers ear^{-1}, finger length (cm), number of grains panicle^{-1}, test weight, seed protein % with grain yield plant^{-1}.

The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation, indicating the masking effect of the environment. Moderate to high variability and high heritability coupled with high genetic advance as per cent of mean were observed for days to 50% flowering, days to maturity, plant height, number of fingers ear^{-1}, finger length, number of grains panicle^{-1}, test weight, seed protein % and grain yield plant^{-1} indicating the predominance of additive gene action and hence, direct phenotypic selection may be useful for these traits.

Correlation and path analysis indicated that the traits like days to 50% flowering, days to maturity, test weight, number of fingers ear^{-1}, number of grains panicle^{-1} and seed protein % may be utilized in selection to evolve high yielding varieties of finger millet.

The results of multivariate analysis indicated the presence of considerable genetic divergence among the 60 genotypes studied. The 60 genotypes were grouped into eight clusters in case of D^2 analysis and also eight clusters through Ward's minimum variance method. This analysis clearly indicated that the genetic diversity and geographical diversity were not related.

By Mahalanobis' D^2 statistic, it could be inferred that days to 50% flowering, days to maturity, number of fingers ear^{-1}, test weight and seed protein % contributed maximum towards genetic divergence. Based on intra-and inter-cluster distance, it is suggested to make crosses between the genotypes of clusters III (GE-4798, GE-506, GE-2963, GE-1746, GPU-48, GE-3099, GE -3453) and VII (GE-2127) or III (GE-4798, GE-506, GE-2963, GE-1746, GPU-48, GE-3099, GE -3453) and VIII (GE-666) or III (GE-4798, GE-506, GE-2963, GE-1746, GPU-48, GE-3099, GE -3453) and VI (GE-258) for evolving transgressive segregants for yield and yield components.

Principal component analysis identified four principal components (PCs), which contributed 74.71 per cent of cumulative variance. The significant factors which contributed maximum genetic divergence in PC_1 were grain yield plant^{-1}, number of grains panicle^{-1}, days to 50% flowering, plant height, days to maturity and number of productive tillers.

Agglomerative cluster analysis revealed that wide genetic distance between the genotypes of clusters II (GE-258, GE-2127, GE-666) and VIII (GE-4798, GE-506, GE-2963, GE-3453) indicating their usefulness in the breeding programmes for finger millet yield improvement.

The genotypes GE-2127, GE-666, GPU-48, GE-4798, GE-506, GE-2963 and GE-3453 showed maximum inter-cluster distance in Mahalanobis' D^2 analysis, principal component analysis and cluster analysis. So they can be exploited for the development of heterotic hybrids in future breeding programmes.

Chapter I

INTRODUCTION

Finger millet (*Eleusine coracana* Gaertn.) commonly known as 'ragi', is one of the important food crops and largely grown in southern states of India. It is indispensable to Indian agriculture as a source of grain and straw in a vast dry land area. It is an important cereal crop amongst the small millets and third in importance among millets, in the country in area and production after sorghum and pearl millet. It is cultivated mostly as a rainfed crop in India for its valued food grains and its adaptability to wide range of geographical areas and agro-ecological diversity, mostly countries in Africa and Asia. India is the major producer of finger millet in Asia. In India the crop is grown in an area of 1.6M ha with a production of 2.1M t and productivity of 1.3 t ha^{-1} (www.indiastat.com).

The major ragi growing states in India are Karnataka, Tamil Nadu, Andhra Pradesh, Orissa, Maharashtra, Uttar Pradesh, Bihar and Gujarat. These eight states together account for more than 95 per cent of the total area under cultivation and more than 98.13 per cent of the total finger millet production in the country. Among them, Karnataka and Tamil Nadu are the major contributors accounting for 56.17 per cent of the total production.

In Andhra Pradesh, finger millet locally termed as Ragi, Chodi or Taidulu is grown mainly in hilly tracts of tribal belt. It is grown in an area of 45,000 ha with a production of 53,000 t and a productivity of 1.17 t ha^{-1} (Ministry of Agriculture, 2010).

Ragi is commonly called as "Nutritious millet" as the grains are nutritionally superior to many cereals providing fair amount of proteins, minerals, calcium and vitamins in abundance to the people. It is the cheapest and preferred food crop of economically suppressed but physically hard working people. It is appreciated by the people; because it can digest slowly thereby furnish energy for hard work throughout the day. Finger millet meets the first and most needs of mankind, the energy and hunger satisfaction. It leaves a sense of being well fed to any farmer. The protein of finger millet has been reported to possess a fairly high biological value, which is needed for the maintenance of nitrogen equilibrium of the body.

The cultivated finger millet is a tetraploid (2n = 4x = 36) and has morphological similarity to both *Eleusine indica* (L.) Gaertn. (2n = 18) and *Eleusine africana* (2n = 36). The cytological evidences indicate that *Eleusine Indica* has contributed one of the genomes (AA) to the cultivated *Eleusine coracana* (AABB). Both tetraploids *Eleusine africana* and *Eleusine coracana* are closely related and gene flow occurring between them in nature suggests that *Eleusine coracana* possibly originated from *Eleusine africana* through selection (Hilu and Wet, 1976).

The higher fibre content of finger millet helps in many ways as it prevents constipation, high cholesterol formation and intestinal cancer. Hence, people suffering from diabetics are advised to eat finger millet and other small millets instead of rice (Hadimani and Malleshi, 1993).

The yield potential of this crop is low and plagued with a number of diseases. Though the crop has been important over centuries, more concentrated research efforts are geared up only in recent years to evolve improved varieties and develop production technology.

In order to achieve the goal of increased production by increasing the yield potential of genotypes, the knowledge of variability, inheritance, direction and magnitude of association between various traits and their stable performance is essential for plant breeder. Expression of grain yield is complex and depends upon the interplay of number of component attributes.

A clear picture of contribution of each component to final expression of a complex character would emerge through the study of correlations and path concept which reveals different ways in which component attributes influence the complex trait.

The choice of suitable parents is of paramount importance for a planned hybridization programme. Hence it is imperative to identify the best parents with wide genetic divergence for characters of economic importance, so that they can be utilized in breeding programme to produce desirable recombinants.

Keeping the above aspects in considerations the present investigation is proposed with the following objectives:

1. To estimate variability, heritability and genetic advance for yield and yield components.
2. To study the genetic divergence among 60 genotypes of finger millet.
3. To assess the character association among yield and yield components in finger millet genotypes.
4. To study the direct and indirect effects of yield components on grain yield in finger millet.

Chapter II

REVIEW OF LITERATURE

Crop varieties show wide fluctuations in their yielding ability when grown over varied environments or agro-climatic zones. This causes difficulty in demonstrating the superiority of particular variety. Each genotype has a specific environment for its maximum performance and similarly in a specific environment, a specific genotype performs better. Hence Information on the relative magnitudes of phenotypic and genotypic variability, heritability, genetic advance and correlations is of immense value in starting any breeding programme. Further, knowledge of the relative contribution of component characters to yield directly as well as indirectly through other characters is also important.

The literature related to the objectives of present study in finger millet is reviewed below under the following headings.

2.1 Genetic variability, heritability and genetic advance as per cent of mean

2.2 Character association

2.3 Path coefficient analysis

2.4 Studies of genetic divergence

2.1 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE AS PER CENT OF MEAN

2.1.1 Variability

The information on the nature and magnitude of variability for both quantitative and qualitative traits in any crop species plays major role in formulating an effective breeding programme and its success. Economic traits, which are polygenically controlled and highly influenced by environment, determine the success in breeding programme through their genotypic variability. It is therefore essential to partition the over-all variability (total variability) into heritable and non-heritable components. Knowledge on the magnitude of heritability coupled with nature and extent of variability in the breeding material gives an idea for effective genetic improvement through selection. High PCV and GCV for a character indicate high variability in that population for that character (Singh, 1998).

Patnaik and Jana (1973) studied 18 ragi varieties and their genetic and environmental variability. A wide range of genotypic and phenotypic variability was observed in the characters studied. Prabhakar and Prasad (1984) studied three intervarietal crosses of ragi in which phenotypic coefficient of variability was found high for grain yield and productive tillers. The available literature on variability in *Eleusine coracana* is presented in Table 2.1.

2.1.2 Heritability and genetic advance as per cent of mean

Hanson *et al*. (1956) defined heritability in broad sense as the ratio of genotypic variance to the total variance in the non-segregating populations. Heritability (h^2) measures the relative amount of heritable portion of the variability, while genetic advance (GA) indicates the amount of progress that can be expected with selection in a character. Johnson *et al*. (1955) reported that estimates of both heritability and genetic advance are more useful in the choice of selection method rather than heritability or genetic advance alone. High heritability coupled with high genetic advance indicates additive gene effect (Johnson *et al*., 1955) and improvement could be made for that character by simple selection based on phenotypic performance. Low genetic advance irrespective of high or low heritability leads to non-additive gene action (Panse, 1957) and improvement of that trait by simple selection may not be rewarding (Verma *et al.*, 1987).

Bandyopadhyay (1998a) reported higher estimates of heritability, GCV and genetic advance for the characters days to 50% flowering, number of productive tillers, number of fingers per ear and days to maturity in finger millet indicating non-additive gene effect. Except days to maturity other characters registered non-significant association with grain yield. Similarly, the available literature on heritability, genetic advance in *Eleusine coracana* is presented in Table 2.1.

2.2 CORRELATIONS

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

2.2.1 Association of component characters with yield

Abraham *et al.* (1989) reported positive significant association of number of productive tillers, days to 50% flowering, days to maturity and test weight with yield at phenotypic level. The number of fingers per ear showed negative non-significant association at both genotypic and phenotypic levels. He also reported positive non-significant association with days to 50% flowering, days to maturity, number of productive tillers and test weight at genotypic level. Similarly, the literature available on association of yield component characters with yield is presented in the Table 2.2.

2.2.2 Association among yield component characters

Bedis *et al.* (2006) reported that positive correlation of plant height, finger length and number of fingers per ear with grain yield and among themselves was observed suggesting that these are the major yield contributing traits in finger millet. The literature on the association among the yield component characters is presented in the Table 2.3.

Table 2.1. Review of literature on genetic variability, heritability [h^2(b)] and genetic advance (GA) in finger millet

S.No	Character studied	Material used	PCV(%)	GCV(%)	h^2 (%)	GA (as % mean)	Reference
1.	Days to 50% Flowering	54 lines	3.22	3.65	78.0	---	Patnaik (1968)
		48 lines	6.4	7.6	70.3	11.1	Chaudhari and Acharya(1969)
		81 genotypes	11.27	11.73	92.38	22.32	Setty *et al.* (1974)
		20 varieties	10.1	---	98.4	23.1	Appadurai *et al.* (1977)
		480 varieties	12.9	13.1	98.7	26.6	Mishra *et al.* (1980)
		40 strains	12.3	---	99.1	25.2	Sarvaiya *et al.* (1982)
		72 lines	---	---	97.7	---	Mishra and Patnaik (1983)
		46 lines	12.29	---	95.51	24.75	Goswami and Asthana (1984)
		30 genotypes	9.48	---	88.1	18.33	Mehta *et al.* (1985)
		20 varieties	10.8	10.9	97.7	21.9	Abraham *et al.* (1989)
		23 cultivars	13.34	13.39	99.13	27.33	Verma (1989)
		192 strains	6.8	7.37	85.12	12.9	Cauvery (1993)
		46 genotypes	---	---	76.4	21.95	Haider *et al.* (1993)
		40 genotypes	14.13	14.42	96.07	28.56	Ramaswamy *et al.* (1994)
		F_2 population of GE 447 × GE156	9.92	9.95	99.27	13.97	Ravikumar and Seetharam (1994)
		F_2 population of GE 30 × GE1409	4.62	4.67	97.85	6.31	Ravikumar and Seetharam (1994)
		40 genotypes	12.2	12.4	97.4	24.8	Chuni Lal *et al.* (1996)
		500 accessions	17.07	17.17	98.91	34.95	Malali Gowda (1996)

Contd…

S.No	Character studied	Material used	PCV(%)	GCV(%)	h^2 (%)	GA (as % mean)	Reference
		256 lines	4.74	5.07	87.36	9.12	Ravishankar (1996)
		29 genotypes	24.74	24.9	98.78	50.63	Bandyopadhyay (1998a)
		29 genotypes	11.94	11.83	---	---	Bendale *et al.* (2002)
		20 genotypes	6.51	6.26	92.55	12.40	John (2006)
		50 hybrids+8 parents	4.38	4.09	87.3	7.87	Sumathi *et al.* (2007)
		65 genotypes	94.67	83.40	77.60	15.13	Kadam *et al.* (2009)
		230 lines	10.67	10.51	97.86	21.71	Ganapathy *et al.* (2011)
		21 hybrids+7parents	8.24	8.21	99.28	16.86	Priyadharshini *et al.* (2011)
		1000 accession	4.65	4.16	80.34	7.70	Haradari *et al.* (2012)
		30 genotypes	9.68	9.64	99.17	19.78	Sahu and Pradhan (2012)
2.	Days to maturity	20 varieties	---	9.80	90.86	19.32	Dhagat *et al.* (1972)
		10 varieties	---	6.30	90.08	12.92	Agalodia *et al.* (1979)
		480 genotypes	9.80	9.70	99.90	19.90	Mishra et al. (1980)
		47 varieties	---	10.45	97.92	22.32	Goswami and Asthana (1984)
		29 genotypes	8.67	8.41	97.00	16.75	Tyagi and Koranne (1989)
		978 varieties	9.78	9.77	---	---	Purushotham Rao (1992)
		40 genotypes	7.80	7.7	97.4	16.30	Chuni Lal et al. (1996)
		500 genotypes	33.72	35.54	98.92	33.96	Malali Gowda (1996)
		29 strains	10.80	10.67	96.63	21.61	Bandyopadhyay (1998a)
		25 genotypes	9.98	9.08	82.67	17.05	Rakesh Kumar *et al.* (2000)
		176 accessions	9.21	7.73	70.50	13.38	Satish (2003)
		20 genotypes	4.69	4.47	90.75	8.77	John (2006)
		66 accessions	8.05	6.52	66	10.92	Kebere Bezaweletaw *et al.* (2006)

Contd…

S.No	Character studied	Material used	PCV(%)	GCV(%)	h^2 (%)	GA (as % mean)	Reference
		19 genotypes	6.46	6.32	95.70	13.34	Sharathababu *et al.* (2008)
		230 accessions	7.51	7.42	98.16	14.91	Ganapathy *et al.* (2011)
		29 genotypes	14.82	12.08	66.42	20.27	Dhamdhere *et al.* (2011)
		1000 accessions	2.00	0.01	13.91	0.57	Haradari *et al.* (2012)
		30 genotypes	6.77	6.76	99.66	13.91	Sahu and Pradhan (2012)
3.	Plant height	54 lines	10.19	12.36	68.4	---	Patnaik (1968)
		14 varieties	91.87	---	87.84	20.33	Rao and Pardhasarathi (1968a)
		47 varieties	12.8	13.1	95.9	25.9	Chaudhari and Acharya (1969)
		22 varieties	24.36	26.25	86.15	46.57	Kempanna *et al.* (1971)
		20 varieties	8.8	---	63.11	14.34	Dhagat *et al.* (1973)
		20 varieties	13.7	14.4	90.3	---	Mahudeswaran and Murugesan (1973)
		18 varieties	4.01	---	37.69	93.65	Patnaik and Jana (1973)
		81 genotypes	13.65	14.03	94.7	27.37	Setty *et al.* (1974)
		20 varieties	9.8	---	37.2	12.4	Appadurai *et al.* (1977)
		33 varieties	12.79	14.69	75.97	22.99	Goud and Lakshmi (1977)
		10 varieties	5.18	---	29.03	4.38	Agalodia *et al.* (1979)
		480 varieties	10.5	11.8	80.1	19.4	Mishra *et al.* (1980)
		72 lines	---	---	84.1	---	Mishra and Patnaik (1983)
		46 varieties	9.73	---	72.58	17.09	Goswami and Asthana (1984)
		20 varieties	4.8	6.0	62.8	7.8	Abraham *et al.* (1989)
		F_4 population of cross B	18.17	20.29	80.24	16.3	Prabhakar and Prasad (1984)
		F_4 population of cross C	12.42	12.43	99.92	16.04	Prabhakar and Prasad (1984)
		27 genetic stocks	7.93	12.78	38.56	10.15	Joshi and Mehra (1989)

Contd.....

S.No	Character studied	Material used	PCV(%)	GCV(%)	h^2 (%)	GA (as % mean)	Reference
		29 genotypes	10.07	14.2	50.26	12.07	Tyagi and Koranne (1989)
		23 cultivars	4.95	5.91	70.2	8.5	Verma (1989)
		F_2 population (GE 447 × GE 1409)	13.24	14.4	84.64	23.84	Ravikumar and Seetharam (1994)
		F_2 population (GE 301 × GE 156)	7.24	9.39	59.52	10.78	Ravikumar and Seetharam (1994)
		46 genotypes	---	---	69.9	21.80	Haider and Mahto (1995)
		29 genotypes	11.47	10.0	---	---	Bendale *et al.* (2002)
		20 genotypes	7.71	5.48	71.08	10.71	John (2006)
		15 hybrids+8parents	6.69	6.12	83.8	11.56	Sumathi *et al.* (2007)
		65 genotypes	52.76	45.64	90.88	28.59	Kadam *et al.* (2009)
		230 lines	17.48	16.87	97.24	34.45	Ganapathy *et al.* (2011)
		21 hybrids+7parents	8.24	8.21	99.28	16.28	Priyadharshini *et al.* (2011)
		1000 accessions	21.11	19.24	83.11	36.14	Haradari *et al.* (2012)
		30 genotypes	11.36	11.29	98.68	23.10	Sahu and Pradhan (2012)
4.	No. of productive tillers	54 lines	6.31	16.31	15.0	---	Patnaik (1968)
		47 varieties	18.3	20.58	79.5	33.8	Chaudhari and Acharya (1969)
		20 varieties	24.6	27.8	78.1	---	Mahudeswaran and Murugesan (1973)
		20 varieties	27.1	---	51.4	40.8	Appadurai *et al.* (1977)
		480 varieties	28.1	33.7	69.5	48.2	Mishra *et al.* (1980)
		40 strains	23.4	---	68.8	40.0	Sarvaiya *et al.* (1982)
		72 lines	---	---	82.0	---	Mishra and Patnaik (1983)
		F_4 population of cross A	18.28	26.52	48.15	28.30	Prabhakar and Prasad (1984)

Contd...

S.No	Character studied	Material used	PCV(%)	GCV(%)	h^2 (%)	GA (as % mean)	Reference
		F_4 population of cross B	28.88	40.79	50.39	25.90	Prabhakar and Prasad (1984)
		20 varieties	14.3	22.7	39.6	18.4	Abraham *et al.* (1989)
		F_2 population (GE 301× GE 1409)	22.16	39.21	31.94	0.79	Ravikumar and Seetharam (1994)
		F_2 population (GE 447 × GE 156)	30.30	42.02	52.00	1.07	Ravikumar and Seetharam (1994)
		46 genotypes	---	---	10.8	0.0224	Haider and Mahto (1995)
		29 genotypes	26.46	33.8	61.3	42.64	Bandyopadhyay (1998a)
		29 genotypes	44.3	53.68	---	---	Bendale *et al.* (2002)
		20 genotypes	43.71	35.69	66.67	60.02	John (2006)
		15 hybrids+8parents	18.96	16.02	71.40	27.89	Sumathi *et al.* (2007)
		65 genotypes	40.65	72.68	81.95	18.61	Kadam *et al.* (2009)
		230 lines	26.39	23.74	81.93	43.98	Ganapathy *et al.* (2011)
		21hybrids+7parents	23.02	22.07	91.87	43.57	Priyadharshini *et al.* (2011)
		1000 accessions	32.98	27.08	66.89	45.44	Haradari *et al.* (2012)
		30 genotypes	17.99	13.81	58.93	21.83	Sahu and Pradhan (2012)
5.	No. of fingers per ear^{-1}	54 lines	5.48	13.91	15.5	---	Patnaik (1968)
		14 varieties	---	27.46	67.33	18.05	Rao and Pardhasarathi (1968a)
		47 varieties	11.7	12.5	87.6	22.5	Chaudhari and Acharya (1969)
		20 varieties	7.8	---	47.42	11.1	Dhagat *et al.* (1972)
		18 varieties	14.27	---	7.92	23.69	Patnaik and Jana (1973)
		81 genotypes	12.38	14.07	77.36	22.42	Setty *et al.* (1974)
		20 varieties	6.6	---	61.27	14.3	Appadurai *et al.* (1977)
		33 varieties	14.6	17.52	69.23	24.73	Goud and Lakshmi (1977)
		10 varieties	20.9	---	90.34	40.85	Agalodia *et al.* (1979)

Contd…

S.No	Character studied	Material used	PCV(%)	GCV(%)	h^2 (%)	GA (as % mean)	Reference
		72 lines	---	---	87.0	---	Mishra and Patnaik (1983)
		F_4 population of cross A	17.88	18.6	95.68	19.3	Prabhakar and Prasad (1984)
		F_4 population of cross B	19.37	26.93	51.54	19.1	Prabhakar and Prasad (1984)
		F_4 population of cross C	29.17	29.43	99.12	18.74	Prabhakar and Prasad (1984)
		20 varieties`	18.1	19.8	83.3	33.9	Abraham *et al.* (1989)
		23 cultivars	8.63	9.61	86.43	16.54	Verma (1989)
		F_2 population (GE 301xGE 156)	53.63	56.4	90.42	8.74	Ravikumar and Seetharam (1994)
		29 genotypes	15.30	17.36	---	---	Bendale *et al.* (2002)
		50 genotypes	12.64	12.28	94.37	24.59	Anantharaju and Meenakshiganesan (2006)
		20 genotypes	22.90	20.67	82.46	38.22	John (2006)
		15 hybrids+8varieties	11.27	10.06	79.8	18.52	Sumathi *et al.* (2007)
		HR911 × *Eleusine africana*	22.56	7.25	10.52	1.61	Gowda *et al.* (2008)
		PR202 × *Eleusine africana*	17.90	14.61	65.38	23.80	Gowda *et al.* (2008)
		150 genotypes	16.01	15.03	88.1	75.25	Arun Prabhu *et al.* (2008)
		65 genotypes	40.03	25.01	39.04	32.19	Kadam *et al.* (2009)
		Indaf-8 × *Eleusine Africana*	25.48	13.49	28.00	14.51	Gowda *et al.* (2008)
		230 lines	14.62	12.36	72.85	21.59	Ganapathy *et al.* (2011)
		21hybrids+7parents	11.93	11.69	95.63	23.55	Priyadharshini *et al.* (2011)
		1000 accessions	16.66	12.71	58.50	20.08	Haradari *et al.* (2012)
		30 genotypes	17.99	15.98	87.92	30.87	Sahu and Pradhan (2012)

Contd…

S.No	Character studied	Material used	PCV(%)	GCV(%)	h^2 (%)	GA (as % mean)	Reference
6.	Finger length	54 varieties	6.95	10.60	42.6	---	Patnaik (1968)
		18 varieties	13.83	---	22.37	6.07	Patnaik and Jana (1973)
		81 genotypes	14.97	15.42	94.29	29.95	Setty *et al.* (1974)
		20 varieties	13.59	---	77.1	24.88	Appadurai *et al.* (1977)
		72 lines	---	---	91.5	---	Mishra and Patnaik (1983)
		46 varieties	27.23	---	92.91	54.07	Goswami and Asthana (1984)
		40 genotypes	32.4	32.7	97.9	66.0	Chuni Lal *et al.* (1996)
		29 genotypes	27.01	27.56	---	---	Bendale *et al.* (2002)
		50 genotypes	22.48	22.08	96.43	44.66	Anantharaju and Meenakshiganesan (2006)
		15 hybrids + 8 parents	11.14	10.37	86.7	19.89	Sumathi *et al.* (2007)
		150 lines	20.97	18.59	78.5	43.51	Arun Prabhu *et al.* (2008)
		Indaf-8 × *Eleusine africana*	19.75	17.02	74.77	30.37	Gowda *et al.* (2008)
		HR911 × *Eleusine Africana*	23.52	20.36	76.26	30.60	Gowda *et al.* (2008)
		PR202 × *Eleusine africana*	23.51	19.58	69.37	33.57	Gowda *et al.* (2008)
		65 genotypes	35.54	72.52	83.76	61.52	Kadam *et al.* (2009)
		230 lines	20.71	18.06	76.10	32.46	Ganapathy *et al.* (2011)
		21hybrids+7parents	17.87	17.33	94.02	34.62	Priyadharshini *et al.* (2011)
		1000 accessions	32.33	28.13	75.00	50.19	Haradari *et al.* (2012)
		30 genotypes	8.49	8.08	90.65	15.86	Sahu and Pradhan (2012)
7.	No. of grains panicle $^{-1}$	40 genotypes	41.30	27.9	45.7	30.9	Chuni Lal *et al.* (1996)
		66 accessions	20.24	12.21	37.00	15.22	Kebere Bezaweletaw *et al.* (2006)
		19 genotypes	8.92	9.83	82.20	26.80	Sharathbabu *et al.* (2008)

Contd…

S.No	Character studied	Material used	PCV(%)	GCV(%)	h^2 (%)	GA (as % mean)	Reference
8.	Test weight	54 lines	10.06	8.94	78.90	---	Patnaik (1968)
		20 varieties	---	6.40	25.58	66.61	Dhagat *et al.* (1972)
		10 varieties	---	6.07	89.71	33.72	Agalodia *et al.* (1979)
		F_2 Population	75.31	47.14	39.18	60.78	Shanthappa (1979)
		F_2 Population	12.36	19.11	71.18	33.37	Shanthappa (1979)
		F_3 Population	42.57	36.44	42.51	53.11	Shanthappa (1979)
		F_3 Population	17.17	11.18	14.46	18.17	Shanthappa (1979)
		40 strains	---	9.00	87.20	17.40	Sarvaiya *et al.* (1982)
		F_4 Population	15.56	15.62	99.11	14.20	Prabhakar and Prasad (1984)
		F_4 Population	24.76	24.17	98.12	28.00	Prabhakar and Prasad (1984)
		F_4 Population	29.76	28.52	95.19	20.61	Prabhakar and Prasad (1984)
		29 genotypes	15.69	9.41	59.97	0.38	Tyagi and Koranne (1989)
		F_2 Population	18.72	16.51	76.00	29.65	Venkatesh Bhat (1991)
		F_2 Population	19.15	13.86	52.17	20.62	Venkatesh Bhat (1991)
		F_3 Population	15.71	13.86	77.70	25.17	Venkatesh Bhat (1991)
		978 genotypes	19.17	19.30	---	---	Purushotham Rao (1992)
		40 genotypes	31.60	31.3	98.2	64.0	Chuni Lal *et al.* (1996)
		364 lines	16.43	10.54	41.18	13.93	Ravi Shankar (1996)
		176 accessions	22.49	20.63	84.10	38.94	Satish (2003)
		20 genotypes	16.37	15.23	86.49	29.00	John (2006)
		66 accessions	17.52	11.34	42.00	15.17	Kebere Bezaweletaw *et al.* (2006)
		19 genotypes	15.57	14.46	86.30	26.80	Sharathababu *et al.* (2008)
		29 genotypes	24.41	19.64	64.71	32.54	Dhamdhere *et al.* (2011)

Contd…

S.No	Character studied	Material used	PCV(%)	GCV(%)	h^2 (%)	GA (as % mean)	Reference
9.	Grain yield per plant	54 varieties	15.3	27.46	31.0	---	Patnaik (1968)
		14 varieties	77.25	---	52.83	40.85	Rao and Pardhasarathi (1968a)
		47 varieties	25.4	28.1	81.5	39.2	Chaudhari and Acharya (1969)
		22 varieties	33.01	41.57	63.03	53.97	Kempanna *et al.* (1971)
		20 varieties	9.65	---	13.47	7.2	Dhagat *et al.* (1972)
		20 varieties	26.2	30.8	72.2	---	Mahudeswaran and Murugesan (1973)
		18 varieties	32.10	---	36.37	24.68	Patnaik and Jana (1973)
		81 genotypes	27.32	30.23	81.68	50.68	Setty *et al.* (1974)
		20 varieties	33.6	---	56.8	32.2	Appadurai *et al.* (1977)
		33 varieties	23.16	36.85	39.27	29.84	Goud and Lakshmi (1977)
		10 varieties	12.8	---	63.38	21.89	Agalodia *et al.* (1979)
		480 varieties	28.1	33.7	69.5	48.2	Mishra *et al.* (1980)
		40 strains	23.4	---	68.8	40.0	Sarvaiya *et al.* (1982)
		F_4 population	35.69	46.52	58.64	38.1	Prabhakar and Prasad (1984)
		30 genotypes	28.82	33.29	75.0	51.41	Mehta *et al.* (1985)
		20 varieties	33.7	41.6	65.7	56.3	Abraham *et al.* (1989)
		29 genotypes	18.17	35.99	50.49	0.76	Tyagi and Koranne (1989)
		23 cultivars	37.5	38.33	95.71	75.59	Verma (1989)
		192 lines	29.58	39.41	56.32	45.68	Cauvery (1993)
		F_2 population (GE 301× GE 56)	40.69	53.47	57.9	8.96	Ravikumar and Seetharam (1994)
		46 genotypes	---	---	13.4	0.212	Haider *et al.* (1993)
		40 genotypes	33.3	33.8	97.0	67.6	Chuni Lal *et al.* (1996)
		F_3 population of (WR13 × GE1409)	27.87	29.06	92.0	59.78	Byre Gowda *et al.* (1997)
		29 genotypes	28.94	35.54	---	---	Bendale *et al.* (2002)
		20 genotypes	14.50	11.83	66.54	19.87	John (2006)

Contd…

S.No	Character studied	Material used	PCV(%)	GCV(%)	h^2 (%)	GA (as % mean)	Reference
		15 hybrids+8 parents	14.16	12.58	78.9	23.03	Sumathi *et al.* (2007)
		Indaf-8 × *Eleusine africana*	25.48	13.49	28.00	14.51	Gowda *et al.* (2008)
		HR911 × *Eleusine africana*	22.56	7.25	10.52	1.61	Gowda *et al.* (2008)
		PR202 × *Eleusine africana*	17.90	14.61	65.38	23.80	Gowda *et al.* (2008)
		150 genotypes	29.75	25.68	74.4	58.5	Arun Prabhu *et al.* (2008)
		230 genotypes	19.77	18.61	88.86	36.17	Ganapathy *et al.* (2011)
		21 hybrids+7 parents	11.58	11.33	95.73	22.83	Priyadharshini *et al.* (2011)
		1000 accessions	48.32	29.89	38.27	38.09	Haradari *et al.* (2012)
		30 genotypes	18.76	14.93	63.33	24.48	Sahu and Pradhan (2012)
10.	Protein %	57 genotype (1995, rainy season)	19.9	20.8	91.4	39.2	Maloo *et al.* (1998)
		57 genotypes (1997, rainy season)	20.6	21.6	90.9	40.5	Maloo *et al.* (1998)
		F_3 population of (Wr 13 X GE 1409)	9.85	11.65	78.0	17.89	Byre Gowda *et al.* (1999)
		F3 population of (Wr 13 X GE 1546)	9.68	9.85	87.3	18.6	Byre Gowda *et al.* (1999)
		21 hybrids+7 parents	14.19	14.18	99.82	29.18	Priyadharshini *et al.* (2011)

PCV : Phenotypic Coefficient of Variation
GCV: Genotypic Coefficient of Variation
h^2 : Heritability (broad sense)
GA : Genetic Advance

Table 2.2. Review of literature on association of component characters with grain yield in finger millet

S.No	Character	Association	S/NS	P/G	Reference
1.	Days to 50% flowering	Positive	S	-	Mahadevappa and Ponnaiya (1965)
				-	Patnaik (1968)
				P,G	Mishra and Patnaik (1983)
				G	Sarvaiya *et al.* (1982)
				-	Shantha Kumar (1988)
				P	Abraham *et al.* (1989)
				G	Haider *et al.* (1993)
				G	Haider and Mahto (1995)
				-	Mahto *et al.* (1996)
				G	Mishra (1996)
				P	Shantha Kumar and Gowda (1997)
				P	Mahto *et al.* (2000)
				P, G	Hari Krishna *et al.* (2005)
				P,G	Bedis *et al.* (2006)
				P	Haradari *et al.* (2012)
		Positive	NS	P,G	Appadurai *et al.* (1977)
				P	Sarvaiya *et al.* (1982)
				G	Abraham *et al.* (1989)
				-	Haider *et al.* (1993)
				P	Haider *et al* (1995)
				P,G	Chuni Lal *et al.* (1996)
				P	Mishra(1996)
				P	Shantha Kumar and Gowda (1997)
				-	Bandyopadhyay (1998b)
				P,G	Ganapathy *et al.* (2011)
				P,G	Sahu and Pradhan (2012)
		Negative	S	P,G	Chaudhari and Acharya (1969)
				-	Ravishankar(1996)
				P,G	Andualem and Tadesse (2011)
		Negative	NS	P,G	Chaduary (1989)
				P,G	Bandyopadhyay (1998a)
				P	Shantha Kumar and Gowda (1997)
				G	Priyadharshini *et al.* (2011)
2.	Days to maturity	Positive	S	P	Chuni Lal *et al.* (1996)
				P,G	Bedis *et al.* (2006)
				P	Haradari *et al.* (2012)
				G	Sahu and Pradhan (2012)

Contd…

S.No	Character	Association	S/NS	P/G	Reference
		Positive	NS	G	Chuni Lal *et al.* (1996)
				P,G	Ganapathy *et al.* (2011)
				P	Sahu and Pradhan (2012)
		Negative	S	P,G	Kebere Bezaweletaw *et al.* (2006)
		Negative	NS	P,G	Bandyopadhyay (1998a)
				P	John (2006)
				P,G	Sumathi *et al.* (2007)
3.	Plant height	Positive	S	-	Patnaik (1968)
				P,G	Chaudhari and Acharya (1969)
				P,G	Dhagat *et al.* (1972)
				G	Dhagat *et al.* (1973)
				P,G	Goud and Lakshmi (1977)
				P,G	Sarvaiya *et al.* (1982)
				P,G	Mishra and Patnaik (1983)
				G	Prabhakar and Prasad (1983)
				P	Chuni Lal *et al.* (1996)
				-	Mahto *et al* (1996)
				G	Mishra (1996)
				P	Shantha Kumar and Gowda (1997)
				P, G	Hari Krishna *et al.* (2005)
				P,G	Bedis *et al.* (2006)
				P,G	Andualem and Tadesse (2011)
				P,G	Ganapathy *et al.* (2011)
				P	Haradari *et al.* (2012)
				P,G	Sahu and Pradhan (2012)
		Positive	NS	P,G	Rao and Pardhasarathi (1968b)
				P,G	Mahudeswaran and Murugesan (1973)
				P,G	Appadurai *et al.* (1977)
				-	Ranganathan *et al.* (1977)
				G	Prabhakar and Prasad (1983)
				P	Abraham *et al.* (1989)
				P,G	Chaudhary (1989)
				-	Haider *et al.* (1993)
				P,G	Haider and Mahto (1995)
				G	Chuni Lal *et al.* (1996)
				P	Mishra (1996)
				P	Shantha Kumar and Gowda (1997)
				P,G	Bandyopadhyay (1998a)
				G	Priyadharshini *et al.* (2011)

Contd…

S.No	Character	Association	S/NS	P/G	Reference
		Negative	S	P	Mahto *et al.* (2000)
		Negative	NS	G	Prabakhar and Prasad (1983)
				G	Abraham *et al.* (1989)
4.	Number of Productive tillers	Positive	S	P,G	Mahdevappa and Ponnaiya (1963)
				-	Patnaik (1968)
				P,G	Chaudhari and Acharya (1969)
				P,G	Mahudeswaran and Murugesan (1973)
				P,G	Appadurai *et al.* (1977)
				-	Ranganathan *et al.* (1977)
				-	Subramanian *et al.* (1977)
				-	Agalodia *et al.* (1979)
				P	Mishra and Patnaik (1983)
				G	Prabakhar and Prasad (1983)
				-	Shantha Kumar (1988)
				-	Chaudhari (1989)
				P	Abraham *et al.* (1989)
				-	Raja Ravindran *et al.* (1996)
				P	Shantha Kumar and Gowda (1997)
				P,G	Hari Krishna *et al.* (2005)
				P,G	Ganapathy *et al.* (2011)
				P,G	Priyadarshini *et al.* (2011)
				P	Haradari *et al.* (2012)
		Positive	NS	G	Mishra and Patnaik (1983)
				G	Abraham *et al.* (1989)
				-	Haider *et al.* (1993)
				-	Bedis *et al.* (2006)
				P	Andualem and Tadesse (2011)
				P,G	Sahu and Pradhan (2012)
		Negative	S	G	Haider and Mahto (1995)
		Negative	NS	P	Haider and Mahto (1995)
				P,G	Bandyopadhyay (1998a)
5.	No. of fingers ear $^{-1}$	Positive	S	-	Patnaik (1968)
				P,G	Rao and Pardhasarathi (1968b)
				G	Goud and Lakshmi (1977)
				-	Agalodia *et al.* (1979)
				P,G	Mishra and Patnaik (1983)
				G	Prabakhar and Prasad (1983)

Contd...

S.No	Character	Association	S/NS	P/G	Reference
				-	Shantha Kumar (1988)
				-	Haider *et al.* (1993)
				G	Haider and Mahto (1995)
				P	Chuni Lal *et al.* (1996)
				-	Ravindran *et al.* (1996)
				P	Shantha Kumar and Gowda (1997)
				P,G	Hari Krishna *et al.* (2005)
				P,G	Bedis *et al.* (2006)
				P	Kadam *et al.* (2009)
				G	Shindey *et al.* (2010)
				P,G	Ganapathy *et al.* (2011)
				G	Priyadharshini *et al.* (2011)
		Positive	NS	P,G	Chaudhari and Acharya (1969)
				P	Goud and Lakshmi (1977)
				P,G	Prabakhar and Prasad (1983)
				P,G	Chaudhary (1989)
				G	Chuni Lal *et al.* (1996)
				P,G	Bandyopadhyay (1998a)
				G	Anantharaju and Meenakshiganesan (2005)
				P	Gowda *et al.* (2008)
				P	Haradari *et al.* (2012)
				P,G	Sahu and Pradhan (2012)
		Negative	S	P,G	Mahudeswaran and Murugesan (1973)
				G	Appadurai *et al.* (1977)
			-	-	Basavaraj and Sheriff (1991)
		Negative	NS	P,G	Dhagat *et al.* (1972)
				G	Dhagat *et al.* (1973)
				P	Appadurai *et al.* (1977)
				G	Prabakhar and Prasad (1983)
				P,G	Abraham *et al.* (1989)
6.	Finger length	Positive	S	-	Patnaik (1968)
				P	Mishra and Patnaik (1983)
				P	Chuni Lal *et al.* (1996)
				P	Shantha Kumar and Goud (1997,1998)
				-	Bendale *et al.* (2002)
				P,G	Hari Krishna *et al.* (2005)
				P,G	Bedis *et al.* (2006)
				G	Padmaja *et al.* (2006)
		Positive	NS	G	Mishra and Patnaik (1983)
				G	Chuni Lal *et al.* (1996)
				P	Shantha Kumar and Goud (1997,1998)

Contd…

S.No	Character	Association	S/NS	P/G	Reference
		Negative	S	P,G	Appadurai *et al.* (1997)
				P,G	Hari Krishna *et al.* (2005)
			-	-	Basavaraj and Sheriff (1991)
7.	No of grains panicle^{-1}	Positive	S	P	Chuni Lal *et al.* (1996)
				G	Kebere Bezaweletaw *et al.* (2006)
		Positive	NS	G	Chuni Lal *et al.* (1996)
				P	Kebere Bezaweletaw *et al.* (2006)
8.	Test weight	Positive	S	G	Dhagat *et al.* (1972)
			-	-	Subramanian *et al.* (1977)
			S	-	Shantappa (1980)
				P,G	Mishra and Patnaik (1983)
				-	Prabhakar and Prasad (1984)
				P,G	Sarvaiya *et al.* (1982)
				-	Dinesh Kumar (1986)
				P	Abraham *et al.* (1989)
				P	Chuni Lal *et al.* (1996)
			S	P,G	Hari Krishna *et al.* (2005)
		Positive	NS	-	Patnaik (1968)
				P	Dhagat *et al.* (1972)
				G	Prabhakar and Prasad (1983)
				G	Abraham *et al.* (1989)
				G	Chuni Lal *et al.* (1996)
		Negative	S	G	Mahudeswaran and Murugesan (1973)
				G	Prabharak and Prasad (1983)
		Negative	NS	G	Dhagat *et al.* (1973)
				P	Mahudeswaran and Murugesan (1973)
				-	Ranganathan *et al.* (1977)
				G	Prabhakar and Prasad (1983)
				P,G	Chaudhary (1989)
				P	John (2007)

Contd…

S.No	Character	Association	S/NS	P/G	Reference
9.	Seed Protein %	Negative	-	-	Dinesh Kumar (1986)
			S	-	Vadivoo *et al.* (1998)
				P	Byre Gowda *et al.* (1999)
				-	Byre Gowda *et al.* (2000)
				P,G	Hari Krishna *et al.* (2005)
				P,G	Padmaja (2006)

S : Significant P : Phenotypic
NS : Non Significant G : Genotypic

Table 2.3. Review of literature on association among component characters of grain yield in finger millet

Character	Association	S/NS	P/G	Reference
1. Association of days to 50% flowering with				
a. Days to maturity	Positive	S	P	Chuni Lal *et al.* (1996)
			P,G	Bandyopadhyay (1998a)
			P	John (2006)
			P,G	Bedis *et al.* (2006)
			P,G	Sumathi *et al.* (2007)
			P,G	Ganapathy *et al.* (2011)
			P	Haradari *et al.* (2012)
			P,G	Sahu and Pradhan (2012)
		NS	G	Chuni Lal *et al.* (1996)
b. Plant height	Positive	S	-	Patnaik (1968)
			G	Appadurai *et al.* (1977)
			P,G	Sarvaiya *et al.* (1982)
			P	Chaudhary (1989)
			-	Haider *et al.* (1993)
			G	Haider and Mahto (1995)
			-	Mahto *et al.* (1996)
			P	Mahto *et al.* (2000)
			-	Bendale *et al.* (2002)
			P,G	Hari Krishna *et al.* (2005)
			P,G	Anantharaju and Meenakshiganesan (2005)
			P,G	Bedis *et al.* (2006)
			P	Kadam *et al.* (2009)
			P,G	Ganapathy *et al.* (2011)
			G	Priyadharshani *et al.* (2011)
			P	Haradari *et al.* (2012)
	Positive	NS	P	Appadurai *et al.* (1977)
			P,G	Abraham *et al.* (1989)
			G	Chaudhary (1989)
			G	Mishra (1996)
			P	Shantha Kumar and Gowda (1997)
			P,G	Bandyopadhyay (1998b)
			P,G	Shindey *et al.* (2010)
			G	Andualem and Tadesse (2011)
	Negative	S	P	Chaudhari and Acharya (1969)
	Negative	NS	G	Chaudhari and Acharya (1969)
			P	Chuni Lal *et al.* (1996)

Contd…

Character	Association	S/NS	P/G	Reference
			P,G	Sahu and Pradhan (2012)
c. No of productive tillers plant^{-1}	Positive	S	P,G	Chaudhari and Acharya (1969)
			G	Haider *et al.* (1993)
			P,G	Haider and Mahto (1995)
			P	Shantha Kumar and Gowda (1997)
			P,G	Bandyopadhyay (1998b)
			P	Kadam *et al.* (2009)
			P,G	Ganapathy *et al.* (2011)
			P	Haradari *et al.* (2012)
	Positive	NS	P,G	Appadurai *et al.* (1977)
			P,G	Abraham *et al.* (1989)
			-	Haider *et al.* (1993)
			P	Shantha Kumar and Gowda (1997)
			P	Andualem and Tadesse (2011)
			P,G	Sahu and Pradhan (2012)
	Negative	S	P	Ravikumar and Seetharam (1993)
			P,G	Bedis *et al.* (2006)
			G	Priyadharshini *et al.* (2011)
	Negative	NS	-	Patnaik (1968)
			P	Shantha Kumar and Gowda (1997)
			G	Kadam *et al.* (2009)
			P,G	Shindey *et al.* (2010)
d. No. of fingers ear^{-1}	Positive	S	P	Chuni Lal *et al.* (1996)
			P,G	Bandyopadhyay (1998b)
			P	Kadam *et al.* (2009)
			P,G	Shindey *et al.* (2010)
	Positive	NS	-	Patnaik (1968)
			P,G	Chaudhari and Acharya (1969)
			P,G	Appadurai *et al.* (1977)
			P,G	Sarvaiya *et al.* (1982)
			P,G	Abraham *et al.* (1989)
			P,G	Chaudhary (1989)
			P	Chuni Lal *et al.* (1996)
			P	Shantha Kumar and Gowda (1997)
			P,G	Anantharaju and Meenakshiganesan (2005)
			P	John (2006)
			P	Haradari *et al.* (2012)

Contd…

Character	Association	S/NS	P/G	Reference
			P,G	Sahu and Pradhan (2012)
	Negative	S	G	Haider and Mahto (1995)
			-	Ravikumar and Seetharam (1993)
			P,G	Hari Krishna *et al.* (2005)
	Negative	NS	-	Haider *et al.* (1993)
			P,G	Ganapathy *et al.* (2011)
			G	Priyadharshini *et al.* (2011)
e. Length of finger	Positive	S	-	Patnaik (1968)
			G	Appadurai *et al.* (1977)
			P	Chuni Lal *et al.* (1996)
			P,G	Bendale *et al.* (2002)
			P,G	Bedis *et al.* (2006)
			P	Kadam *et al.* (2009)
			P,G	Ganapathy *et al.* (2011)
			G	Priyadharshani *et al.* (2011)
	Positive	NS	P	Shantha Kumar and Gowda (1997)
			P,G	Hari Krishna *et al.* (2005)
			P,G	Shindey *et al.* (2010)
	Negative	NS	P	Appadurai *et al.* (1977)
			P	Shantha Kumar and Gowda (1997)
			P,G	Hari krishna *et al.* (2005)
f. No of grains panicle^{-1}	Positive	NS	P,G	Chuni Lal *et al.* (1996)
g. Test Weight	Positive	S	-	Patnaik (1968)
			G	Sarvaiya *et al.* (1982)
	Positive	NS	P	Sarvaiya *et al.* (1982)
			P,G	Abraham *et al.* (1989)
			P,G	Chuni Lal *et al.* (1996)
	Negative	NS	G	Chaudhary (1989)
h. Grain yield plant^{-1}	Positive	S	P,G	Kadam *et al.* (2009)
			P,G	Shindey *et al.* (2010)
		NS	P,G	Anantharaju and Meenakshiganesan (2005)
	Negative	S	P	John (2006)

Contd…

Character	Association	S/NS	P/G	Reference
2. Association of Days to maturity with				
a. Plant height	Positive	S	P	Chuni Lal *et al.* (1996)
			P,G	Bedis *et al.* (2006)
			G	Sumathi *et al.* (2007)
			P,G	Kebere Bezaweletaw *et al.* (2006)
			P,G	Ganapathy *et al.* (2011)
			P	Haradari *et al.* (2012)
	Positive	NS	G	Chuni Lal *et al.* (1996)
			P	John (2006)
			P	Sumathi *et al.* (2007)
	Negative	NS	P,G	Bandyopadhyay (1998a)
			P,G	Sahu and Pradhan (2012)
b. Productive tillers	Positive	S	P	Chuni Lal *et al.* (1996)
			P	Haradari *et al.* (2012)
	Positive	NS	G	Chuni Lal *et al.* (1996)
			P,G	Bandyopadhyay (1998a)
			P,G	Sumathi *et al.* (2007)
			P,G	Ganapathy *et al.* (2011)
			P,G	Sahu and Pradhan (2012)
	Negative	S	G	Bedis *et al.* (2006)
	Negative	NS	P	John (2006)
			P	Bedis *et al.* (2006)
			P,G	Kebere Bezaweletaw *et al.* (2006)
c. No of fingers ear^{-1}	Positive	S	P	Chuni Lal *et al.* (1996)
			G	Kebere Bezaweletaw *et al.* (2006)
	Positive	NS	G	Chuni Lal *et al.* (1996)
			P	Bandyopadhyay (1998a)
			P,G	Bedis *et al.* (2006)
			P	Kebere Bezaweletaw *et al.* (2006)
			P	Sahu and Pradhan (2012)

Contd…

Character	Association	S/NS	P/G	Reference
	Negative	S	G	Bandyopadhyay (1998a)
			P	John (2006)
	Negative	NS	P,G	Sumathi *et al.* (2007)
			P,G	Ganapathy *et al.* (2011)
			G	Sahu and Pradhan (2012)
			P	Haradari *et al.* (2012)
d. Length of finger	Positive	S	P	Chuni Lal *et al.* (1996)
			P,G	Bedis *et al.* (2006)
			P,G	Sumathi *et al.* (2007)
			P,G	Ganapathy *et al.* (2011)
			P	Haradari *et al.* (2012)
	Positive	NS	G	Chuni Lal *et al.* (1996)
			P,G	Kebere Bezaweletaw *et al.* (2006)
	Negative	S		
	Negative	NS	P	John (2006)
			P,G	Sahu and Pradhan (2012)
e. No of grains panicle^{-1}	Positive	S	P	Chuni Lal *et al.* (1996)
			P,G	Kebere Bezaweletaw *et al.* (2006)
	Positive	NS	G	Chuni Lal *et al.* (1996)
	Negative	S		
	Negative	NS		
f. Test weight	Positive	S	P	Chuni Lal *et al.* (1996)
	Positive	NS	G	Chuni Lal *et al.* (1996)
			P	John (2006)
	Negative	S	P,G	Kebere Bezaweletaw *et al.* (2006)
	Negative	NS	P,G	Sumathi *et al.* (2007)
3. Association of plant height with				
a. No. of productive tillers	Positive	S	-	Patnaik (1968)
			G	Chaudhari and Acharya (1969)
			G	Appadurai *et al.* (1977)
			G	Prabhakhar and Prasad

Contd...

Character	Association	S/NS	P/G	Reference
				(1983)
			P	Ravikumar and Seetharam (1993)
			P	Shantha Kumar and Gowda (1997)
			G	Priyadharshini *et al.* (2011)
			P	Haradari *et al.* (2012)
	Positive	NS	P	Chaudhari and Acharya (1969)
			P	Appadurai *et al.* (1977)
			-	Ranganathan *et al.* (1977)
			G	Prabakhar and Prasad (1983)
			P	Abraham *et al.* (1989)
			P	Ravikumar and Seetharam (1993)
			P,G	Haider *et al.* (1993)
			P,G	Ravindran *et al.* (1996)
			P	Shantha Kumar and Gowda (1997)
			P,G	Bandyopadhyay (1998b)
			G	Anantharaju and Meenakshiganesan (2005)
			P,G	Andualem and Tadesse (2011)
			P,G	Sahu and Pradhan (2012)
	Negative	S	-	Goud and Lakshmi (1977)
			G	Prabakhar and Prasad (1983)
	Negative	NS	P,G	Mahudeswaran and Murugesan (1973)
			G	Abraham *et al.* (1989)
			P	Prabakhar and Prasad (1983)
			P	Ravikumar and Seetharam (1993)
			-	Haider *et al.* (1993)
			P	Shantha Kumar and Gowda (1997)
			P	Anantharaju and Meenakshiganesan (2005)
			P,G	Ganapathy *et al.* (2011)
b. No. of fingers ear^{-1}	Positive	S	-	Patnaik (1968)
			G	Dhagat *et al.* (1972)
			P	Goud and Lakshmi (1977)
			P,G	Sarvaiya *et al.* (1982)
			G	Prabakhar and Prasad (1983)
			P	Chaudhary (1989)

Contd…

Character	Association	S/NS	P/G	Reference
			P	Ravikumar and Seetharam (1993)
			P	Chuni Lal *et al.* (1996)
			P,G	Ravindran *et al.* (1996)
			P	Bandyopadhyay (1999b)
			-	Bedis *et al.* (2006)
			G	Gowda *et al.* (2008)
			P,G	Andualem and Tadesse (2011)
			G	Priyadharshini *et al.* (2011)
	Positive	NS	P,G	Chaudhari and Acharya (1969)
			P,G	Mahudeswaran and Murugesan (1973)
			G	Prabakhar and Prasad (1983)
			P,G	Abraham *et al.* (1989)
			G	Chaudhary (1989)
			P	Shantha Kumar and Gowda (1997)
			P,G	Bandyopadhyay (1998b)
			P,G	Shindey *et al.* (2010)
			P	Haradari *et al.* (2012)
			P,G	Sahu and Pradhan (2012)
	Negative	S	G	Goud and Lakshmi (1977)
			G	Prabakhar and Prasad (1983)
			-	Haider *et al.* (1993)
	Negative	NS	P,G	Rao and Pardharasarathi (1968b)
			G	Dhagat *et al.* (1973)
			P,G	Appadurai *et al.* (1977)
			G	Prabakhar and Prasad (1983)
			-	Haider *et al.* (1993)
			P,G	Ganapathy *et al.* (2011)
	Negative	NS	P	Shantha Kumar and Gowda (1997)
			P	Gowda *et al.* (2008)
			P	Kadam *et al.* (2009)
c. Length of finger	Positive	S	-	Patnaik (1968)
			P	Chuni Lal *et al.* (1996)
			P	Shantha Kumar and Gowda (1997)
			-	Bedis *et al.* (2006)
			P	Gowda *et al.* (2008)
			P	Kadam *et al.* (2009)
			P,G	Andualem and Tadesse (2011)
			P,G	Ganapathy *et al.* (2011)
			P	Haradari *et al.* (2012)
	Positive	NS	P,G	Appadurai *et al.* (1977)
			P	Shantha Kumar and Gowda(1997)
			P,G	Shindey *et al.* (2010)

Contd…

Character	Association	S/NS	P/G	Reference
			P,G	Sahu and Pradhan (2012)
d. No of grain panicle^{-1}	Positive	S	P	Chuni Lal *et al.* (1996)
	Positive	NS	G	Chuni Lal *et al.* (1996)
	Negative	S	P,G	Kebere Bezaweletaw *et al.* (2006)
	Negative	NS		
e. Test weight	Positive	S	-	Patnaik (1968)
			P,G	Sarvaiya *et al.* (1982)
			G	Prabakhar and Prasad (1983)
			P	Chuni Lal *et al.* (1996)
	Positive	NS	-	Ranganathan *et al.* (1977)
			G	Prabakhar and Prasad (1983)
			G	Abraham *et al.* (1989)
			P,G	Chaudhary (1989)
	Negative	S	G	Dhagat *et al.* (1972)
	Negative	NS	P	Dhagat *et al.* (1972)
			G	Dhagat *et al.* (1973)
			P	Mahudeswaran and Murugesan (1973)
			P	Abraham *et al.* (1989)
f. Grain yield plant^{-1}	Positive	S	P,G	Shindey *et al.* (2010)
		NS	P	Gowda *et al.* (2008)
	Negative	NS	-	John (2006)
			P	Gowda *et al.* (2008)

4. Association of No. of productive tillers with

Character	Association	S/NS	P/G	Reference
a. No. of fingers ear^{-1}	Positive	S	-	Patnaik (1968)
			G	Prabakhar and Prasad (1983)
			-	Chaudhary (1989)
			-	Ravindran *et al.* (1996)
			P	Shantha Kumar and Gowda (1997)
			G	Bandyopadhyay (1998b)
			P	Kadam *et al.* (2009)
			G	Andualem and Tadesse (2011)
			G	Priyadharshini *et al.* (2011)
	Positive	NS	P,G	Appadurai *et al.* (1977)
			G	Prabakhar and Prasad (1983)

Contd...

Character	Association	S/NS	P/G	Reference
			P	Ravikumar and Seetharam (1993)
			P	Shantha Kumar and Gowda (1997)
			P	Bandyopadhyay (1998b)
			P,G	Sahu and Pradhan (2012)
	Negative	NS	G	Abraham *et al.* (1989)
			P	Ravikumar and Seetharam (1993)
			-	Haider *et al.* (1993)
			P	Haider and Mahto (1995)
			P	Gowda *et al.* (2008)
			P,G	Shindey *et al.* (2010)
	Negative	S	P,G	Chaudhari and Acharya (1969)
			P,G	Mahudeswaran and Murugesan (1973)
			G	Prabakhar and Prasad (1983)
			P	Ravi Kumar and Seetharam (1993)
			G	Haider *et al.* (1993)
			P	Shantha Kumar and Gowda (1997)
			P	Haradari *et al.* (2012)
b. Length of finger	Positive	S	P	Gowda *et al.* (2008)
			P	Kadam *et al.* (2009)
		NS	-	Patnaik (1968)
			P	Chuni Lal *et al.* (1996)
			P	Shantha Kumar and Gowda (1997)
			P,G	Shindey *et al.* (2010)
			P	Haradari *et al.* (2012)
			P,G	Sahu and Pradhan (2012)
	Negative	S	G	Appadurai *et al.* (1977)
			P	Shantha Kumar and Gowda (1997)
			P,G	Hari Krishna *et al.* (2005)
	Negative	NS	P,G	Anantharaju and Meenakshiganesan (2005)
c. No of grains panicle^{-1}	Positive	NS	P,G	Chuni Lal *et al.* (1996)

Contd…

Character	Association	S/NS	P/G	Reference
	Negative	NS	P,G	Kebere Bezaweletaw *et al.* (2006)
d. Test weight	Positive	S	G	Prabakhar and Prasad (1983)
	Positive	NS	-	Ranganathan *et al.* (1977)
			G	Prabakhar and Prasad (1983)
			P,G	Abraham *et al.* (1989)
	Negative	S	-	Patnaik (1968)
			G	Mahudeswaran and Murugesan (1973)
	Negative	NS	P	Mahudeswaran and Murugesan (1973)
			G	Prabakhar and Prasad (1983)
e. Grain yield plant^{-1}	Positive	NS	P	Gowda *et al.* (2008)
			P,G	Shindey *et al.* (2010)
	Negative	NS	P	John (2006)
5. Association of number of fingers per ear with				
a. Length of finger	Positive	S	-	Patnaik (1968)
			P	Chun Lal *et al.* (1996)
			P,G	Sahu and Pradhan (2012)
	Positive	NS	P	Shantha Kumar and Goud (1997)
			P	Haradari *et al.* (2012)
	Negative	S	P,G	Appadurai *et al.* (1977)
			P	Shantha Kumar and Goud (1997)
	Negative	NS	P	Shantha Kumar and Goud (1998)
b. No of grains panicle^{-1}	Positive	S	P	Chuni Lal *et al.* (1996)
	Positive	NS	G	Chuni Lal *et al.* (1996)
	Negative	NS	P,G	Kebere Bezaweletaw *et al.* (2006)
c. Test weight	Positive	S	G	Prabhakar and Prasad (1983)
			G	Sarvaiya *et al.* (1982)

Contd…

Character	Association	S/NS	P/G	Reference
	Positive	NS	P - P	Chuni Lal *et al.* (1996) Patnaik (1968) Sarvaiya *et al.* (1982)
	Negative	S	G G G P	Dhagat *et al.* (1972) Mahudeswaran and Murugesan (1973) Prabakhar and Prasad (1983) Abraham *et al.* (1989)
	Negative	NS	P G P G G	Dhagat *et al.* (1972) Dhagat *et al.* (1973) Mahudeswaran and Murugesan (1973) Prabakhar and Prasad (1983) Abraham *et al.* (1989)
d. Grain yield	Positive	S	P,G	Shindey *et al.* (2010)
		NS	P	Gowda *et al.* (2008)
	Negative	NS	P	John (2006)
6. Association of length of finger with				
a. No. of grains panicle^{-1}	Positive	S	P	Chuni Lal *et al.* (1996)
	Positive	NS	G	Chuni Lal *et al.* (1996)
	Negative	S	G	Kebere Bezaweletaw *et al.* (2006)
	Negative	NS	P	Kebere Bezaweletaw *et al.* (2006)
b. Test weight	Positive	NS	-	Patnaik (1968)
	Negative	S	P	Chuni Lal *et al.* (1996)
c. Grain yield plant	Positive	NS	P,G	Shindey *et al.* (2010)

Contd…

Character	Association	S/NS	P/G	Reference
7. Association of No of grains panicle^{-1} with				
a. Test weight	Positive	S	P	Chuni Lal *et al.* (1996)
			G	Kebere Bezaweletaw *et al.* (2006)
	Positive	NS	G	Chuni Lal *et al.* (1996)
			P	Kebere Bezaweletaw *et al.* (2006)
b. Grain yield	Positive	S	G	Kebere Bezaweletaw *et al.* (2006)
	Positive	NS	P,G	Chuni Lal *et al.* (2006)
			P	Kebere Bezaweletaw *et al.* (2006)
8. Association of seed protein with				
a. Plant height	Negative	NS	P	Byre Gowda *et al.* (2000)
b. No. of Productive tillers	Negative	S	P	Byre Gowda *et al.* (2000)
	Negative	NS	P	Byre Gowda *et al.* (2000)
c. No of fingers ear^{-1}	Negative	S	P	Byre Gowda *et al.* (2000)
	Negative	NS	P	Byre Gowda *et al.* (2000)
d. Test weight	Negative	-	-	Byre Gowda *et al.* (2000)

S : Significant
NS : Non Significant

P : Phenotypic
G : Genotypic

2.3 PATH COEFFICIENT ANALYSIS

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

Chaudhary (1989) reported positive direct effect of plant height, tillers per plant, ears per plant and fingers on main ear on seed yield in finger millet.

Raja Ravindran *et al.* (1996) reported that number of productive tillers per plant and number of fingers on main ear had high direct effect on grain yield. While plant height showed negative and indirect effect on yield. They suggested that, selection programme based on number of productive tillers per plant and number of fingers on main ear will be effective for grain yield improvement.

Byre Gowda (1997) observed high effect of productive tillers and fingers per ear on grain yield and suggested that due weightage has to be given to the characters in breeding programme for high yield. Mahto *et al.* (2000) noticed that number of tillers per plant and days to maturity had high positive direct effect on grain yield.

Similarly the literatures available on direct and indirect effects of yield components on yield in *Elesuine coracana* are reviewed here in Table 2.4 and Table 2.5.

Table 2.4. Review of literature on direct effects of component characters on grain yield in finger millet

S.No	Character	Effect	Reference
1.	Days to 50% flowering	Positive	Appadurai *et al.* (1977) Bandyopadhyay (1998b) Mahto *et.al* (2000) Bendale *et al.* (2002) Hari Krishna *et al.* (2005) Kadam *et al.* (2009) Priyadharshini *et al.* (2011) Ganapathy *et al.* (2011)
		Negative	Chaudhary (1989) Singh *et al.* (1995) Chuni Lal *et al.* (1996) Mishra (1996) Bedis *et al.* (2006) Kadam *et al.* (2009) Andualem and Tadesse (2011) Haradari *et al.* (2012)
2.	Days to maturity	Positive	Chuni Lal *et al.* (1996) Bedis *et al.* (2006) Haradari *et al.* (2012)
		Negative	Sumathi *et al.* (2007) Kebere Bezaweletaw *et al.* (2006) Ganapathy *et al.* (2011)
3.	Plant height	Positive	Mahudeswaran and Murugesan (1973) Prabhakhar and Prasad (1983) Singh *et al.* (1995) Chuni Lal *et al.* (1996) Mishra (1996) Mahto *et.al* (2000) Bedis *et al.* (2006) Kadam *et al.* (2009)
		Negative	Dhagat *et al.* (1973) Appadurai *et al.* (1977) Ranganathan *et al.* (1977) Subramanian *et al.* (1977) Sarvaiya *et al.* (1982) Prabhakhar and Prasad (1983) Shantha Kumar and Gowda (1997)

Contd...

S.No	Character	Effect	Reference
			Bendale *et al.* (2002) Shindey *et al.* (2010) Andualem and Tadesse (2011) Ganapathy *et al.* (2011) Haradari *et al.* (2012)
4.	No. of productive tillers	Positive	Chaudhari and Acharya (1969) Mahudeswaran and Murugesan (1973) Appadurai *et al.* (1977) Prabhaakhar and Prasad (1983) Chaudhari (1989) Singh *et al.* (1995) Ravindran *et al.* (1996) Hari Krishna *et al.* (2005) Bedis *et al.* (2006) Kadam *et al.* (2009) Shindey *et al.* (2010) Priyadharshini *et al.* (2011) Haradari *et al.* (2012)
		Negative	Prabhakhar and Prasad (1983) Shantha Kumar and Gowda (1997) Bendale *et al.* (2002)
5.	No. fingers ear^{-1}	Positive	Chaudhari and Acharya (1969) Agalodia *et al.* (1979) Prabhakhar and Prasad (1983) Chaudhary (1989) Ravikumar and Seetharam (1993) Chuni Lal *et al.* (1996) Ravindran *et al.* (1996) Bedis *et al.* (2006) Andualem and Tadesse (2011) Ganapathy *et al.* (2011) Priyadharshini *et al.* (2011)
		Negative	Appadurai *et al.* (1977) Prabakhar and Prasad (1983) Chaudhary (1989) Bendale *et al.* (2002) Hari Krishna *et al.* (2005) Haradari *et al.* (2012)

Contd…

S.No	Character	Effect	Reference
6.	Length of finger	Positive	Dhagat *et al.* (1973) Chuni Lal *et al.* (1996) Marimuthu (1997) Shantha Kumar and Gowda (1997) Bendale *et al.* (2002) Anantharaju and Meenakshiganesan (2005) Kadam *et al.* (2009) Shindey *et al.* (2010) Andualem and Tadesse (2011) Ganapathy *et al.* (2011)
		Negative	Marimuthu (1997) Shantha Kumar and Gowda (1997) Hari Krishna *et al.* (2005) Bedis *et al.* (2006) Priyadharshini *et al.* (2011) Haradari *et al.* (2012)
7.	No of grains panicle^{-1}	Positive	Chuni Lal *et al.* (1996)
		Negative	Chuni Lal *et al.* (1996) Kebere Bezaweletaw *et al.* (2006)
8.	Test weight	Positive	Dhagat *et al.* (1973) Mahudeswaran and Murugesan (1973) Ranganathan *et al.* (1977) Prabakhar and Prasad (1983) Sarvaiya *et al.* (1982) Singh *et al.* (1995) Hari Krishna *et al.* (2005) Padmaja *et al.* (2006)
		Negative	Prabakhar and Prasad (1983) Chaudhary (1989) Chuni Lal *et al.* (1996) Marimuthu (1997) Bendale *et al.* (2002)

Contd…

S.No	Character	Effect	Reference
9.	Seed Protein %	Positive	Sarala *et al.* (2007)
		Negative	Hari Krishna *et al.* (2005) Padmaja *et al.* (2006) Sarala *et al.* (2007)

Table 2.5. Review of literature on indirect effects of component characters on grain yield in finger millet

S.No	Character	Effect	Through	Reference
1.	Days to 50% flowering	Positive	number of tillers	Appadurai *et al.* (1977)
			plant height, fingers on main ear	Chaudhary (1989)
			plant height,	Singh *et al.* (1995)
			plant height	Mishra (1996)
			plant height	Mahto *et al.* (2000)
			plant height, number of fingers, finger length,	Bendale *et al.* (2002)
			plant height, number of tillers	Anuradha and Surya Kumari (2005)
			number of tillers	Bedis *et al.* (2006)
			plant height, number of tillers, number of fingers	Shindey *et al.* (2010)
			productive tillers per plant, days to maturity	Haradari *et al.* (2012)
		Negative	plant height, fingers per ear	Appadurai *et al.* (1977)
			finger length, fingers per ear, plant height	Chuni Lal *et al.* (1996)
			plant height, productive tillers per plant, fingers per ear, finger length	Shantha Kumar and Gowda (1997)
			plant height, number of tillers	Mahto *et al.* (2000)
			number of fingers	Anuradha and Surya Kumari (2005)
			plant height, main ear length, number of fingers per ear,	Bedis *et al.* (2006)
			plant height, finger length, finger number, days to maturity	Haradari *et al.* (2012)

Contd…

S.No	Character	Effect	Through	Reference
2	Days to maturity	Positive	test weight, grains per ear, finger length, number of finger, productive tiller, plant height, days to maturity, days to flowering	Chuni Lal *et al.* (1996)
			number of finger, number of grains	Kebere Bezaweletaw *et al.* (2006)
			days to flowering, plant height, number of finger	Bedis *et al.* (2006)
			days to 50% flowering, number of productive tillers, finger length	Sumathi *et al.* (2007)
			days to 50% flowering, plant height, number of productive tillers, finger length	Ganapathy *et al.* (2011)
			Productive tillers per plant, finger length	Haradari *et al.* (2012)
		Negative	productive tiller, test weight	Kebere Bezaweletaw *et al.* (2006)
			Number of productive tiller	Bedis *et al.* (2006)
			Plant height, number of finger, test weight	Sumathi *et al.* (2007)
			number of finger	Ganapathy *et al.* (2011)
3.	Plant height	Positive	days to 50% flowering, fingers per ear	Appadurai *et al.* (1977)
			productive tillers per plant,	Ranganathan *et al.* (1977)
			productive tillers, finger number	Prabhakar and Prasad (1983)
			fingers on main ear	Chaudhary (1989)
			number of tillers, number of fingers	Ravikumar and Seetharam (1993)
			days to 50% flowering, number of tillers	Ramaswamy *et al.* (1994)
			number of tillers	Singh *et al.* (1995)
			number of tillers, day to 50% flowering	Haider and Mahto (1995)
			finger length, fingers per ear	Chuni Lal *et al.* (1996)

Contd…

S.No	Character	Effect	Through	Reference
			day to 50% flowering, fingers per ear, finger length	Shantha Kumar and Gowda (1997)
			days to 50% flowering	Mahto *et al.* (2000)
			days to 50% flowering	Anuradha and Surya Kumari (2005)
			days to 50% flowering, number of fingers ear^{-1}	Bedis *et al.* (2006)
			days to 50% flowering,, number of fingers ear^{-1}	Kadam *et al.*(2009)
			Productive tillers per plant, days to maturity	Haradari *et al.* (2012)
		Negative	productive tillers per plant,	Mahudeswaran and Murugesan (1973)
			productive tillers, finger number,	
			days to 50 % flowering,	Chaudhary (1989)
			productive tillers	Ravikumar and Seetharam (1993)
			days to 50 % flowering	Singh *et al.* (1995)
			days to 50 % flowering	Mishra (1996)
			days to 50 % flowering, productive tillers,	
			finger length, finger number per ear	Shantha Kumar and Gowda (1997)
			finger length, finger number per ear	
			days to 50% flowering	Mahto *et al.* (2000)
			Finger length, Finger number,	Haradari *et al.* (2012)
			Days to 50% flowering	
4.	No. of productive tillers	Positive	days to 50 % flowering	Appadurai *et al.* (1977)
			plant height,	Ranganathan *et al.* (1977)
			number of fingers	Agalodia *et al.* (1979)
			plant height, finger number,	Prabhakar and Prasad (1983)

Contd…

S.No	Character	Effect	Through	Reference
			plant height, finger number	Ravikumar and Seetharam (1993)
			plant height, finger number, days to 50% flowering	Haider and Mahto (1995)
			plant height, inflorescence length	Anuradha and Surya Kumari (2005)
			plant height, number of fingers, finger length	Shindey *et al.* (2010)
			Productive tillers per plant, finger number, Days to maturity	Haradari *et al.* (2012)
		Negative	fingers per ear	Chaudhari and Acharya (1969)
			plant height,	Mahudeswaran and Murugesan (1973)
			plant height, fingers per ear	Appadurai *et al.* (1977)
			plant height, finger number,	Prabakhar and Prasad (1983)
			plant height, finger number per ear	Ravikumar and Seetharam (1993)
			days to 50% flowering, plant height, finger length	Bendale *et al.* (2002)
			days to 50% flowering, finger length	Bedis *et al.* (2006)
			finger length	Shindey *et al.* (2010)
			Plant height, finger length, days to 50% flowering	Haradari *et al.* (2012)
5.	No. of fingers ear^{-1}	Positive	plant height, tillers per plant, day to 50% flowering	Appadurai *et al.* (1977)
			plant height, productive tillers	Prabhakar and Prasad (1983)
			plant height	Chaudhary (1989)
			days to 50% flowering, finger length, plant height	Shantha Kumar and Gowda (1997)
			days to 50% flowering	Haradari *et al.* (2012)
		Negative	productive tillers	Chaudhari and Acharya (1969)
			plant height, productive tillers	Prabhakhar and Prasad (1983)
			days to 50%flowering	Chaudhary (1989)
			days to 50% flowering, plant height, productive tillers, finger length	Shantha Kumar and Gowda (1997)

Contd...

S.No	Character	Effect	Through	Reference
			Plant height, finger length, productive tillers, Days to maturity	Haradari *et al.* (2012)
6.	Length of finger	Positive	days to 50% flowering, productive tillers, finger number, length of finger	Shantha Kumar and Gowda (1997)
			plant height, days to 50% flowering, number of productive tillers per plant	Bedis *et al.* (2006)
			productive tillers, days to maturity	Haradari *et al.* (2012)
		Negative	plant height, productive tillers, fingers per ear	Shantha Kumar and Gowda (1997)
			number of productive tillers	Hari Krishna *et al.* (2005)
			plant height, finger length, finger number, days to 50% flowering	Haradari *et al.* (2012)
			plant height, finger number per ear	Ravikumar and Seetharam (1993)
			days to 50% flowering, plant height, finger length	Bendale *et al.* (2002)
			days to 50% flowering, finger length	Bedis *et al.* (2006)
			finger length	Shindey *et al.* (2010)
7.	No of grain panicle^{-1}	Positive	test weight, finger length, finger per ear, productive tillers, plant height, days to maturity, days to flowering	Chuni Lal *et al.* (1996)
			days to maturity, test weight	Kebere Bezaweletaw *et al.* (2006)

Contd…

S.No	Character	Effect	Through	Reference
		Negative	test weight, finger length, finger per ear, productive tillers, plant height, days to maturity, days to flowering	Chuni Lal *et al.* (1996)
			days to 50% flowering, productive tillers, finger number	Kebere Bezaweletaw *et al.* (2006)
8.	Test weight	Positive	plant height	Dhagat *et al.* (1973)
			Plant height, productive tiller	Ranganathan et al. (1977)
			Plant height, productive tiller, finger number	Prabakhar and Prasad (1983)
			Plant height	Singh *et al.* (1995)
			Plant height	Chaudhary (1989)
			Length of finger	Padmaja *et al.* (2006)
		Negative	plant height, productive tillers	Mahudeswaran and Murugesan (1973)
			Plant height, productive tillers, finger number	Prabakhar and Prasad (1983)
			Plant height	Sarvaiya *et al.* (1982)
			No of fingers per panicle	Chaudhary (1989)
			Days to 50% flowering	Singh *et al.* (1995)
			Days to 50% flowering, plant height, fingers per ear, Finger length, biological yield	Chuni Lal *et al.* (1996)
			Productive tillers plant^{-1}	Hari Krishna *et al.* (2005)
9.	Seed Protein %	positive	tillers per plant	Hari Krishna *et al.* (2005)
		Negative	test weight, yield	Hari Krishna *et al.* (2005)
			Days to 50% flowering	Padmaja *et al.* (2006)

2.4 STUDIES ON GENETIC DIVERGENCE

The assessment of genetic diversity using quantitative traits has got prime importance in many contexts particularly in differentiating well defined population. The germplasm in a self-pollinated crop can be considered as a heterogeneous set of groups since each group being homozygous within it. Selecting parents for hybridization programme in these crops is difficult because, the success depends upon the segregates of hybrid derivatives between the parents, particularly when the aim is to improve the quantitative characters like yield.

To identify the parents that nick better, several methods of divergence analysis based on quantitative characters have been proposed to suit various objectives. Among them, Mahalanobis’s generalized distance occupies a unique place and is an efficient method to measure the extent of diversity among genotypes, which quantify the differences among several quantitative traits.

Suyambulingam and Jebarani (1977) studied 34 short duration finger millet varieties for their divergence and reported that maximum diversity was contributed by number of tillers per plant, followed by plant height. These 34 varieties were grouped into six clusters with the help of D^2 analysis.

Jain *et al.* (1981) grouped 30 germplasm lines of finger millet from diverse geographical sources into 13 clusters using D^2 statistic. They reported that the clustering pattern did not follow geographical origin. This was expected because of Shigeta (1985) conducted D^2 analysis in 150 samples of finger millet collected from Kenya and found two clusters indicating the narrow variation among native collections.

Jayaprakash Naik (1991) observed the formation of 13 clusters in Indian germplasm in a study of genetic diversity in Indian and African finger millet collections using D^2 analysis. The characters that contributed to divergence were days to flowering, days to maturity, tiller number, flag leaf length, finger number, spikelet number, glume length and harvest index.

Purushotham Rao (1992) based on D^2 values, grouped 978 finger millet accessions were grouped into 38 clusters. The clustering pattern revealed that, there were 14 clusters predominantly occupied with Indian germplasm, two clusters with only African accessions, two clusters with unknown origin and remaining 20 clusters were having germplasm from different origins. Majority of accessions do not follow the pattern of geographic distinction. Hence, it is presumed that, there was no association of geographic diversity with the genetic diversity.

Vadivoo *et al.* (1998) grouped finger millet genotypes into eight clusters. Based on genetic diversity and performance, genotypes MS 1168, M174 and CO13 were suitable parents in hybridization for improving yield.

Surya Kumar *et al.* (1998) grouped 99 genotypes into 10 clusters using D^2 statistic. They reported that clustering pattern did not follow geographical origin. The genotypes from the clusters II, X, V and VII having moderate to high genetic divergence coupled with high mean performance may be selected for yield and its important components.

Jain *et al.* (2002) evaluated 40 genotypes in two consecutive years to assess the genetic divergence based on morphological characters related to grain yield and blast resistance in finger millet. The genetic diversity did not relate to geographic origin in same subcontinent, but it relates to some extent between the subcontinents.

Satish (2003) based on D^2 statistics, grouped 178 genotypes into 10 clusters. Clustering pattern revealed that there was no relationship between genetic divergence and geographical diversity. Highest contribution to genetic divergence of finger millet genotypes was contributed by floret number per spikelet followed by ear head length, flag leaf length, finger length and number of fingers per ear.

Balwant Kumar and Rai (2005) evaluated 30 genotypes of finger millet from diverse sources and grouped them into two clusters using D^2 statistics. The characters that contributed to divergence were days to 50% flowering, days to maturity and plant height.

Jaya Lakshmi (2007) studied 30 genotypes of finger millet and grouped them into ten clusters. Total tillers per plant followed by test weight contributed more towards total diversity.

Anantharaju and Meenakshiganesan (2008) grouped 50 finger millet genotypes into 14 clusters. Among the characters studied, days to 50% flowering contributed more towards total diversity.

Arun Prabhu *et al.* (2008) studied 150 finger millet germplasm for their variability and diversity. Based on Mahalanobis' D^2 statistic, genotypes were grouped in to 18 clusters. Finger breadth and number of fingers contributed maximum towards diversity.

Kadam (2008) assessed 70 genotypes of finger millet using Mahalanobis' D^2 analysis based on 15 characters and grouped them into eight clusters. Days to 50% flowering followed by flag leaf blade length contributed maximum towards total divergence and parallelism was observed between geographical diversity and geographical origin.

Dinesh Kumar *et al.* (2010) grouped 140 finger millet genotypes into ten non-overlapping clusters and observed that the genetic diversity was independent of the geographical origin of the genotypes.

Sahu and Pradhan (2012) group 30 finger millet genotypes into 12 cluster and observed that maximum contribution for the genetic divergence was by days to maturity followed by days to 50% flowering.

Chapter - III

MATERIAL AND METHODS

The present investigation entitled **“**Study of Genetic divergence for grain yield and yield components in finger millet (*Eleusine coracana* (L.) Gaertn)” was taken up during *kharif* 2012 in randomized block design with 60 genotypes at Agricultural College Farm, Baptla, Guntur district, Andhra Pradesh. The site of the experiment is situated at an altitude of 5.4m MSL, $15^{o}54$’N latitude and $80^{o}90$’E longitude. The soils are sandy type. The material used and methods followed in this investigation are given below

3.1 MATERIAL

The experimental material used in the present study comprised 60 diverse genotypes of finger millet [*Eleusine coracana* (L.) Gaertn] obtained from collections maintained at All India Coordinated Small Millets Improvement Project (AICSMIP), Bangalore. The source of origin of these genotypes is presented in Table 3.1

3.2 METHODS

The detailed experimental technique for the present investigation is furnished here under.

3.2.1 Experimental details of the present investigation

The experimental details were presented here under in the Table 3.2. The lay-out of the experiment with label was shown in plate 3.1.

Table 3.2. Experimental details of the present investigation

Location	:	Agricultural College Farm, Bapatla
Season	:	*Kharif, 2012*
Entries	:	60 genotypes
Design	:	Randomized complete block design
Replications	:	3
Plot size	:	3 rows of 3 m length
Spacing	:	30 cm between rows and 15 cm within rows
Fertilizers	:	60 N: 30 P_2O_5: 20 K_2O kg ha^{-1}
Plant protection	:	Need based

Table 3.1. Name and origin of finger millet genotypes employed in the present study

Sl No	Genotype	Origin
1	GE-361 (E)	-
2	GE -636 (E)	H D Kote, Mysore
3	GE -5257 (L)	ICRISAT
4	MR-6 (L)	VC farm, Mandya, Karnataka
5	GE -2078 (E)	Almora
6	GE-666 (E)	-
7	GE-1074	-
8	GE-1680 (E)	Karnataka
9	Indaf-5 (E)	Karnataka
10	GPU -45 (E)	AICSMIP, Karnataka
11	GE-3986 (E)	Maharashtra,Shirivande 9
12	GE- 4764 (L)	ICRISAT, Kenya
13	GE -3266 (L)	A P
14	GE- 3689 (E)	Maharastra, Medali 1
15	GE-667 (E)	-
16	GE-492 (L)	Almora
17	GE-1298 (L)	-

Sl No	**Genotype**	**Origin**
18	GE- 2931 (E)	ICRISAT, Africa
19	GE- 4798 (L)	ICRISAT, Kenya
20	GPU-67 (L)	AICSMIP, Karnataka
21	GE- 2963 (L)	ICRISAT,Africa
22	GE-2811	Kenya, Africa
23	GPU -26 (E)	AICSMIP, Karnataka
24	GE-2723 (L)	Collection from Kenya, Africa
25	GE-3099 (E)	ICRISAT,Africa
26	GPU-28 (M)	AICSMIP, Karnataka
27	GE-145 (L)	Kerala (KRL)
28	GE-4976 (L)	ICRISAT, Zumbia
29	GE-4437 (E)	Cindri, Koraput, Orissa
30	GE-995	-
31	GE-3140 (E)	New Delhi
32	GE-1673 (E)	Karnataka
33	GE-2737 (L)	Collected in Kenya, Africa
34	GE-4440 (L)	Orissa
35	GE-2672 (L)	Collected in Kenya, Africa
36	GE-3775 (E)	Dapoli 588, Maharastra Devatha 2
37	GE-258 (L)	U P
38	GE-506 (L)	Karnataka
39	GE-844 (L)	Nihivapahi.Kavalre. Hassan Dist. Karnataka
40	GE-4736 (L)	ICRISAT, Kenya
41	GE-3090 (E)	ICRISAT,Africa
42	GE-3521	Received from project coordinator (Millets) june 1982 (814 Collections) Ref no 3/866 10/2/82, Africa
43	GE-2127 (E)	Almora

Sl No	**Genotype**	**Origin**
44	GPU -48 (E)	AICSMIP, Karnataka
45	GE 225 (L)	-
46	GE-3453 (L)	Received from project coordinator (Millets) june 1982 (814 Collections) Ref no 3/866 , 10/2/82, Africa
47	GE-1274 (E)	Tamil Nadu
48	GE-4777 (E)	ICRISAT, Kenya
49	GE-5159 (E)	ICRISAT
50	GE-3067(L)	ICRISAT,Africa
51	GE-4842 (L)	ICRISAT, Malawi
52	GE-4707 (L)	ICRISAT, Kenya
53	GE-66 (M)	-
54	GE-2073 (E)	JN
55	GE-4999 (L)	ICRISAT, Tanzania
56	GE-1746 (L)	Almora
57	HR-911 (M)	India-Karnataka
58	GE-3225 (L)	Andhra pradesh
59	L-5 (L)	India-Karnataka
60	GE-1126 (E)	-

Plate 3.1. Experimental field with label indicating all the details of the experimental site

3.2.2 Recording Observations

The data was recorded on 10 randomly selected competitive plants per entry per replication and labelled for recording observations on yield and yield component traits.

However, the data on days to 50% flowering, test weight, days to maturity and seed protein% was recorded on plot basis.

The mean value of 10 competitive plants is expressed as mean of the respective character. The details of data recorded were:

3.2.2.1 Days to 50% flowering

The number of days taken by each genotype, from sowing to the day when 50 per cent of the plants were seen flowering in the population in each plot and in each replication.

3.2.2.2 Days to Maturity

Days to maturity was taken from date of sowing to stage when 50 per cent of main tillers have mature ears i.e., the ear colour changes from green to brownish.

3.2.2.3 Plant height (cm)

Height of the main tiller from the ground level to the tip of the inflorescence measured in centimetre.

3.2.2.4 Number of productive tillers per plant

Numbers of basal ear bearing tillers were counted at harvest.

3.2.2.5 Finger length (cm)

The length from the base to tip of the longest finger on main tiller was measured in centimetre and mean of ten plants was computed.

3.2.2.6 Number of fingers per ear head

The number of fingers on main ear of each tagged plant was counted and averaged per plant.

3.2.2.7 Number of grains per panicle

Numbers of grains per panicle were counted at harvest.

3.2.2.8 Test weight (g)

It is the absolute weight of 1000 randomly selected grains from the total seed yield of plot.

3.2.2.9 Grain yield per plant (g)

All the ears of a plant were dried and threshed before weighing and expressed in grams.

3.2.2.10 Seed Protein (%)

The protein content in the seed sample was estimated by standard procedure following Micro- Kjeldhal method.

The seeds were ground into flour and percentage of nitrogen was estimated as follows.

Procedure of protein estimation

a. Material

A known weight of flour is digested with diacid digestion mixture (sulphuric acid and per-chloric acid in the ratio of 9:1), 40% sodium hydroxide, 4% boric acid, mixed indicator (5 parts of bromocresol and 1 part of methyl red and N/50 sulphuric acid).

b. Apparatus

Micro-Kjeldhal flasks, distillation set, pipettes, burette, 100ml and analytical balance.

c. Procedure

The nitrogen was estimated using the procedure described by Williams Horowitz (A.O.A.C, 1980). The percentage of nitrogen was calculated by using the formula

‘N’ per cent in grain = (T-B) x N/50 x 1.4/S x 25/10

Where,

T = Sample titration, ml standard acid

B = Blank titration, ml standard acid

N/50 = Normality of standard acid

S = Sample weight (g)

25 = Volume of aliquot made after digestion

10 = Volume of aliquot used in distillation.

From the per cent nitrogen of crude protein was calculated as follows (A.O.A.C, 1980)

Per cent protein = per cent N x 6.25

3.3 STATISTICAL ANALYSIS

The data recorded on various characters were subjected to following statistical analysis

3.3.1 Analysis of variance

The data for different characters was statistically analysed on the basis of the model given by Cochran and Cox (1950) for Randomized complete Block Design.

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

Where,

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

μ = General mean

b_i = Effect of i^{th} block

t_j = Effect of j^{th} genotype

e_{ij} = Random error associated with j^{th} genotype and i^{th} block

The analysis of variance for each character was carried out as indicated below

Source of variation	**d.f**	**SS**	**MSS**	**F ratio**
Replications	r-1	RSS	Mr = σ^2e+ σ^2r	Mr/Me
Treatments(genotypes)	t-1	TrSS	Mt= σ^2e+ σ^2g	Mt/Me
Error	(r-1)(t-1)	ESS	Me= σ^2e	
Total	**(rt-1)**	**TSS**		

Where,

r = Number of replications

t = Number of genotypes

df = Degrees of freedom

SS = Sum of squares

MSS = Mean sum of squares

σ^2e = Error variance

σ^2g = Variance due to genotypes

σ^2r = Variance due to replications

M/ r = Mean sum of squares due to replications

M/ t = Mean sum of squares due to treatments

M/ e = Mean sum of squares due to error

The test of significance was carried out against the corresponding error degrees of freedom using ‘F’ table values given by Fisher and Yates (1963).

3.3.2 Estimation of genetic parameters

3.3.2.1 Coefficient of variation

Phenotypic and Genotypic Coefficients of Variation (PCV and GCV) were computed according to Burton (1952).

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

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

As suggested by Siva Subramanian and Menon (1973), GCV and PCV were categorized into:

Low = Less than 10 per cent

Moderate = 10-20 per cent

High = More than 20 per cent

3.3.2.2 Heritability in broad sense [h^2 (b)]

Heritability in broad sense refers to the proportion of genotypic variance to total variance. This was estimated as per Lush (1940) and Allard (1960).

$$h^2\,(b) = \frac{\text{Genotypic variance } (\sigma^2 g)}{\text{Phenotypic variance } (\sigma^2 p)} \times 100$$

As suggested by Johnson *et al.* (1955), h^2 (b) estimates were categorized into:

Low = 0-30 per cent

Moderate = 31-60 per cent

High = 61 per cent and above

3.3.2.3 Genetic advance (GA)

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

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

Where,

k = Selection differential at 5% selection intensity which accounts to a constant value of 2.06

h^2 (b) = Heritability in broad sense

σ_p = Phenotypic standard deviation

3.3.2.4 Genetic advance as per cent of mean (GAM)

$$GAM = \frac{\text{Genetic Advance}}{\text{Grand mean } (\overline{X})} \times 100$$

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

Low = Less than 10 per cent

Moderate = 10-20 per cent

High = More than 20 per cent

3.3.3 Correlation Analysis

Analysis of Covariance

Analysis of Covariance was computed by following procedure.

$$Y_{ij} = M + t_i + b_j + B\,(X_{ij} - X) + e_{ij}$$

Where,

Y_{ij} = Performance of i^{th} genotype in the j^{th} replication

M = General mean

t_i = True effect of i^{th} treatment

b_j = True effect of j^{th} block

b_{yx} = Regression coefficient of y on x

$X_{ij} - X$ = Covariate

e_{ij} = Random error

The structure of analysis of covariance is as follows

Source	df	SSY	SSX	SPXY	MSSY	MSSX	MSPXY
Replications	(r-1)	RY	RX	RXY	Ry	rx	Rxy
Genotypes	(t-1)	TY	TX	TXY	Ty	tx	Txy
Error	(r-1)(t-1)	EY	EX	EXY	Ey	ex	Exy

Where,

df = Degrees of freedom

SS = Sum of squares

SP = Sum of products

MSS = Mean sum of squares

MSP = Mean sum of products

r = Number of replications

t = Number of genotypes

Genotypic covariance $(x_i.x_j)_g = (MSPr - MSPe) / r$

$(x_i.x_j)_g$ = Genotypic covariance between i^{th} and j^{th} characters

MSPr = Mean sum of products of genotypes

MSPe = Error mean sum of products

Phenotypic covariance $(x_i.x_j)_p = (x_i.x_j)_g + e_ie_j$

$(x_i.x_j)_p$ = Phenotypic covariance between i^{th} and j^{th} characters

$(x_i.x_j)_g$ = Genotypic covariance between i^{th} and j^{th} characters

e_ie_j = Environmental covariance between i^{th} and j^{th} characters

Phenotypic and genotypic correlations were worked out by using the formulae suggested by Falconer (1964).

Phenotypic coefficients of correlation (r_p)

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

Where,

$r(X_i.X_j)_p$ = Phenotypic correlation between i^{th} and j^{th} characters

$COV(X_i.X_j)_p$ = Phenotypic covariance between i^{th} and j^{th} characters

$V(X_i)_p$ = Phenotypic variance of i^{th} character

$V(X_j)_p$ = Phenotypic variance of j^{th} character

Genotypic coefficient of correlation (r_g)

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

Where,

$r(x_i.x_j)_g$ = Genotypic correlation between i^{th} and j^{th} characters

$COV(x_i.x_j)_g$ = Genotypic covariance between i^{th} and j^{th} characters

$V(x_i)_g$ = Genotypic variance of i^{th} character

$V(x_j)_g$ = Genotypic variance of j^{th} character

3.3.3.1 Test of significance

Significance of correlation coefficients was tested by comparing phenotypic correlation coefficients with the table values (Fisher and Yates, 1963) at (n-2) degrees of freedom at 5% and 1% level where ‘n’ denotes the number of paired observations used in the calculation where genotypic correlation coefficient were tested for significance using ‘Z’ transformation.

3.3.4 Path coefficient analysis

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

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

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

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

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

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

Where,

r_{1y} to r_{ky} = Coefficient of correlations between causal factors 1 to K and Dependent character Y

r_{12} to r_{k-1},k = Coefficient of correlations among causal factors

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

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

$$\begin{pmatrix} r_{1y} \\ r_{2y} \\ - \\ - \\ r_{iy} \end{pmatrix} = \begin{pmatrix} 1 & r_{12} & r_{i1} \\ r_{21} & 1 & r_{i2} \\ - & - & - \\ - & - & - \\ - & - & - \\ r_{i1} & r_{i2} & i \end{pmatrix} \begin{pmatrix} p_{1y} \\ p_{2y} \\ - \\ - \\ p_{iy} \end{pmatrix}$$

Then B = $[C]^{-1}$ A

Where

$$[C\ ]^{-1} = \begin{pmatrix} c_{11} & c_{12} & c_{13} & & & c_{1i} \\ c_{21} & c_{22} & c_{23} & & & c_{2i} \\ c_{i1} & c_{i2} & c_{i3} & - & - & c_{ii} \end{pmatrix}$$

The direct effects were calculated as follows

$$p_{1y} = \sum c_{1i} r_{iy}$$

$$p_{2y} = \sum c_{2i} r_{iy}$$

$$p_{iy} = \sum c_{ii} r_{iy}$$

3.3.4.1 Residual effect

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

$$I = P^2 R_y + \Sigma P_{iy} r_{iy}$$

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

Lenka and Mishra (1973) have suggested scales for path coefficients in rice as below:

0.00 to 0.09 = Negligible

0.10 to 0.19 = Low

0.20 to 0.29 = Moderate

0.30 to 0.99 = High

More than 1.00 = Very high

3.3.5 Genetic divergence

3.3.5.1 Mahalanobis' D^2 analysis

The data collected on different yield contributing characters was analysed using Mahalanobis' D^2 analysis to determine the genetic divergence among the genotypes (Mahalanobis, 1928).

3.3.5.1.1 Test of significance

Variances were calculated for all the characters investigated and test of significance was done. Analysis of covariance for the character pairs was estimated on the basis of mean values (Panse and Sukhatme, 1985). After testing the difference between genotypes for each of the characters, a simultaneous test of significance for differences in the mean values of a number of correlated variables with regard to the pooled effect of characters was carried out using 'V' statistic, which in turn utilizes Wilk's criterion. The sum of squares and sum of products of error and error + variety, variance – covariance matrix were used for this purpose. The estimation of Wilk's criterion was done using the following relationship.

$$\Lambda = \frac{(E)}{(E+V)}$$

Where,

Λ = Wilk's criterion

(E) = Determinant of error matrix and

(E+V) = Determinant of error + variety matrix

n = degree of freedom for error + varieties and

$$\log e\ `\Lambda'\ V_{(stat)} = -\ m\ log_e^{\wedge} = -\left(n - \frac{P+Q+1}{2}\right) log_e^{\hat{}}$$

Where,

$m = n - (P+Q+1)/2 = 2.3026 \log 10\ '\Lambda'$

P = number of variables (or) characters (16)

Q = number of varieties –1 (or d.f.) / (or) populations

$V_{(stat)}$ is distributed as χ^2 with PQ (864) degrees of freedom .

Transformation of correlated variables

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

3.3.5.1.2 Computation of D^2 values

For the given combination of i and j genotypes, the mean deviation *i.e.,* Y_{it}-Y_{jt} for t=1, 2…p variables are computed and the D^2 values were calculated as

$$D^2_{ij} = \Sigma_{t=1}(y_i^t - y_j^t)^2$$

Where,

y_i^t is uncorrelated mean value of i^{th} genotype for character ‘t’

y_j^t is uncorrelated mean value of j^{th} genotype for character ‘t’

D^2_{ij} is D^2 between i^{th} and j^{th} genotypes.

3.3.5.1.3 Testing the significance of D^2 values

The D^2 value obtained for a pair of population is taken as calculated value of $\chi 2$ and is tested against the tabulated value of $\chi 2$ for P degrees of freedom where P is the number of characters considered *i.e.* 16 in the present study.

3.3.5.1.4 Contribution of individual characters towards divergence

In all combinations, each character was ranked on the basis of their contribution towards divergence between two entries ($d_i = Y_{it} - Y_{jt}$). Rank 1 is given to the highest mean difference and the rank P to the lowest difference, where, P is the total number of characters.

Percentage contribution towards genetic divergence was calculated using the following formula.

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

Where,

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

M = All possible combinations of number of genotypes considered. *i.e.* 1770 in the present study.

3.3.5.1.5 Grouping of genotypes into various clusters

The grouping of genotypes into different clusters was done using the Tocher's method as described by Rao (1952). The criterion was that the two varieties belonging to the same cluster at least on an average show a smaller D^2 value than those belonging to different clusters. For this purpose, D^2 values of all combinations of each genotype were arranged in ascending order of magnitude in a tabular form as described by Singh and Chaudhary (1977).

To start with, two populations having the closest distance from each other were considered, to which the third population having the smallest D^2 value from the first two populations was added. Similarly, the next nearest fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a particular population there was an abrupt increase in the average D^2, that population was not considered for including in that cluster.

The genotypes of the first cluster were then eliminated and the rest were treated in a similar way. This procedure was continued till all the genotypes were included into one or other cluster.

3.3.5.1.6 Average intra- cluster distance

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

3.3.5.1.7 Average inter-cluster distance

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

$$\text{Average inter cluster distance} = \frac{D^2}{(n_1 \times n_2)}$$

Where,

D^2 = difference in the mean values between two populations when all the characters are considered simultaneously.

n_1 and n_2 are number of genotypes of two clusters.

3.3.5.2 Principal component analysis and cluster analysis

Principal component analysis was carried according to procedure described by Banfield (1978). PCA can be performed on two types of data matrices *viz.*, variance-covariance matrix and correlation matrix. With characters of different scale, a correlation matrix standardizing the original data set is preferred. If the characters are of same scale, a variance – covariance matrix can be used. In the present study, PCA was performed on the correlation matrix of traits, thereby removing the effects of scale (Jackson, 1991).

3.3.5.2.1 Eigen values and eigen vectors

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

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

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

The principal components were identified by following procedure.

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

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

Where,

Aij are found such that Yj is uncorrelated Y1, Y2,……..Yj-1 the j^{th} largest variance. The Aij are the elements of the normalized eigen vector associated with largest j^{th} eigen value. The variance of the j^{th} principal component of the λj and the total system variance trace (S) = $\lambda 1+\lambda 2 +\ldots+ \lambda\ p$. The importance of the j^{th} principal component is given by

$$\frac{\lambda\ j}{\text{Trace (S)}}$$

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

$$\rho(X_i, Y_j) = \frac{A_{ij}.\sqrt{\lambda_j}}{\sqrt{S_i}}$$

Where S_i is the standard deviation of X_i.

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

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

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

PCA scores for each genotype under concerned PCs were computed and utilized to derive a 2D or 3D (dimensional) scatter plot of individuals.

3.3.5.2.2 Cluster analysis

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

3.3.5.2.2.1 Obtaining data matrix

PCA scores for 60 genotypes were used as input for clustering because principal component analysis provides variable independence and balanced weighting of traits, which leads to an effective contribution of different characters on the basis of respective variation.

3.3.5.2.2.2 Standardizing the data matrix

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

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

$$Z_{ij} = X_{ij} - \overline{X_j} / S_{ij}$$

Where $\overline{X_j} = \sum_{i=1}^{n} X_{ij} / n$

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

For, i= genotypes *i.e.*, 60

j = total variables *i.e.*, 11

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

3.3.5.2.2.3 Computing the resemblance matrix

A resemblance coefficient, which measures the overall resemblance (the degree of similarity or distance) between a pair of genotypes, was computed. Here 60 genotypes were taken in data matrix therefore resemblance coefficient was computed for a total of 1770 combinations *i.e.*, ${}^{60}C_2$ ways.

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

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

Where,

P = Number of genotypes *i.e.*, 60

X_{ik} = Value of i^{th} genotype for k PCA scores

X_{jk} = Value of j^{th} genotype for k PCA scores

3.3.5.2.2.4 Execution of the clustering method

Distance matrix was converted into dendrogram by using Ward’s method where the distance between two clusters is the sum of squares between two clusters summed over all variables. At each stage in the clustering procedure within cluster sum of squares is minimized over all partitions obtained by combining 2 clusters from previous stage.

Chapter IV

RESULTS AND DISCUSSION

A systematic study was conducted to estimate the genetic variability, heritability, character association of yield and yield components and direct and indirect effects of yield components on grain yield in finger millet at Agricultural College, Bapatla, A.P., India. The results obtained are presented under the following headings.

4.1 Genetic variability, heritability and genetic advance as per cent of mean

4.2 Character association

4.3 Path coefficient analysis

4.4 Studies of Genetic divergence

ANALYSIS OF VARIANCE

The results of analysis of variance for ten characters in finger millet are furnished in Table 4.2. The variance due to genotypes for all the 10 characters studied were observed to be highly significant indicating the presence of genetic variability among the genotypes.

4.1 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE AS PER CENT OF MEAN

In any successful crop improvement programme, the availability of adequate variability in basic genetic stocks and their proper use through breeding for developing improved genotypes are very much necessary. The genetic improvement of plant population depends on the presence of genetic variability and the extent to which the traits are heritable. Besides genetic variability, knowledge on heritability and genetic advance plays a predictive role in breeding, expressing the reliability of phenotype as a guide to its breeding value. Higher the heritability, greater would be the response to selection, as heritability is directly proportional to genetic advance making selection more effective (Burton, 1952 and Swarup and Chaugle, 1962). The magnitude of heritable variability is the most important aspect of genetic contribution of the breeding material, which has close relationship on its response to selection (Panse, 1957).

In the present investigation estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability [h^2 (b)] in broad sense and genetic advance as per cent of mean (GAM) were calculated and are presented in Table 4.3 and described character-wise. The mean performance of 60 genotypes is presented in Table 4.1 here under:

Table 4.1. Mean performance of 60 genotypes for 10 characters in finger millet

Sl.No	Genotype	Days to 50% flowering	Plant height (cm)	Days to maturity	Number productive tillers	No. of fingers ear^{-1}	Finger length (cm)	Test weight (g)	No. of grains per panicle	Seed protein %	Grain yield per plant (g)
1	GE-361	60.67	98.81	91.67	5.30	7.10	9.28	2.85	1874.12	7.08	18.19
2	GE-636	60.00	97.49	97.33	4.57	6.83	8.69	3.13	2370.40	7.50	21.80
3	GE-5257	65.33	107.30	119.67	5.10	7.17	8.24	2.64	2347.87	8.29	21.44
4	MR-6	69.00	114.40	120.67	5.17	7.30	10.44	2.87	2035.38	8.13	18.42
5	GE-2078	52.00	87.54	93.00	5.23	4.93	7.43	2.87	2072.26	7.20	22.26
6	GE-666	62.33	140.54	94.67	5.63	7.10	14.63	2.91	1907.67	6.37	18.34
7	GE-1074	62.67	105.63	96.67	4.57	6.07	9.25	3.28	2677.27	8.46	27.78
8	GE-1680	59.33	104.86	99.00	4.90	6.93	8.53	2.87	1904.53	9.24	19.27
9	INDAF-5	63.33	100.41	98.67	4.67	7.00	10.02	3.12	2383.20	7.17	23.88
10	GPU-45	65.00	93.14	98.67	4.37	7.17	8.62	2.89	2712.71	7.88	26.09
11	GE-3986	58.67	106.63	98.00	4.93	7.50	8.57	3.23	2314.13	10.11	21.32
12	GE-4764	66.33	97.93	120.33	4.83	6.47	7.74	3.07	1463.80	7.18	13.89
13	GE-3266	69.67	107.24	118.00	5.03	5.97	9.53	3.42	2701.27	9.70	26.54
14	GE-3689	61.00	98.18	95.33	4.87	7.43	9.29	2.83	2307.80	8.89	22.08
15	GE-667	57.33	103.68	95.67	4.40	6.73	8.95	3.06	2644.67	9.25	26.24
16	GE-492	58.00	101.54	119.00	4.33	6.63	9.36	2.90	2388.73	8.47	23.95
17	GE-1298	66.00	105.68	119.33	5.13	5.30	7.55	3.37	2084.80	9.19	18.67
18	GE-2931	66.00	107.97	96.67	5.80	7.20	9.37	3.24	1933.47	8.37	17.83
19	GE-4798	69.00	108.17	119.67	5.07	6.53	9.96	3.40	2559.67	10.51	25.84
20	GPU-67	61.00	91.96	119.33	4.73	7.33	8.85	3.52	2391.67	9.14	24.85
21	GE-2963	78.00	131.18	121.67	5.37	7.10	10.03	2.69	2066.85	10.51	18.37
22	GE-2811	65.00	101.51	99.00	4.97	7.87	8.19	2.66	2230.93	10.03	23.05
23	GPU-26	60.67	99.59	99.33	5.07	7.33	8.69	3.06	1568.93	9.58	16.03
24	GE-2723	72.67	118.67	121.00	5.37	4.87	9.56	2.90	2673.73	7.47	26.48
25	GE-3099	64.00	126.64	94.00	5.90	6.90	14.37	2.49	2446.13	10.74	23.20
26	GPU-28	65.67	100.13	112.67	5.13	6.33	9.79	3.12	1998.13	9.78	19.72
27	GE-145	71.33	97.02	118.67	4.87	6.30	9.64	2.82	2834.40	7.13	29.39
28	GE-4976	71.00	112.37	119.33	4.67	6.80	11.35	3.09	2226.80	8.85	19.86
29	GE-4437	53.00	89.01	92.00	4.73	5.97	7.33	3.25	2110.50	9.44	20.69
30	GE-995	53.00	82.77	87.00	5.10	3.47	5.72	2.62	1952.97	8.24	17.62
31	GE-3140	60.33	100.67	90.33	5.43	5.77	7.39	2.71	1569.27	8.20	15.24
32	GE-1673	60.67	102.11	92.00	6.37	6.80	9.38	3.02	1600.00	10.13	14.42
33	GE-2737	63.67	122.55	121.33	5.27	6.53	8.27	2.55	2673.67	7.37	26.24
34	GE-4440	55.00	90.06	122.33	5.03	4.57	6.80	3.77	1986.33	9.44	19.76
35	GE-2672	66.67	111.33	119.33	5.40	5.63	8.42	3.49	2627.00	7.59	25.27
36	GE-3775	60.33	116.83	97.67	5.17	6.23	9.08	2.81	2233.73	8.47	21.31
37	GE-258	53.00	108.36	120.67	5.50	5.30	8.26	2.93	2342.40	6.67	21.46
38	GE-506	77.33	100.43	118.33	5.30	6.67	8.82	3.18	2640.33	10.47	24.72
39	GE-844	75.00	102.28	118.33	4.83	7.53	9.15	2.53	2655.33	7.57	25.95
40	GE-4736	74.67	134.06	118.33	4.60	6.87	9.16	3.39	2271.93	9.58	21.98
41	GE-3090	51.67	99.79	89.67	4.47	7.03	9.07	2.84	2351.20	9.13	22.33
42	GE-3521	62.67	121.73	91.67	5.80	6.77	8.82	2.33	2718.00	8.24	26.38
43	GE-2127	50.67	78.49	88.00	4.30	3.50	6.83	2.73	1860.20	6.18	17.95
44	GPU-48	62.00	87.46	98.33	4.67	7.83	9.11	2.83	2822.33	10.72	28.27
45	GE-225	61.33	103.48	122.00	4.60	6.70	10.45	3.52	2636.60	8.88	26.42
46	GE-3453	74.67	123.72	120.00	5.50	8.17	8.60	3.93	2481.05	11.12	24.28
47	GE-1274	61.33	92.75	98.33	5.10	7.40	9.45	2.82	1879.80	9.13	17.80
48	GE-4777	62.00	109.15	95.67	5.10	7.07	8.62	2.54	1972.17	10.17	20.47
49	GE-5159	65.33	106.65	88.00	4.83	6.37	6.17	2.83	2772.30	7.70	27.75
50	GE-3067	67.33	106.18	121.00	5.60	6.33	6.60	3.29	2795.67	10.06	28.47
51	GE-4842	77.67	121.13	119.33	5.93	7.23	10.48	2.24	1881.61	8.32	18.38

Contd. . .

Sl.No	Genotype	Days to 50% flowering	Plant height (cm)	Days to maturity	Number productive tillers	No. of fingers ear^{-1}	Finger length (cm)	Test weight (g)	No. of grains per panicle	Seed protein %	Grain yield per plant (g)
52	GE-4707	72.00	107.78	120.33	5.47	7.97	9.72	3.20	1843.60	9.31	19.21
53	GPU-66	61.00	104.38	110.67	5.50	7.00	9.17	3.40	2677.60	9.30	27.77
54	GE-2073	54.33	116.55	94.67	5.60	5.90	9.34	3.14	1991.00	9.93	21.17
55	GE-4999	62.33	110.09	122.33	5.67	6.83	7.62	2.32	2411.60	8.63	24.51
56	GE-1746	61.00	122.40	123.33	5.47	6.50	9.40	3.33	2760.40	10.31	27.68
57	HR-911	63.33	95.91	109.33	5.17	6.03	9.71	3.44	2053.49	8.09	19.59
58	GE-3225	52.67	91.25	120.00	5.03	7.80	9.53	2.87	2353.93	8.73	22.45
59	L-5	62.67	108.32	121.67	5.20	7.03	8.87	3.13	2581.27	9.51	25.80
60	GE-1126	59.33	102.03	97.00	4.93	7.23	9.49	3.22	2661.33	8.09	26.65
	Mean	**63.32**	**105.60**	**107.43**	**5.11**	**6.60**	**9.01**	**3.01**	**2288.17**	**8.78**	**22.38**
	C.V.	2.44	5.55	3.23	4.81	4.51	6.79	4.71	10.24	0.79	9.56
	F ratio	57.28	13.27	40.95	9.50	31.09	17.80	18.39	7.17	879.03	10.00
	S.E.	0.89	3.38	2.00	0.14	0.17	0.35	0.08	135.33	0.04	1.24
	C.D. 5%	2.50	9.48	5.61	0.40	0.48	0.99	0.23	378.99	0.11	3.46
	C.D. 1%	3.30	12.53	7.42	0.53	0.64	1.31	0.30	501.07	0.15	4.57

CV= coefficient of variation SE= standard error CD= critical difference

4.1.1 Days to 50% flowering

Days to 50% flowering ranged from 50.67 (GE 2127) to 78.00 days (GE 2963) with a mean of 63.32 days. The estimation of PCV and GCV were moderate (10.84 and 10.56). Similar results were reported by Mishra *et al.* (1980), Verma (1989), Malali Gowda (1996), Bandyopadhyay (1998a), Bendale *et al.* (2002) and Ganapathy *et al.* (2011).

High heritability (94.94%) coupled with high GAM (21.29) observed for days to 50% flowering, indicates the preponderance of additive gene action making selection effective. These results are in agreement with the findings of Haider and Mahto (1995), Chuni Lal *et al.* (1996), Malali Gowda (1996), Bandyopadhyay (1998a) and Ganapathy *et al.* (2011).

4.1.2 Days to maturity

Days to maturity ranged from 87 (GE-995) to 123.33 days (GE-1746) with a mean of 107.43 days. The estimation of PCV and GCV were moderate (12.22 and 11.79). Similar results were reported by Goswami and Asthana (1984), Bandyopadhyay (1998a) and Dhamdhere *et al*. (2011).

High heritability (93.01) coupled with high GAM (23.42) observed for days to maturity, indicates the preponderance of additive gene action making selection effective. These results are in agreement with the findings of Goswami and Asthana (1984), Malali Gowda (1996) and Bandyopadhyay (1998a).

Table 4.2. Analysis of variance for 10 characters in 60 finger millet genotypes

Mean sum of squares of characters											
Source of variation	df	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of productive tillers plant^{-1}	No. of fingers ear $^{-1}$	Finger length (cm)	No. of grains panicle^{-1}	Test weight (g)	Yield plant $^{-1}$ (g)	Seed Protein %
Replication	2	0.45	15.45	35.272	0.151	0.057	0.07	39199.561	0.017	2.345	0.005
Treatment	59	136.457**	493.122**	455.800**	0.573**	2.754**	6.66**	393982.748**	0.369**	45.811**	4.273**
Error	118	2.382	12.043	34.341	0.06	0.089	0.37	54942.672	0.020	4.581	0.005

** Significant at 1% level df = Degrees of freedom

Table 4.3. Genetic variability parameters for 10 different characters in 60 finger millet genotypes

Sl.NO	Character	Mean	Range		Coefficient of variation		Variance		h^2 (b) (%)	Genetic advance	Genetic advance as % of mean
			Min	Max	Genotypic (%)	Phenotypic (%)	Genotypic	Phenotypic			
1	Days to 50% flowering	63.32	50.67	78.00	10.56	10.84	44.69	47.07	95.94	13.42	21.19
2	Days to maturity	107.43	87.00	123.33	11.79	12.22	160.36	172.40	93.01	25.16	23.42
3	Plant height (cm)	105.60	78.49	140.54	11.22	12.52	140.49	174.83	80.36	21.89	20.73
4	No. of productive tillers plant^{-1}	5.11	4.30	6.37	8.09	9.41	0.17	0.23	73.91	0.73	14.33
5	No. of fingers ear $^{-1}$	6.60	3.47	8.17	14.27	14.97	0.89	0.98	90.93	1.85	28.04
6	Finger length (cm)	9.01	5.72	14.63	16.07	17.44	2.10	2.47	84.85	2.75	30.49
7	No. of grains panicle^{-1}	2288.17	1463.80	2834.40	14.69	17.91	113013.36	167956.03	67.29	568.07	24.83
8	Test weight (g)	3.01	2.24	3.93	11.34	12.28	0.12	0.14	85.29	0.65	21.58
9	Grain Yield plant $^{-1}$ (g)	22.38	13.89	29.39	16.57	19.13	13.74	18.32	75.01	6.61	29.55
10	Seed Protein %	8.78	6.18	11.12	13.58	13.60	1.42	1.43	99.66	2.45	27.93

4.1.3 Plant height

The range of plant height varied from 78.49 (GE-2127) to 140.54 cm (GE-666) with a mean of 105.60 cm. The estimates of PCV and GCV were moderate (12.52 and 11.22). These results agree with the findings of Goud and Lakshmi (1977), Mishra *et al.* (1980), Prabhakar and Prasad (1984), Ravikumar and Seetharam (1994), Bendale *et al.* (2002) and Ganapathy *et al* (2011).

High heritability (80.36%) coupled with high GAM (20.73%) was observed for plant height. For this trait direct phenotypic selection may be effective due to preponderance of additive gene action. Similar results were reported by Ravikumar and Seetharam (1994), Haider and Mahto (1995), Kadam *et al.* (2009) and Ganapathy *et al.* (2011).

4.1.4 Number of Productive tillers

The number of productive tillers ranged from 4.30 (GE-2127) to 6.37 (GE-1673) with a mean of 5.11. The estimates of PCV and GCV (9.41 and 8.09) were low.

High heritability (73.91%) coupled with moderate GAM (14.33%) were observed for this trait indicating the operation of both additive and non-additive gene action and further improvement of this character would be easier through mass selection, progeny selection or any modified selection procedure aiming to exploit the additive gene effect rather than simple selection. Similar results were reported by Kadam *et al.* (2009).

4.1.5 Number of fingers ear^{-1}

The parameter number of fingers ear head^{-1} ranged from 3.47 (GE-995) to 8.17 (GE-3453) with a mean of 6.60. The variation for this character among different genotypes was shown in Plate 4.1. Estimates of PCV and GCV (14.97 and 14.27) were moderate. Similar results were observed by Chowdary and Acharya (1969), Setty *et al.* (1974), Prabhakar and Prasad (1984), Bendale *et al.* (2002), Anantharaju and Meenakshiganesan (2006), Gowda *et al.* (2008), Ganapathy *et al.* (2011) and Priyadharshani *et al.* (2011).

High heritability (90.93%) coupled with high GAM (28.04) was observed for this trait making selection effective due to additive gene action. Similar results were reported by Agalodia *et al.* (1979), Abraham *et al.* (1989), Anantharaju and Meenakshiganesan (2005), John (2006), Gowda *et al.* (2008), Ganapathy *et al.* (2011) and Priyadharshini *et al.* (2011).

Plate 4.1. Variation among different genotypes for number of fingers ear^{-1}

GE-5159 **GE-225** **GE-1680**

INDAF-5 **GE-2723** **GE-145**

Plate 4.2. Variation among different genotypes for finger length

GE-225 **GE-1680** **GE-2723** **GE-145**

4.1.6 Finger length

The parameter finger length ranged from 5.72 (GE-995) to 14.63 (GE-666) with a mean of 9.01. The variation for this character among different genotypes was shown in plate 4.2. Estimates of PCV and GCV (17.44 and 16.07) were moderate. Similar results were observed by Setty *et al.* (1974), Sumathi *et al.* (2007), Gowda *et al.* (2008) and Priyadharshini *et al.* (2011).

High heritability (84.85%) couple with high GAM (30.49) was observed for this trait making selection effective due to additive gene action. These results are in conformity with the findings by Setty *et al.* (1974), Appadurai *et al.* (1977), Goswami and Asthana (1984), Chuni Lal *et al.* (1996), Anantharaju and Meenakshiganesan (2006), Arun Prabhu *et al.* (2008), Gowda *et al.* (2008), Kadam *et al.* (2009), Ganapathy *et al.* (2011), Priyadharshini *et al.* (2011) and Haradari *et al.* (2012).

4.1.7 Number of grains panicle^{-1}

The parameter number of grains per panicle ranged from 1463.80 (GE-4764) to 2834.40 (GE-145) with a mean of 2288.17. Estimates of PCV and GCV (17.91 and 14.69) were moderate. Similar results were observed by Kebere Bezaweletaw *et al.* (2006).

High heritability (67.29%) couple with high GAM (24.83) was observed for this trait making selection effective due to additive gene action. Similar results were reported by Chuni Lal *et al.* (1996) and Sharathbabu *et al.* (2008).

4.1.8 Test weight

The parameter test weight ranged from 2.24 (GE-4842) to 3.93 (GE-3453) with a mean of 3.01. Estimates of PCV and GCV (12.28 and 11.34) were moderate. Similar results were reported by Shanthappa (1979), Prabhakar and Prasad (1984), Venkatesh Bhat (1991), Purushotham Rao (1992), Ravi Shankar (1996), Satish (2003), John (2006), Kebere Bezaweletaw et al. (2006) and Sharathababu et al. (2008).

High heritability (85.29%) couple with high GAM (21.58) was observed for this trait making selection effective due to additive gene action. These results are in agreement with the findings of Agalodia *et al.* (1979), Shanthappa (1979), Prabhakar and Prasad (1984), Venkatesh Bhat (1991), Chunilal *et al.* (1996), Satish (2003), John (2006), Sharathababu *et al.* (2008) and Dhamdhere *et al*. (2011).

4.1.9 GrainYield plant $^{-1}$

The parameter yield per plant ranged from 13.89 (GE-4764) to 29.39 (GE-145) with a mean of 22.38. Estimates of PCV and GCV (19.13 and 16.57) were moderate. These results agree with the findings of John (2006), Sumathi *et al.* (2007), Gowda *et al.* (2008), Ganapathy *et al.* (2011), Priyadharshini *et al.* (2011) and Sahu and Pradhan (2012).

High heritability (75.01%) couple with high GAM (29.55) was observed for this trait making selection effective due to additive gene action. Similar results were reported by Chaudhari and Acharya (1969), Setty *et al.* (1974), Agalodia *et al.* (1979), Mishra *et al.* (1980), Verma (1989), Chuni Lal *et al.* (1996), Sumathi *et al.* (2007), Ganapathy *et al.* (2011), Priyadharshini *et al.* (2011) and Sahu and Pradhan (2012).

4.1.10 Seed Protein %

The parameter Protein ranged from 6.18 (GE-2127) to 11.12 (GE-3453) with a mean of 8.78. Estimates of PCV and GCV (13.60 and 13.58) were moderate. Similar results were observed by Priyadharshini *et al.* (2011).

High heritability (99.66%) couple with high GAM (27.93) was observed for this trait making selection effective due to additive gene action. These results are in conformity with the findings of Maloo *et al.* (1998) and Priyadharshini *et al.* (2011).

4.2 CHARACTER ASSOCIATION

Yield is a complex quantitative trait, considerably affected by environment. Therefore, selection of genotypes based on yield will not be effective. Genetic correlation measures the magnitude of relationship between various plant characters that determine the component characters on which selection can be made for improvement in yield (Johnson *et al.,* 1955). Genotypic correlation is the inherent association between two variables. It may be either due to pleiotropic action of genes or linkage. If the correlation between finger millet grain yield and a character is due to the direct effect of the character, it reflects a true relationship between them and selection can be practiced for such characters in order to improve yield. However, if the correlation is mainly due to indirect effect of the character through other component traits, the breeder has to select for the trait through which the indirect effect is expected. Thus, correlation coefficients are useful, if indirect selection of a secondary trait is to be used for improving the primary trait of interest. A great yield response is obtained when the character for which indirect selection is practiced has a high heritability and a positive correlation with yield. Thus, correlation is an important tool to finger millet breeder in deciding the breeding procedure for genetic improvement of grain yield.

In the present investigation, phenotypic and genotypic correlation coefficients between finger millet grain yield and other related component characters and among themselves were estimated and presented in Table 4.4.

4.2.1 Days to 50% flowering

Days to 50% flowering showed significant positive phenotypic association with days to maturity (0.5135), plant height (0.4687), number of productive tillers (0.1782), number of fingers ear^{-1} (0.3430), finger length (0.2727), number of grains panicle^{-1} (0.1522) and seed protein % (0.1958) indicating close association among the characters. Hence genetic improvement in one character would lead to increase in second and *vice-versa*.

These results are in agreement with the findings of John (2006) and Haradari *et al.* (2012) for days to maturity, Kadam *et al.* (2009) and Haradari *et al.* (2012) for plant height, Kadam *et al.* (2009) and Haradari *et al.* (2012)) for number of productive tillers, Chuni Lal *et al.* (1996) and Kadam *et al.* (2009) for number of fingers ear^{-1} and Chuni Lal *et al.* (1996) and Kadam *et al.* (2009) for finger length.

This trait also showed significant positive genotypic association with days to maturity (0.5347), plant height (0.5304), number of productive tillers (0.2353), number of fingers ear^{-1} (0.3672), finger length (0.2965), number of grains panicle^{-1} (0.2048) and seed protein % (0.203) indicating close association among the characters. Hence genetic improvement in one character would lead to increase in second and *vice-versa*.

This trait showed significant positive association with grain yield plant^{-1} at genotypic level (0.1503) only. These results are in agreement with the findings of Sarvaiya *et al.* (1982), Haider *et al.* (1993) and Mishra (1996).

4.2.2 Days to maturity

This trait showed significant positive phenotypic association with days to 50% flowering (0.5135), plant height (0.2395), number of grains panicle^{-1} (0.2158) and test weight (0.2696).

Similar results were given by John (2006) and Haradari *et al.* (2012) for days to 50% flowering, Chuni Lal *et al.* (1996) and Haradari *et al.* (2012) for plant height and Chuni Lal *et al.* (1996) for number of grain panicle^{-1} and test weight.

Similarly this trait recorded positive genotypic association with days to 50% flowering (0.5347), plant height (0.2395), number of grains panicle^{-1} (0.2855) and test weight (0.3045).

Positive significant association of this trait was observed with grain yield plant^{-1} (0.1844, 0.2579) at both phenotypic and genotypic levels, suggesting that this association can be exploited in selection leading towards varietal improvement. Similar results were given by Bedis *et al.* (2006).

4.2.3 Plant height

Plant height showed significant positive association with days to 50% flowering (0.4687), days to maturity (0.2395), number of productive tillers (0.3608), number of fingers ear^{-1} (0.2755), finger length (0.4828) and seed protein % (0.1468) at phenotypic level indicating close association among the characters. Hence genetic improvement in one character would lead to increase in second and *vice-versa.*

Similar results were reported by Mahto *et al.* (2000) and Haradari *et al.* (2012) for days to 50% flowering, Chuni Lal *et al.* (1996) and Haradari *et al.* (2012) for days to maturity, Shantha Kumar and Gowda (1997) and Haradari *et al.* (2012) for number of productive tillers, Ravikumar and Seetharam (1993) and Bandyopadhyay (1999b) for number of fingers ear^{-1} and Gowda *et al.* (2008) and Haradari *et al.* (2012) for finger length at phenotypic level.

Table 4.4. Phenotypic (r_p) (above diagonal) and Genotypic (r_g) (below diagonal) correlation coefficients among 10 traits in 60 finger millet genotypes

Sl. No	Character	Days to 50 % flowering	Days to maturity	Plant height	No. of productive tillers	No. of fingers ear^{-1}	Finger length	No. of grain panicle^{-1}	Test weight	Seed protein%	Grain yield plant^{-1}
1	Days to 50 % flowering	----	0.5135 **	0.4687 **	0.1782 *	0.3430 **	0.2727 **	0.1522 *	0.0304	0.1958 **	0.1174
2	Days to maturity	0.5347 **	---	0.2395 **	0.082	0.0994	0.067	0.2158 **	0.2696 **	0.1271	0.1844 *
3	Plant height	0.5304 **	0.2978 **	---	0.3608 **	0.2755 **	0.4828 **	0.1062	-0.0655	0.1468 *	0.0775
4	No. of productive tillers	0.2353 **	0.0947	0.5293 **	---	0.0404	0.1848 *	-0.1867 *	-0.1354	0.1603 *	-0.1760 *
5	No. of fingers ear^{-1}	0.3672 **	0.1115	0.2867 **	0.0593	---	0.3951 **	0.0913	-0.0549	0.3465 **	0.0873
6	Finger length	0.2965 **	0.0796	0.5697 **	0.2261 **	0.4502**	---	0.0285	-0.0568	0.0734	0.0073
7	No. of grain panicle^{-1}	0.2048 **	0.2855 **	0.1401	-0.2297 **	0.1302	0.0234	---	0.089	0.081	0.8342 **
8	Test weight	0.0331	0.3045 **	-0.0739	-0.1585 **	-0.0406	-0.0553	0.1419 *	---	0.2706 **	0.1292
9	Seed protein%	0.203 **	0.1328	0.1629 **	0.1831 **	0.3621 **	0.0773	0.0921	0.2948 **	---	0.0907
10	Grain yield plant^{-1}	**0.1503 ***	**0.2579 ****	**0.088**	**-0.2383 ****	**0.1329**	**-0.0106**	**1.0651 ****	**0.1474 ***	**0.104**	**---**

*, ** significant at 0.05 and 0.01 levels of probability respectively

Similarly this trait recorded positive genotypic association with days to 50 % flowering (0.5304), days to maturity (0.2978), number of productive tillers (0.5293), number of fingers ear^{-1} (0.2867), finger length (0.5697) and seed protein % (0.1629).

Positive non-significant association of this trait was recorded with grain yield plant^{-1} (0.0775, 0.088) at both phenotypic and genotypic levels. These results are in agreement with the findings of Chaudhary (1989), Haider and Mahto (1995) and Bandyopadhyay (1998a).

4.2.4 Number of productive tillers

This trait showed significant positive association with days to 50% flowering (0.1782), plant height (0.3608), finger length (0.1848) and seed protein % (0.1603) and negative significant association with number of grains panicle^{-1} (-0.1867) indicates that this trait may not be improved simultaneously.

These results are in conformity with the findings of Shantha Kumar and Gowda (1997) and Haradari *et al.* (2012) for days to 50% flowering, Ravikumar and Seetharam (1993) and Haradari *et al.* (2012) for plant height and Gowda *et al.* (2008) and Kadam *et al.* (2009) for finger length.

Similarly this trait recorded significant positive genotypic association with days to 50% flowering (0.2353), plant height (0.5293), finger length (0.2261) and seed protein % (0.1831) and negative significant association with grain number (-0.2297) and test weight (-0.1585).

It showed negative significant association of this trait with grain yield plant^{-1} (-0.1760, -0.2383) at both phenotypic and genotypic levels. Similar results were given by Haider and Mahto (1995).

4.2.5 Number of fingers ear^{-1}

This trait showed significant positive association with days to 50% flowering (0.3430, 0.3672), plant height (0.2755, 0.2867), finger length (0.3951, 0.4502) and seed protein % (0.3465, 0.3621) at both phenotypic level and genotypic level.

These results agree with the findings of Bandyopadhyay (1998b) and Shindey *et al.* (2010) for days to 50% flowering, Ravindran *et al.* (1996) and Andualem and Tadesse

(2011) for plant height and Sahu and Pradhan (2012) for finger length at both phenotypic and genotypic level.

Positive non-significant association of this trait with grain yield plant^{-1} (0.0873, 0.1329) at both phenotypic and genotypic levels. These results are in conformity with the findings of Chaudhary (1989), Bandyopadhyay (1998a) and Sahu and Pradhan (2012).

4.2.6 Finger length

Finger length showed significant positive association with days to 50% flowering (0.2727, 0.2965), plant height (0.4828, 0.5697), number of productive tillers (0.1848, 0.2261) and number of fingers ear^{-1} (0.3951, 0.4502) at both phenotypic level and genotypic level.

Similar results were reported by Bendale et al. (2002) and Ganapathy *et al.* (2011) for days to 50% flowering, Andualem and Tadesse (2011) and Ganapathy *et al.* (2011) for plant height, Gowda *et al.* (2008) and Kadam *et al.* (2009) for number of productive tillers and Sahu and Pradhan (2012) for number of fingers ear^{-1} at both phenotypic and genotypic level.

This trait showed positive non-significant association with yield plant^{-1} at phenotypic level only (0.0073). These results are in agreement with the findings of Shantha Kumar and Goud (1997, 1998).

4.2.7 Number of Grain panicle^{-1}

This trait showed significant positive association with days to 50% flowering (0.1522), days to maturity (0.2158) at both phenotypic and genotypic level and test weight (0.1419) at genotypic level and negative association with number of productive tillers (-0.2297) at both phenotypic and genotypic level.

These results are in conformity with the findings of Kebere Bezaweletaw *et al.* (2006) for days to 50% flowering and days to maturity at phenotypic level and for days to 50% flowering, days to maturity and test weight at genotypic level.

It showed positive significant association with grain yield plant^{-1} at both phenotypic (0.8342) and genotypic level (1.0651). These results are in conformity with the findings of Chuni Lal *et al.* (1996) and Kebere Bezaweletaw *et al.* (2006).

4.2.8 Test weight

Test weight showed significant positive association with days to maturity (0.2696) which is similar to the findings of Chuni Lal *et al.* (1996) and seed protein % (0.2706) at phenotypic level. It also show significant positive association with days to maturity (0.3045), number of grains panicle^{-1} (0.1419) and seed protein % (0.2948) at genotypic level and significant negative association with number of productive tillers (-0.1585) at genotypic level.

This trait showed significant positive association with grain yield plant^{-1} at genotypic level (0.1474) and positive non-significant association at phenotypic level (0.1292). These results are in agreement with the findings of Dhagat *et al.* (1972).

4.2.9 Seed Protein %

This trait showed significant positive association with days to 50% flowering (0.1958, 0.203), plant height (0.1468, 0.1629), number of productive tillers (0.1603, 0.1831), number of finger ear^{-1} (0.3465, 0.3621) and test weight (0.2706, 0.2948) at phenotypic and genotypic level. This trait showed positive non-significant association with grain yield plant^{-1} (0.0907, 0.104) at both phenotypic and genotypic level indicating no major improvement can be made in the total grain yield plant^{-1} by improving this trait.

4.2.10 Grain yield plant^{-1}

The trait grain yield plant^{-1} showed significant positive association with days to maturity (0.1844, 0.2579), number of grains panicle^{-1} (0.8342, 1.0651) at both phenotypic and genotypic level. It also showed positive association with days to 50% flowering (0.1503) and test weight (0.1474) at genotypic level and significant negative association with number of productive tillers (-0.1760, -0.2383) at both phenotypic and genotypic level.

The negative significant association of number of productive tillers with grain yield plant^{-1} indicates the antagonistic nature of this character. However since most of the important yield component traits are showing strong significant positive association with grain yield plant^{-1} rational improvement in yield is possible through simultaneous selection for these component characters.

4.3 PATH COEFFICIENT ANALYSIS

The information on the extent of association between the yield and other components is important to bring the simultaneous improvement in correlated traits. With the increase in number of variables, it becomes imperative to measure the contribution of each variable towards the observed correlation. Therefore, partitioning the observed correlation coefficients into direct and indirect effects facilitates the characterization of more complex traits like grain yield as devised by Wright (1921) and utilized by Dewey and Lu (1959) in selection programmes. Path coefficient analysis, which splits the correlation coefficients, provides precise information on the direct and indirect effects in order to perceive the most influencing characters to be utilized as selection criteria in breeding programme.

Sometimes correlation coefficients may be negative, but the direct effect is positive and high. Under these conditions, a restricted simultaneous selection model has to be followed *i.e.,* restrictions are to be imposed to nullify the undesirable indirect effects, in order to make use of the direct effect (Singh and Chaudhary, 1977).

Hence in the present study direct and indirect effects of different yield component traits on grain yield plant^{-1} were estimated through path analysis at phenotypic and genotypic levels and are presented in Tables 4.5 and 4.6, respectively. The phenotypic and genotypic path diagrams are given in Fig.4.1 and 4.2, respectively.

4.3.1 Days to 50% flowering

At phenotypic level, the direct contribution of this character on grain yield plant^{-1} was negative (-0.0127). The indirect effects via plant height (0.0033), number of fingers ear^{-1} (0.0083), number of grains panicle^{-1} (0.1259), test weight (0.0017) and seed protein % (0.0012) were positive. While days to maturity (-0.0025), number of productive tillers (-0.0022) and finger length (-0.0056) showed negative indirect effects through this trait.

At genotypic level, the direct contribution of this character on grain yield plant^{-1} was negative (-0.0525). The indirect effects via productive tillers (0.016), number of finger ear^{-1} (0.0106), number of grains panicle^{-1} (0.2258), test weight (0.0001) and seed protein %

(0.0012) were positive. While days to maturity (-0.009), plant height (-0.04) and finger length (-0.0015) were negative.

This trait had significant positive correlation with grain yield plant^{-1} (0.1503, 0.1174) at genotypic and phenotypic level. These results indicated the true relationship between the traits. The negative direct effect indicates that the direct selection with due consideration for suitable positive indirect effects through other traits is necessary for selection programme. This is in agreement with Chaudhary (1989), Andualem and Tadesse (2011) and Haradari *et al.* (2012).

4.3.2 Days to Maturity

At phenotypic level, the direct contribution of this character on grain yield plant^{-1} was negative (-0.0048). The indirect effects via plant height (0.0017), number of fingers ear^{-1} (0.0024), number of grains panicle^{-1} (0.1785), test weight (0.0147) and seed protein % (0.0008) were positive. While days to 50% flowering (-0.0065), number of productive tillers (-0.001) and finger length (-0.0014) showed negative indirect effects through this trait.

At genotypic level, the direct contribution of this character on grain yield plant^{-1} was negative (-0.0168). The indirect effects via productive tillers (0.0064), number of finger ear^{-1}(0.0032), number of grains panicle^{-1} (0.3147), test weight (0.0008) and seed protein % (0.0006) were positive. While days to 50% flowering (-0.0281), plant height (-0.0225) and finger length (-0.0004) were negative.

This trait had positive significant correlation with grain yield plant^{-1} (0.2579, 0.1844) at both genotypic and phenotypic levels respectively, indicating that the trait days to maturity had a significant effect on grain yield plant^{-1} of its own and its effect on grain yield plant^{-1} may be through its component traits as the direct effect of this trait is low and negative. Similar results were reported by Sumathi *et al.* (2006), Kasetsart *et al.* (2006) and Ganapathy *et al.* (2011).

4.3.3 Plant Height

At phenotypic level, the direct contribution of this character on grain yield plant^{-1} was positive (0.007). The indirect effects via number of fingers ear^{-1} (0.0067), number of grains panicle^{-1} (0.0879) and seed protein % (0.0009) were positive. While days to 50%

flowering (-0.006), days to maturity (-0.0011), number of productive tillers (-0.0044), finger length (-0.0099) and test weight (-0.0036) showed negative indirect effects through this trait.

At genotypic level, the direct contribution of this character on grain yield plant^{-1} was negative (-0.0755). The indirect effects via number of productive tillers (0.0359), number of finger ear^{-1} (0.0083), number of grains panicle^{-1} (0.1544) and seed protein % (0.0007) were positive. While days to 50% flowering (-0.0278), days to maturity (-0.005), finger length (-0.0029) and test weight (-0.0002) were negative.

This trait had positive non-significant correlation with grain yield plant^{-1} (0.088, 0.0775) at genotypic level and phenotypic levels respectively. Dhagat *et al.* (1973), Andualem and Tadesse (2011), Ganapathy *et al.* (2011) and Haradari *et al.* (2012) also reported similar results for this trait.

4.3.4 Number of Productive tillers

At phenotypic level, the direct contribution of this character on grain yield plant^{-1} was negative (-0.0122). The indirect effects via plant height (0.0025), number of fingers ear^{-1} (0.001) and seed protein % (0.001) were positive. While days to 50% flowering (-0.0023), days to maturity (-0.0004), finger length (-0.0038), number of grains panicle^{-1} (-0.1544) and test weight (-0.0074) showed negative indirect effects through this trait.

At genotypic level, the direct contribution of this character on grain yield plant^{-1} was positive (0.0678). The indirect effects via number of finger ear^{-1} (0.0017) and seed protein % (0.0008) were positive. While days to 50% flowering (-0.0123), days to maturity (0.0016), plant height (-0.0399), finger length (-0.0011), number of grains panicle^{-1} (-0.2532) and test weight (-0.0004) were negative.

This trait had negative significant correlation with grain yield plant^{-1} (-0.2383, -0.176) at genotypic level and phenotypic levels respectively. The high and negative direct effect at genotypic level indicated that the genotypes with less number of productive tillers will give higher yields and the indirect positive effects were also to be considered while selection. Selection for varieties with less number of productive tillers may also bring about yield improvement. The results are in agreement with Prabhakhar and Prasad (1983), Shantha Kumar and Gowda (1997) and Bendale *et al.* (2002).

Table 4.5. Direct and indirect effects (phenotypic) of yield components on grain yield in 60 finger millet genotypes

Sl.no	Character	Days 50 % flowering	Days to maturity	Plant height	Number of productive tillers	No. of fingers ear^{-1}	Finger length	No. of grains panicle^{-1}	Test weight	Seed protein%
1	**Days to 50 % flowering**	**-0.0127**	-0.0065	-0.006	-0.0023	-0.0044	-0.0035	-0.0019	-0.0004	-0.0025
2	**Days to maturity**	-0.0025	**-0.0048**	-0.0011	-0.0004	-0.0005	-0.0003	-0.001	-0.0013	-0.0006
3	**Plant height**	0.0033	0.0017	**0.007**	0.0025	0.0019	0.0034	0.0007	-0.0005	0.001
4	**No. of productive tillers**	-0.0022	-0.001	-0.0044	**-0.0122**	-0.0005	-0.0023	0.0023	0.0017	-0.002
5	**No. of fingers ear^{-1}**	0.0083	0.0024	0.0067	0.001	**0.0242**	0.0095	0.0022	-0.0013	0.0084
6	**Finger length**	-0.0056	-0.0014	-0.0099	-0.0038	-0.0081	**-0.0205**	-0.0006	0.0012	-0.0015
7	**No. of grains panicle^{-1}**	0.1259	0.1785	0.0879	-0.1544	0.0755	0.0236	**0.8272**	0.0736	0.067
8	**Test weight**	0.0017	0.0147	-0.0036	-0.0074	-0.003	-0.0031	0.0049	**0.0546**	0.0148
9	**Seed protein%**	0.0012	0.0008	0.0009	0.001	0.0021	0.0004	0.0005	0.0017	**0.0061**
10	**Grain yield Plant^{-1} (r_p)**	**0.1174****	**0.1844****	**0.0775**	**-0.176****	**0.0873**	**0.0073**	**0.8342****	**0.1292****	**0.0907**

Table 4.6. Direct and indirect effects (genotypic) of yield components on grain yield in 60 finger millet genotypes

Sl.no	Character	Days to 50 % flowering	Days to maturity	Plant height	Number of productive tillers	No. of fingers ear^{-1}	Finger length	No. of grains panicle^{-1}	Test weight	Seed protein%
1	**Days to 50 % flowering**	**-0.0525**	-0.0281	-0.0278	-0.0123	-0.0193	-0.0156	-0.0107	-0.0017	-0.0106
2	**Days to maturity**	-0.009	**-0.0168**	-0.005	-0.0016	-0.0019	-0.0013	-0.0048	-0.0051	-0.0022
3	**Plant height**	-0.04	-0.0225	**-0.0755**	-0.0399	-0.0216	-0.043	-0.0106	0.0056	-0.0123
4	**No. of productive tillers**	0.016	0.0064	0.0359	**0.0678**	0.004	0.0153	-0.0156	-0.0108	0.0124
5	**No. of fingers ear^{-1}**	0.0106	0.0032	0.0083	0.0017	**0.0288**	0.013	0.0038	-0.0012	0.0104
6	**Finger length**	-0.0015	-0.0004	-0.0029	-0.0011	-0.0023	**-0.005**	-0.0001	0.0003	-0.0004
7	**No. of grains panicle^{-1}**	0.2258	0.3147	0.1544	-0.2532	0.1436	0.0258	**1.1024**	0.1564	0.1015
8	**Test weight**	0.0001	0.0008	-0.0002	-0.0004	-0.0001	-0.0001	0.0004	**0.0025**	0.0008
9	**Seed protein%**	0.0009	0.0006	0.0007	0.0008	0.0016	0.0003	0.0004	0.0013	**0.0044**
10	**Grain yield Plant^{-1} (r_g)**	**0.1503****	**0.2579****	**0.088**	**-0.2383****	**0.1329****	**-0.0106**	**1.0651****	**0.1474****	**0.104****

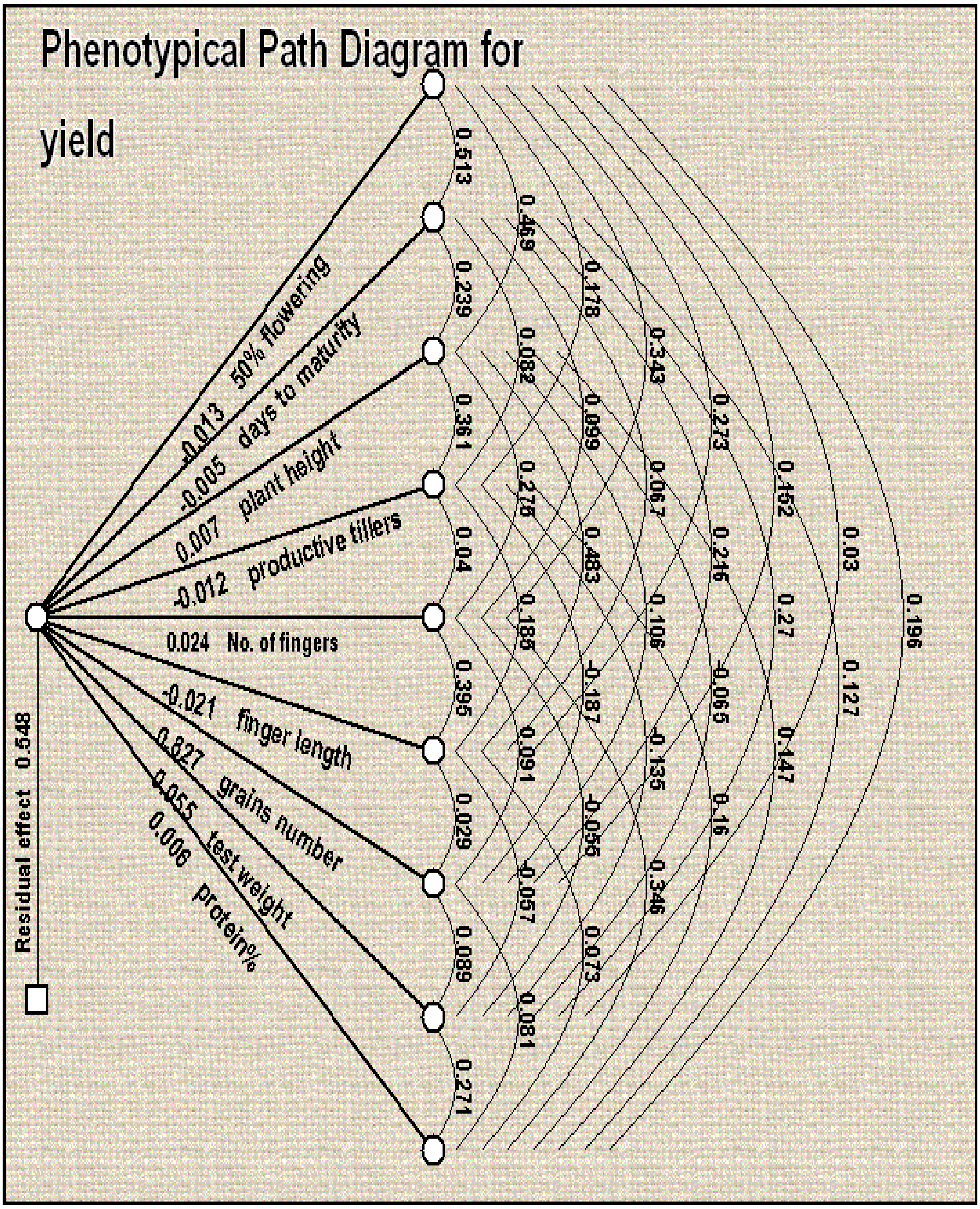

Fig 4.1. Phenotypic path diagram showing cause-effect relationship of yield components with grain yield per plant in finger millet

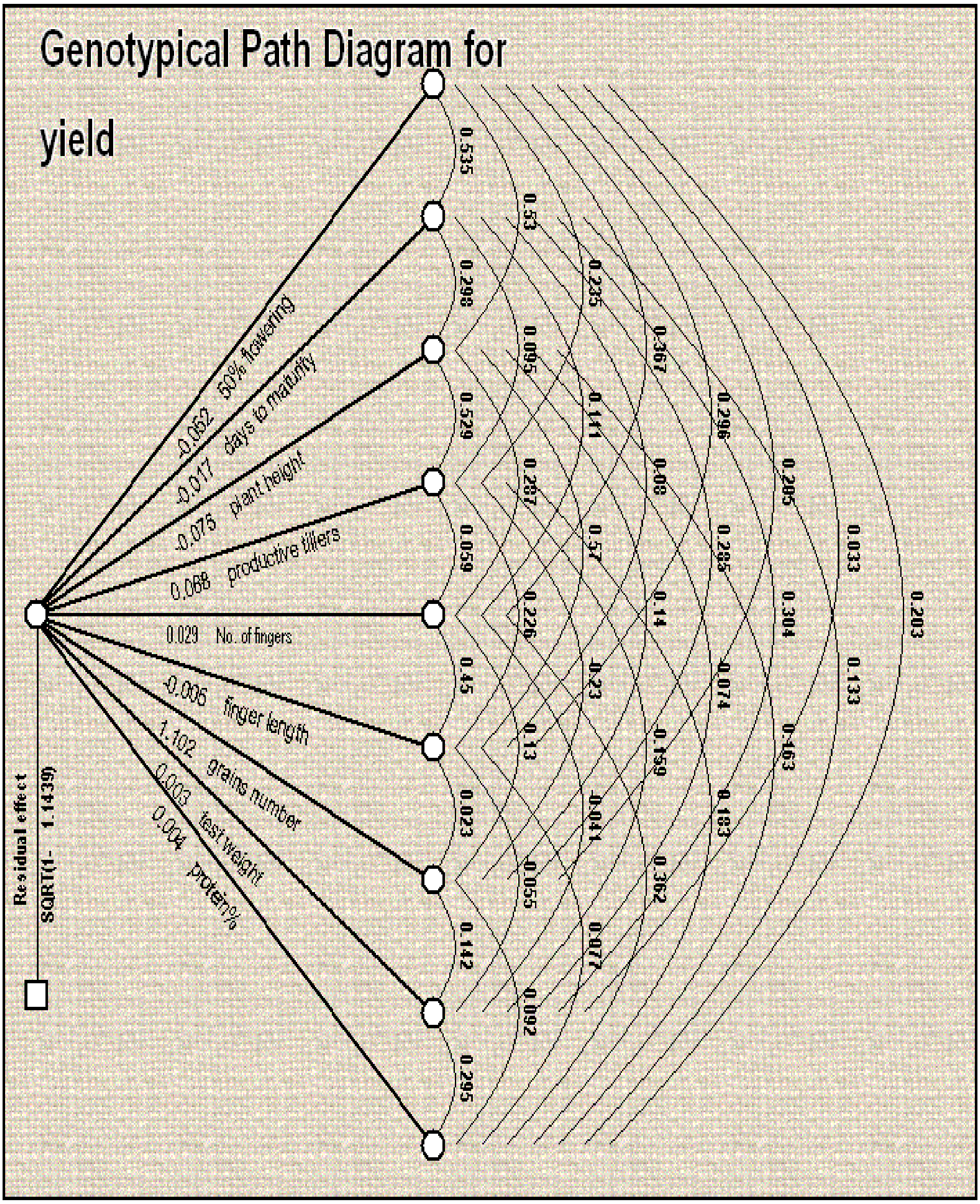

Fig 4.2. Genotypic path diagram showing cause-effect relationship of yield components with grain yield per plant in finger millet

4.3.5 Number of fingers ear^{-1}

At phenotypic level, the direct contribution of this character on grain yield plant^{-1} was positive (0.0242). The indirect effects via plant height (0.0019), grain number (0.0755) and seed protein % (0.0021) were positive. While days to 50% flowering (-0.0044), days to maturity (-0.0005), number of productive tillers (-0.0005), finger length (-0.0081) and test weight (-0.003) showed negative indirect effects through this trait.

At genotypic level, the direct contribution of this character on grain yield plant^{-1} was positive (0.0288).The indirect effects via number of productive tillers (0.004), number of grains panicle^{-1} (0.1436) and seed protein % (0.0016) were positive. While days to 50% flowering (0.0193), days to maturity (-0.0019), plant height (-0.0216), finger length (-0.0023) and test weight (-0.0001) were negative.

This trait had significant positive correlation with grain yield plant^{-1} (0.1329) at genotypic and non-significant positive correlation with grain yield plant^{-1} (0.0873) at phenotypic level. The non-significant correlation and low direct effect of this trait at phenotypic level indicates the influence of the environment on this trait. The low direct effects at genotypic level indicate that the trait had little effect on the grain yield plant^{-1} of its own but its effect on grain yield plant^{-1} may be through its components traits. Ravindran *et al.* (1996), Bedis *et al.* (2006), Ganapathy *et al.* (2011) and Priyadharshini *et al.* (2011) also reported similar results for this trait.

4.3.6 Finger Length

At phenotypic level, the direct contribution of this character on grain yield plant^{-1} was negative (-0.0205).The indirect effects via plant height (0.0034), number of fingers ear^{-1} (0.0095), number of grains panicle^{-1} (0.0236) and seed protein % (0.0004) were positive. While days to 50% flowering (-0.0035), days to maturity (-0.0003), number of productive tillers (-0.0023) and test weight (-0.0031) showed negative indirect effects through this trait.

At genotypic level, the direct contribution of this character on grain yield plant^{-1} was negative (-0.005). The indirect effects via number of productive tillers (0.0153), number of finger ear^{-1} (0.013), number of grains panicle^{-1} (0.0258) and seed protein % (0.0003) were positive. While days to 50% flowering (-0.0156), days to maturity (-0.0013), plant height (-0.043) and test weight (-0.0001) were negative.

This trait had non-significant negative correlation with grain yield plant^{-1} (-0.0106) at genotypic and non-significant positive correlation with grain yield plant^{-1} (0.0073) at phenotypic level, indicating that this trait had a significant effect on grain yield plant^{-1} directly and also through its component traits. The low direct effects indicate that the finger length had little effect on grain yield plant^{-1} as its own but its effect on grain yield plant^{-1} may be through its component traits. Further, non-significant correlation indicates the independent association of this trait in improving grain yield plant^{-1}. The results were in agreement with Kadam *et al.* (2009), Shindey *et al.* (2010) and Ganapathy *et al.* (2011).

4.3.7 Number of Grains Panicle^{-1}

At phenotypic level, the direct contribution of this character on grain yield plant^{-1} was positive (0.8272). The indirect effects via plant height (0.0007), number of productive tillers (0.0023), number of finger ear^{-1} (0.0022), test weight (0.0049) and seed protein % (0.0005) were positive. While days to 50% flowering (-0.0019), days to maturity (-0.001) and finger length (-0.0006) showed negative indirect effects through this trait.

At genotypic level, the direct contribution of this character on grain yield plant^{-1} was positive (1.1024). The indirect effects via number of finger ear^{-1} (0.0038), test weight (0.0004) and seed protein % (0.0004) were positive. While days to 50% flowering (-0.0107), days to maturity (-0.0048), plant height (-0.0106), number of productive tillers (-0.0156) and finger length (-0.0001) were negative.

This trait had significant positive correlation with grain yield plant^{-1} (1.0651, 0.8342) at genotypic and phenotypic level respectively, indicating that this trait had a significant effect on grain yield plant^{-1} directly and also through its component traits. These results were in agreement with the earlier works of Chuni Lal *et al.* (1996).

4.3.8 Test Weight

At phenotypic level, the direct contribution of this character on grain yield plant^{-1} was positive (0.0546). The indirect effects via number of productive tillers (0.0017), finger length (0.0012), number of grains panicle^{-1} (0.0736) and seed protein % (0.0017) were positive. While days to 50% flowering (-0.0004), days to maturity (-0.0013), plant height (-0.0005) and number of finger ear^{-1} (-0.0013) showed negative indirect effects through this trait.

At genotypic level, the direct contribution of this character on grain yield plant^{-1} was positive (0.0025). The indirect effects via plant height (0.0056), finger length (0.0003), number of grains panicle^{-1} (0.1564) and seed protein % (0.0013) were positive. While days to 50% flowering (-0.0017), days to maturity (-0.0051), number of productive tillers (-0.0108) and number of finger ear^{-1} (-0.0012) were negative.

This trait had significant positive correlation with grain yield plant^{-1} (0.1474, 0.1292) at genotypic and phenotypic level respectively, indicating that this trait had a significant effect on grain yield plant^{-1} of its own and its effect on grain yield plant^{-1} may be through its component traits. These results were in conformity with the work of Ranganathan *et al.* (1977), Prabakhar and Prasad (1983), Singh *et al.* (1995), Hari Krishna *et al.* (2005) and Padmaja *et al.* (2006).

4.3.9 Seed Protein %

At phenotypic level, the direct contribution of this character on grain yield plant^{-1} was positive (0.0061). The indirect effects via plant height (0.001), number of finger ear^{-1} (0.0084), number of grains panicle^{-1} (0.067) and test weight (0.0148) were positive. While days to 50% flowering (-0.0025), days to maturity (-0.0006), number of productive tillers (-0.002) and finger length (-0.0015) showed negative indirect effects through this trait.

At genotypic level, the direct contribution of this character on grain yield plant^{-1} was positive (0.0044). The indirect effects via number of productive tillers (0.0124), number of finger ear^{-1} (0.0104), number of grains panicle^{-1} (0.1015) and test weight (0.0008) were positive. While days to 50% flowering (-0.0106), days to maturity (-0.0022), plant height (-0.0123) and finger length (-0.0004) were negative.

This trait had significant positive correlation with grain yield plant^{-1} (0.104) at genotypic and non-significant positive correlation with grain yield plant^{-1} (0.0907) at phenotypic level. The non-significant correlation and very low direct effect of this trait at phenotypic level indicates the influence of the environment on this trait. These results were in agreement with the earlier works of Sarala *et al.* (2007)

The path analysis indicated that number of productive tillers, number of fingers ear^{-1}, grain number, test weight and seed protein % showed direct positive effects on grain yield plant^{-1}.

In plant breeding, it is very difficult to have complete knowledge of all component traits of yield. The residual effect permits precise explanation about the pattern of interaction of other possible components of yield. In other words, residual effect measures the role of the possible independent variables which were not included in the study on the dependent variable. In the present study, the residual effect observed was low both at phenotypic (0.548) and genotypic [sqrt (1-1.1439)] levels, so the characters included in the study clearly explains extent of the direct and indirect effects on the dependent variable.

The present study revealed that due weightage should be given while undergoing selection for number of days to 50% flowering, days to maturity, plant height, number of productive tillers, number of finger ear^{-1}, number of grains panicle^{-1} and test weight and there should be economic balance among these traits to get higher grain yield plant^{-1}.

4.4 GENETIC DIVERGENCE

Genetic divergence plays a key role in analysing the general distance among the genotypes and subsequently selection of distant parents. Hybridization among diverse set of parents is likely to enhance the level of heterosis and generate wide range of variability in segregating generations.

Generally, geographical diversity was considered as a measure of genetic diversity when no scientific tools were available. But, geographical distribution of genotypes is not the only factor that causes genetic diversity. This may be due to exchange of breeding material over the locations and further selections at different locations which could result in genetic drift. However, this is an inferential criterion and may not be used for discrimination among the populations occupying ecologically marginal habitats (Arunachalam and Ram, 1967). So, selection of parents for hybridization programme should be based on genetic divergence rather than geographical diversity as there is no parallelism between genetic divergence and geographical divergence of genotypes.

The multivariate analyses like Mahalanobis' D^2 statistic and principal component analysis provide useful statistical tool for measuring the genetic diversity in a given population with respect to the characters that are considered together. Further, the problem of selecting diverse parents for hybridization programme can be narrowed, if one can identify the characters responsible for the discriminations between the populations.

The data collected on 10 yield and yield contributing characters from 60 genotypes of finger millet were subjected to multivariate analysis like Mahalanobis' D^2 statistic, principal component and cluster analysis. The magnitude of values suggested that there is considerable variability in the genotypes studied, which led to genetic diversity.

4.4.1 Mahalanobis' D^2 analysis

4.4.1.1Test with *Wilk's* criterion 'Λ'

Significant differences among the genotypes for individual characters were first determined and later the statistical significant differences between the genotypes based on the pooled effects of all the characters were carried out using the *Wilk's criterion* 'Λ'. The *Wilk's* criterion, thus obtained was used in calculations of 'V' statistic. The value of 'V' statistic was 3221.9 in the present investigation. This highly significant statistic indicated that genotypes differ significantly when all the characters were considered simultaneously.

4.4.1.2 Mahalanobis' D^2 values

To estimate the D^2 values, correlated means of characters were transformed into standardized uncorrelated characters using Pivotal Condensation Method. It measures the degree of diversification and determines the relative proportion of each component character to total divergence. The statistical differences (D^2) between pairs of genotypes was obtained as the sum of squares of the differences between the pairs of corresponding uncorrelated values of any two genotypes considered at a time. Thus a possible 1770 combinations and the corresponding D^2 values were obtained.

The per cent contribution towards genetic divergence for all the 10 contributing characters is presented in Table 4.7.The knowledge on characters influencing divergence is an important aspect to a breeder. Out of the total contribution of different characters towards genetic divergence protein content (79.66%) showed maximum contribution which was followed by days to 50% flowering (8.14%), days to maturity (5.42%), number of fingers per ear head (3.28%), test weight (1.19%), finger length (0.90%), number of productive tillers (0.56%), number of grains per panicle (0.34%), plant height (0.28%) and yield per plant (0.23%).

4.4.1.3 Grouping of genotypes into various clusters

The 60 genotypes were grouped into eight clusters using the Tocher's method with the criterion that the intra-cluster average D^2 values should be less than the inter-cluster D^2 values (Table 4.8).

The distribution of 60 genotypes into eight clusters was at random with maximum number of genotypes in cluster I and cluster II (24 genotypes) from different locations.

Cluster III was the second largest with 7 genotypes. Clusters IV, V, VI, VII and VIII were solitary clusters, and showed nil intra-cluster D^2 values. The formation of distinct solitary clusters may be due to the fact that geographic barriers preventing gene flow or intensive natural and human selection for diverse and adaptable gene complexes must be responsible for this genetic diversity (Arunachalam and Ram, 1967).

This pattern of grouping has indicated that the diversity need not be necessarily related to geographical diversity and it may be the outcome of several other factors like natural selection, exchange of breeding material, genetic drift and environmental variation. Therefore, selection of varieties for hybridization should be based on genetic diversity rather than geographical diversity.

The mutual relationships between the clusters were represented diagrammatically by taking average intra and inter cluster D^2 values. The tree like structure called dendrogram (Fig 4.3) was constructed based on clustering by Tocher's method.

4.4.1.4 Average intra and inter- cluster D^2 value

The average intra -and inter- cluster D^2 values were estimated as per the procedure given by Singh and Chaudhary (1977) and were presented in the Table 4.9. The proximity and divergence among eight clusters were indicated in Table 4.10.

The maximum intra cluster distance was 221.84 in cluster II followed by 186.45 in cluster III followed by 182.14 in cluster I while, it was zero for clusters IV, V, VI, VII, VIII.

Cluster I, with 24 genotypes, was the largest of all clusters. It was closest to cluster IV (334.83) followed by cluster III (486.09) and it was farthest from cluster VII (2678.51) followed by cluster VIII (2546.73).

Cluster II, with 24 genotypes, was also the largest of all clusters along with cluster I. It was closest to cluster IV (370.31) followed by cluster V (416.68) and it was farthest from cluster III (1892.88) followed by cluster VII (962.78).

Seven genotypes were grouped into cluster III. It was nearest to cluster IV (1105.78) followed by cluster V (1693.98) and it was farthest from cluster VII (4761.34) followed by cluster VIII (4426.68).

Cluster IV was monogenotypic (GE-3225). It was nearest to the cluster II (416.68) followed by cluster V (459.72) and it was farthest from cluster VII (1693.98) followed by cluster VIII (1542.81).

Cluster V was monogenotypic (GE-995). It was closest to the cluster II (416.68) followed by cluster I (662.42) and was farthest from cluster III (1693.98) followed by cluster VIII (1426.56).

Cluster VI was monogenotypic (GE-258). It was closest to the cluster VII (269.55) followed by cluster VIII (289.04) and was farthest from cluster VIII (337.09) followed by cluster IV (284.85).

Cluster VII was monogenotypic (GE-2127). It was closest to the cluster VI (269.55) followed by cluster VIII (498.58) and was farthest from cluster III (4761.34) followed by cluster I (2678.51).

Cluster VIII was monogenotypic (GE-666). It was closest to the cluster VI (289.04) followed by cluster VII (498.58) and was farthest from cluster III (4426.68) followed by cluster I (2546.73).

The high intra-cluster distance in cluster II indicates the presence of wide genetic diversity among the genotypes present within this cluster.

Genotypes grouped into the same cluster presumably differ little from one another as the aggregate of characters measured. General notion exists that the larger is the divergence between the parental genotypes, the higher will be the heterosis in crosses. In the present study, inter-cluster distances were worked out considering 10 characters and these distances ranged from 269.55 (between cluster VI and VII) to 4761.34 (between cluster III and VII).

The inter-cluster distance was maximum between cluster III and VII (4761.34), followed by cluster III and VIII (4426.68), cluster III and VI (3750.44), cluster I and VII (2678.51), cluster I and VIII (2546.73), cluster I and VI (1977.98) and cluster II and Cluster III (1892.88). This suggested that there is wide genetic diversity between these clusters. Based on these studies, crosses can be made between genotypes of these clusters to obtain desirable transgressive segregants.

Table 4.7. Contribution of different characters towards genetic divergence in 60 Finger millet genotypes

Sl.no	Source	No. of times ranked first	Per cent contribution
1	Days to 50% flowering	144	8.14%
2	Days to maturity	96	5.42%
3	Plant height	5	0.28%
4	Number of productive tillers	10	0.56%
5	No. of fingers ear^{-1}	58	3.28%
6	Finger length	16	0.90%
7	No. of Grains panicle^{-1}	6	0.34%
8	Test weight	21	1.19%
9	Seed Protein%	1410	79.66%
10	Grain yield plant^{-1}	4	0.23%

Table 4.8. Clustering pattern of 60 finger millet genotypes by Tocher's method

Cluster number	No. of genotypes	Name of genotype (s)
I	24	GE-1680, GE-1274, GE-3689, GE-667, GE-3090, GE-4437, GPU-26, GPU-66, GPU-67, L-5, GE-1298, GE-225, GPU-28, GE-4707, GE-4976, GE-3266, GE-4736, GE-4440, GE-2073, GE-3986, GE-2811, GE-4777, GE-3067, GE-1673
II	24	GE-361, INDAF-5, GE-636, GE-4764, GE-145, GE-2737, GE-2672, GE-844, GE-2723, GPU-45, GE-5159, GE-1126, HR-911, MR-6, GE-5257, GE-3521, GE-2931, GE-3775, GE-1074, GE-3140, GE-492, GE-4999, GE-4842, GE-2078
III	7	GE-4798, GE-506, GE-2963, GE-1746, GPU-48, GE-3099, GE -3453
IV	1	GE-3225
V	1	GE-995
VI	1	GE-258
VII	1	GE-2127
VIII	1	GE-666

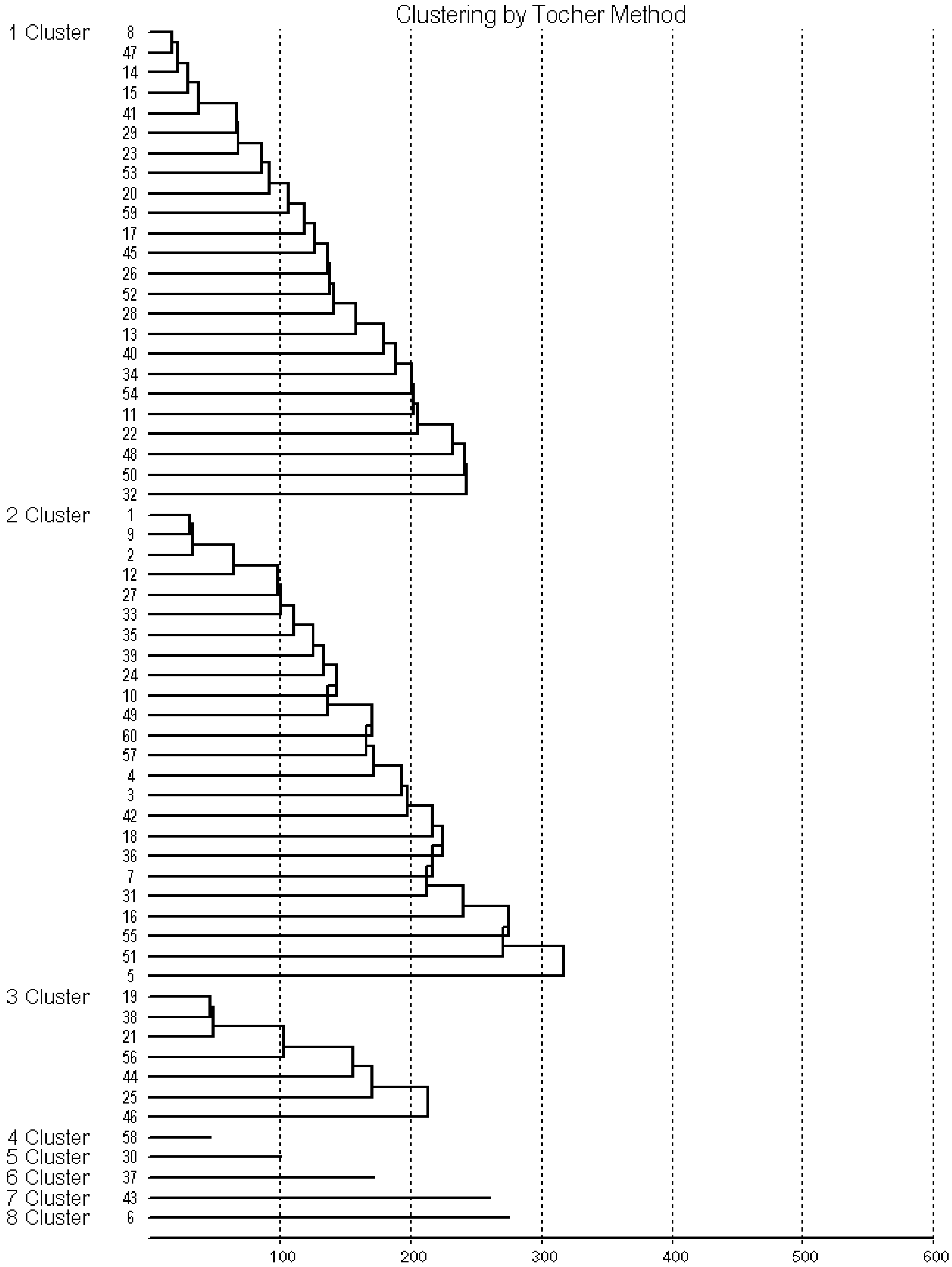

Fig 4.3. Dendrogram showing relationship of 60 finger millet genotypes in eight clusters based on Mahalanobis' D^2 values (Genotype numbers as per Table 3.1)

Table 4.9. Average intra (diagonal) and inter-cluster D^2 values among eight clusters with 60 finger millet genotypes

Cluster number	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**
I	182.14	789.09	486.09	334.83	662.42	1977.98	2678.51	2546.73
II		221.84	1892.88	370.31	416.68	542.57	962.78	826.88
III			186.45	1105.78	1693.98	3750.44	4761.34	4426.68
IV				0	459.72	1005.33	1693.98	1542.81
V					0	854.43	962.55	1426.56
VI						0	269.55	289.04
VII							0	498.58
VIII								0

Table 4.10. The nearest and the farthest cluster from each cluster based on D^2 values using Tocher's method in 60 finger millet genotypes

Cluster number	Nearest cluster with D^2 values	Farthest cluster with D^2 values
I	IV (334.83)	VII (2678.51)
II	IV (370.31)	III (1892.88)
III	IV (1105.78)	VII (4761.34)
IV	V (459.72)	VII (1662.37)
V	VI (854.43)	VIII (1426.56)
VI	VII (269.55)	VIII (289.04)
VII	VI (269.55)	III (4761.34)
VIII	VI (289.04)	III (4426.68)

Table 4.11. Mean values for 10 character in eight clusters estimated by Tocher's method from 60 finger millet genotypes

Cluster number	**Days to 50% flowering**	**Days to maturity**	**Plant height**	**No. of productive tillers**	**No. of fingers ear^{-1}**	**Finger length**	**No. of grains panicle^{-1}**	**Test weight**	**Seed protein~~%~~**	**Grain yield plant^{-1}**
I	62.18	107.24	103.98	5.05	6.76	8.89	2211.31	**3.15**	9.49	21.83
II	64.54	106.94	105.79	5.11	6.55	8.84	2334.36	2.88	7.86	22.86
III	**69.43**	113.62	114.29	5.32	7.10	10.04	**2539.54**	3.12	**10.63**	**24.62**
IV	52.67	120.00	91.25	5.03	**7.80**	9.53	2353.93	2.87	8.73	22.45
V	53.00	**87.00**	82.77	5.10	**3.47**	**5.72**	1952.97	**2.62**	8.24	**17.62**
VI	53.00	**120.67**	108.36	5.50	5.30	8.26	2342.40	2.93	6.67	21.46
VII	**50.67**	88.00	**78.49**	**4.30**	3.50	6.83	**1860.20**	2.73	**6.18**	17.95
VIII	62.33	94.67	**140.54**	**5.63**	7.10	**14.63**	1907.67	2.91	6.37	18.34

Note: Bold figures indicate minimum and maximum values in each character

Choice of the particular cluster and selection of particular genotype from selected cluster are the two important points to be considered before initiating the crossing programme. The hybrids between varieties of different clusters will express high heterosis and give more useful segregants. Hence genotypes from different clusters may be chosen for further genetic studies either by diallel or line × tester analysis.

4.4.1.5 Cluster mean values

The cluster mean values for 10 characters are presented in Table 4.11. The data indicated a wide range of mean values between the clusters. Days to 50% flowering had a range of 50.67 for cluster VII to 69.43 for cluster III; days to maturity had a range of 87.00 for cluster V to 120.67 for cluster VI; plant height had a range of 78.49 for cluster VII to 140.54 for cluster VIII; number of productive tillers ranged from 4.30 for cluster VII to 5.63 for cluster VIII; number of fingers ear^{-1} varied from 3.47 for cluster V to 7.80 for cluster IV; finger length varied from 5.72 for cluster V to 14.63 for cluster VIII; number of grains per panicle varied from 1860.20 for cluster VII to 2539.54 for cluster III; test weight varied from 2.62 for cluster V to 3.15 for cluster I; seed protein % varied from 6.18 for cluster VII to 10.63 for cluster III and grain yield plant^{-1} ranged from 17.62 for cluster V to 24.62 for cluster III.

Higher mean values for protein % were seen in cluster III and cluster I and higher means for days to 50% flowering were seen in cluster III and II and higher means for days to maturity were observed in clusters VI, IV and higher means for number of finger ear^{-1} were observed in clusters IV, VIII and higher means for test weight were observed in clusters I, III which were major contributors in improving grain yield plant^{-1} in finger millet. Based on mean values, series of crosses in diallel analysis may prove highly successful for genetic improvement of the above mentioned traits.

The success and usefulness of Mahalanobis' D^2 analysis in quantifying genetic divergence in finger millet has been studied by Suyambulingam and Jebarani (1977), Jain *et al.* (1981), Shigeta (1985), Jayaprakash Naik (1991), Purushotham Rao (1992), Vadivoo *et al.* (1998), Surya Kumar *et al.* (1998), Jain *et al.* (2002), Satish (2003), Balwant Kumar *et al.* (2005), Jayalakshmi *et al.* (2007), Anantharaju and Meenakshiganesan (2008), Arun Prabhu *et al.* (2008), Kadam (2008), Dinesh Kumar *et al.* (2010) and Sahu and Pradhan (2012).

4.4.2 Principal component analysis

Principal component analysis or Canonical (vector) analysis is a sort of multivariate analysis where canonical vectors or roots representing different axis of differentiation and amount of variation accounted for by each of such axis, respectively, are derived (Rao, 1952). It is called principal component analysis as it reflects the importance of the largest contributor to the total variation at each axis of differentiation. It measures divergence between varieties in terms of spatial distance rather than quantifying it as D^2 does. It gives group constellations as varietal distribution in two-way pictorial graph fixing the relative position of each variety or genotype.

In principal component analysis on correlation matrix, the standardization of columns (here characters) created 10 new variables for 60 genotypes without changing their relative positions. These 10 new variables are the principal components (PC_1, PC_2 …….PC_{10}). Each principal component is a linear combination of the 10 attributes of data matrix. The loading values are scaled or standardized in such a manner that the sum of square of loadings within a principal component is equal to one. The loadings are viewed as weights defining the contribution of characters in respective principal component. Like regression coefficients, loadings sign (+ / -) are indicative of the direction of contribution. But unlike regression, only the relative contributions are important, so all signs can be changed without affecting the analysis (Jackson, 1991).

The loadings for first principal component were chosen so as to make its variance as large as possible. Loadings of second principal component were chosen such that the variance of PC_2 is as large as possible, subject to the constraint that PC_1 and PC_2 are uncorrelated. The process was continued to create 10 principal components, but PC's having eigen value less than one is not having any practical significance (Legendre and Legendre, 1984).

Results obtained from PCA on the correlation matrix of the traits reduce the dimensionality of the data set by creating several significant principal components having eigen value more than one. The PCA scores for individual genotypes were used for clustering the genotypes as suggested by Anderberg (1993). Results of PCA and cluster analysis are discussed here under.

Principal components (Eigen value greater than one), Eigen values (Latent Root), per cent variability, cumulative per cent variability and component loading of different characters are presented in Table 4.12.

Table 4.12. Eigen values, proportion of the total variance represented by first four Principal components, cumulative per cent variance and component loading of different characters in finger millet.

	PCA_1	**PCA_2**	**PCA_3**	**PCA_4**
Eigen Value (Root)	**3.548**	**1.653**	**1.311**	**0.959**
% Var. Exp.	**35.479**	**16.532**	**13.110**	**9.591**
Cum. Var. Exp.	**35.479**	**52.011**	**65.121**	**74.712**
Days to 50% Flowering	0.384	0.204	0.138	0.075
Days to Maturity	0.322	-0.159	0.365	-0.182
Plant Height (cm)	0.351	0.430	0.157	-0.091
Number of Productive Tillers	0.261	0.550	0.116	-0.218
No. of Fingers ear^{-1}	0.243	-0.038	-0.608	0.327
Finger Length	0.155	0.370	-0.449	0.252
Number of Grains Panicle^{-1}	0.410	-0.247	0.193	0.373
Test Weight	0.251	-0.292	-0.230	-0.501
Seed Protein %	0.247	-0.138	-0.378	-0.533
Grain Yield Plant^{-1}	0.426	-0.377	0.079	0.247

In the present study, the first eight principal components with eigen values more than one contributed 74.71 per cent towards the total variability. It was therefore inferred that the essential features of data set had been represented in the first four principal components. The first principal component contributed maximum towards variability (35.48). The characters *viz.*, days to 50% flowering (0.38), plant height (0.35), number of grains panicle^{-1} (0.41), grain yield plant^{-1} (0.43) contributed maximum variance in the first principal component (PC_1) and signifying their importance in divergence.

The second principal component (PC_2) described 16.53 per cent of total variance and the characters *viz.*, plant height (0.43), number of productive tillers (0.55), finger length (0.37), grain yield plant^{-1} (-0.38) showed the maximum variance in this principal component.

The third principal component (PC_3) was characterized by 13.11 per cent contribution towards the total variability. The characters *viz.*, days to maturity (0.37), number of fingers ear^{-1} (-0.61), finger length (-0.45), seed protein % (-0.38), contributed maximum variance in this principal component.

The fourth principal component (PC_4) was conspicuously characterized by high loading of number of fingers ear^{-1} (0.33), number of grains panicle^{-1} (0.37), test weight (-0.50), seed protein % (-0.53). Contribution of this principal component towards the total variability was 9.59 per cent.

The PCA scores for 60 finger millet genotypes in the first three principal components were computed. Principal component I, II and III were considered as three axis as X, Y and Z and squared distance of each genotype from these three axis were calculated and presented in Table 4.13.

The analysis thus identified the maximum contributing variables *i.e.*, days to 50% flowering, days to maturity, plant height, number of productive tillers, number of fingers ear^{-1} and finger length. It is important to study the variance as the relative contribution than the signs (indicative of direction) in principal component analysis.

These three PCA scores for 60 genotypes were plotted in graph to get two dimensional and three dimensional scatter diagrams (Fig.-4.4 and Fig.-4.5) and revealed diversity between the genotypes. The genotypes GE-666, GE-4842, GE-2723, GE-361 and GE-3521 showed maximum variance through PC_1 axis and these genotypes are considered to be highly divergent with required variability for further improvement in plant breeding programme. These genotypes may be used in crop improvement programmes for generating transgressive segregants. While the genotypes GPU-48, GE-4440, GPU-67, GE-3067 and GE-4437 showed low variance on both sides of the axis so it may be considered that these genotypes are less efficient in breeding programme to improve yield unless they have special added advantage in them.

Table 4.13. PCA scores of 60 finger millet genotypes

Sl.no	Genotype	Vector 1	Vector 2	Vector 3
1	GE-361	51.064	0.473	-22.244
2	GE-636	52.670	-2.327	-22.986
3	GE-5257	57.461	-2.109	-23.049
4	MR-6	57.898	-0.175	-23.565
5	GE-2078	48.756	-1.749	-19.820
6	GE-666	52.039	6.077	-20.277
7	GE-1074	56.014	-3.399	-24.931
8	GE-1680	56.201	-3.167	-28.231
9	INDAF-5	53.207	-1.174	-22.260
10	GPU-45	54.887	-3.409	-24.039
11	GE-3986	59.289	-5.063	-31.821
12	GE-4764	53.056	-0.806	-19.865
13	GE-3266	61.922	-4.332	-27.154
14	GE-3689	56.144	-3.144	-28.127
15	GE-667	56.738	-4.954	-28.406
16	GE-492	56.352	-4.156	-24.536
17	GE-1298	58.274	-3.394	-24.404
18	GE-2931	56.172	-0.189	-25.813
19	GE-4798	64.052	-5.211	-30.578
20	GPU-67	59.412	-5.981	-27.925
21	GE-2963	64.900	-1.272	-29.518
22	GE-2811	59.854	-4.518	-31.143
23	GPU-26	56.953	-3.354	-30.337
24	GE-2723	56.951	0.581	-17.263
25	GE-3099	62.096	-0.049	-33.619
26	GPU-28	59.551	-3.475	-28.899
27	GE-145	56.214	-1.467	-18.868
28	GE-4976	59.542	-1.617	-26.077
29	GE-4437	54.404	-5.609	-28.820
30	GE-995	48.391	-2.645	-21.239
31	GE-3140	51.713	-0.424	-23.556
32	GE-1673	57.935	-1.424	-31.552
33	GE-2737	56.192	-0.454	-18.296
34	GE-4440	56.790	-6.251	-25.334
35	GE-2672	56.804	-1.504	-19.333
36	GE-3775	55.039	-0.958	-24.337
37	GE-258	51.386	-0.285	-16.112
38	GE-506	64.698	-4.749	-29.817
39	GE-844	57.856	-1.253	-21.155
40	GE-4736	62.661	-2.579	-26.963
41	GE-3090	54.366	-4.422	-29.177
42	GE-3521	55.791	0.317	-23.104
43	GE-2127	43.103	-1.181	-15.764
44	GPU-48	61.535	-7.367	-34.260
45	GE-225	59.442	-4.727	-26.294
46	GE-3453	68.292	-5.533	-33.482
47	GE-1274	56.117	-2.805	-29.129
48	GE-4777	58.611	-3.330	-30.894
49	GE-5159	53.744	-2.353	-21.313
50	GE-3067	63.149	-5.747	-26.979
51	GE-4842	59.454	2.412	-22.737
52	GE-4707	61.606	-2.263	-28.287
53	GPU-66	60.160	-4.362	-27.627
54	GE-2073	57.325	-2.716	-29.491
55	GE-4999	58.275	-2.137	-22.642
56	GE-1746	63.662	-4.822	-28.818
57	HR-911	55.165	-1.902	-23.779
58	GE-3225	56.945	-4.640	-27.045
59	L-5	61.170	-4.583	-27.258
60	GE-1126	55.478	-2.960	-25.255

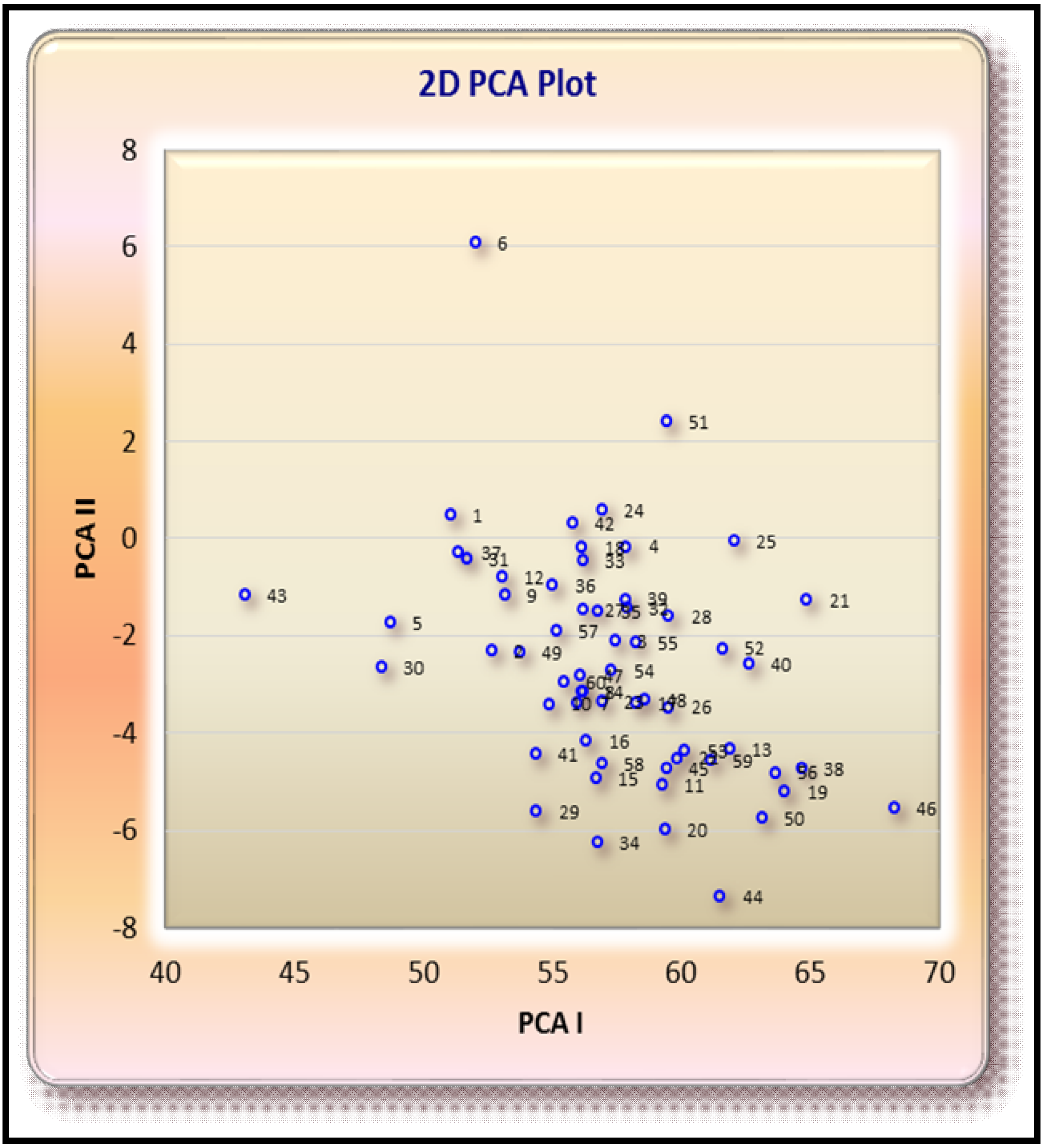

Fig 4.4. **Two dimensional graph showing relative position of 60 finger millet genotypes based on PCA Scores.**

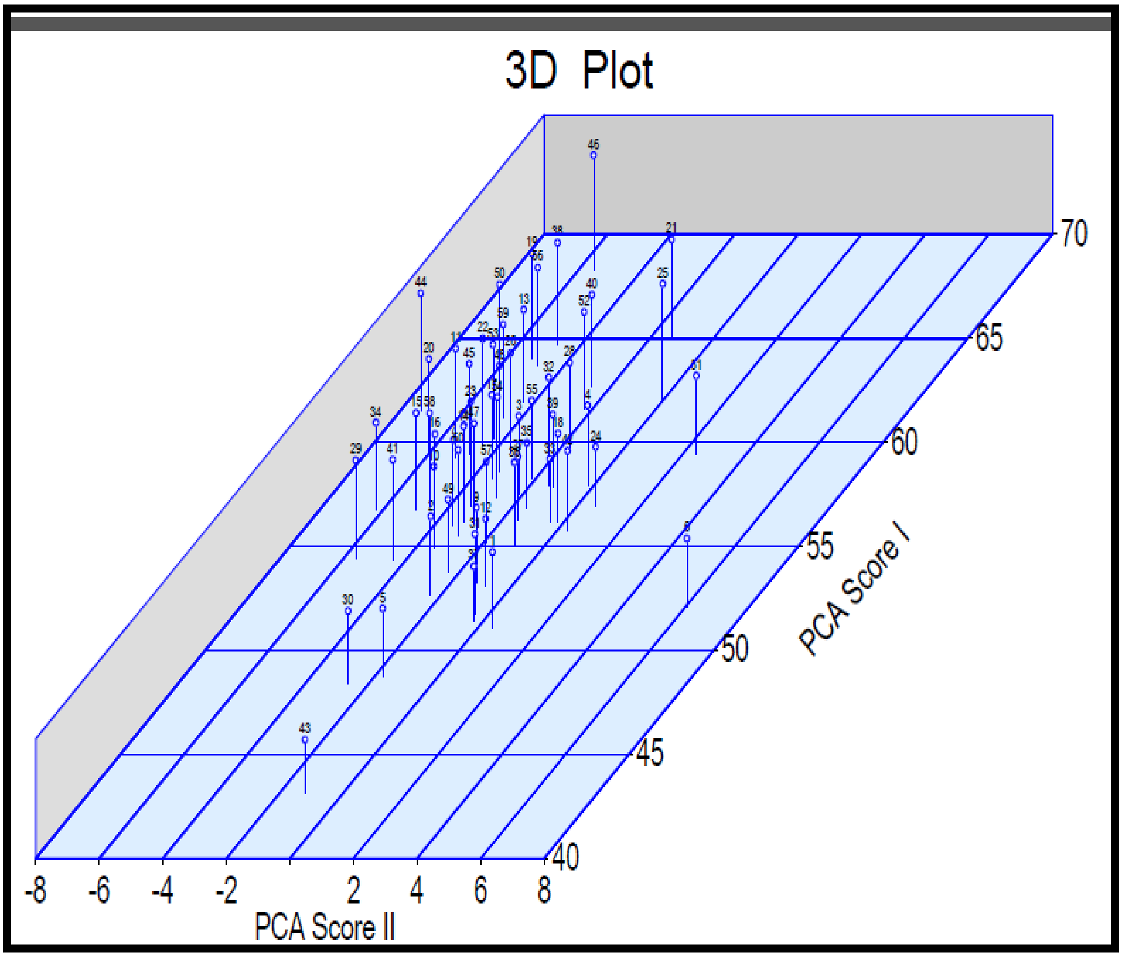

Fig 4.5. **Three dimensional graph showing relative position of 60 finger millet genotypes based on PCA scores. (Genotype numbers as per Table 4.1)**

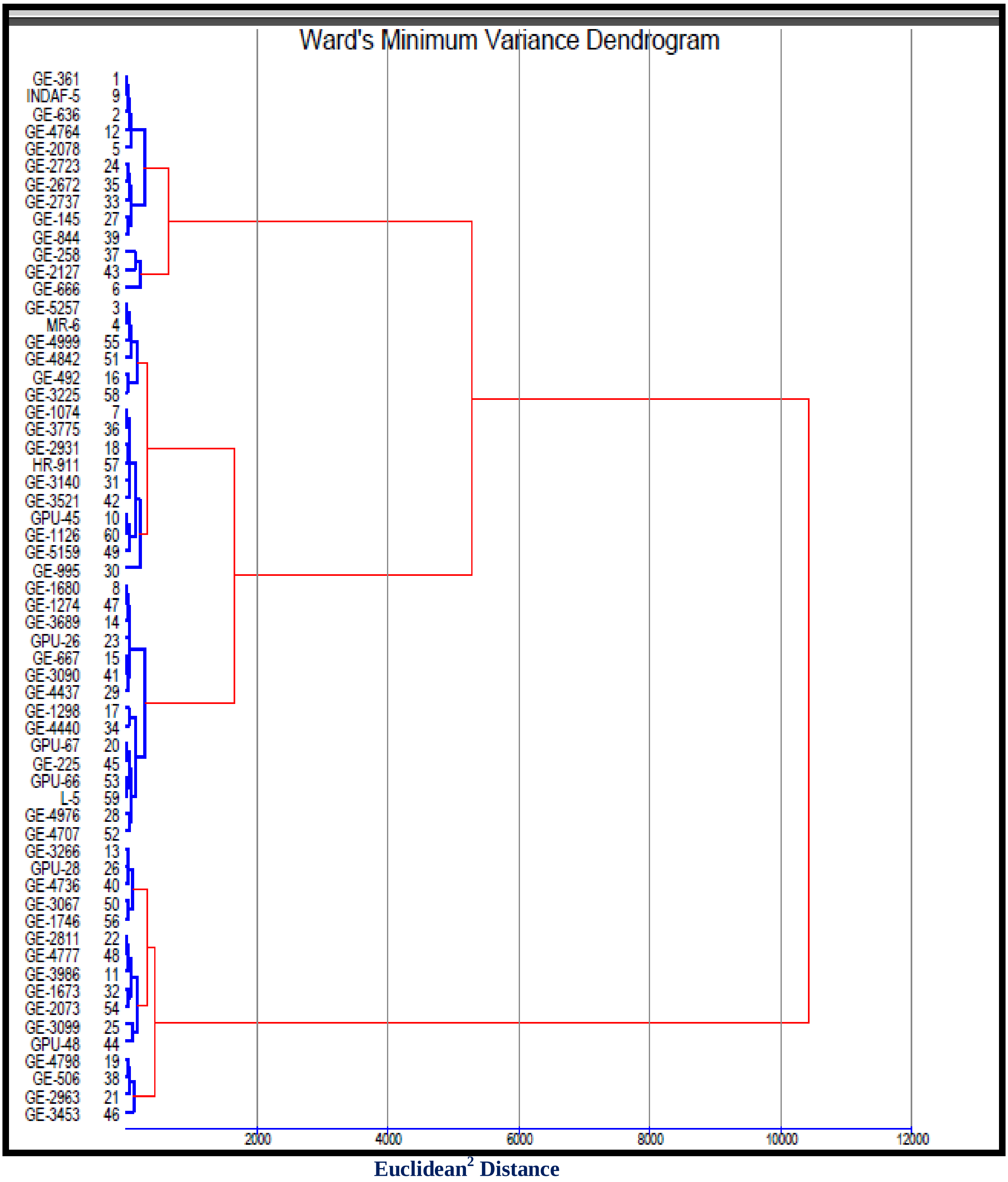

Fig 4.6. Dendrogram showing relationship of 60 finger millet genotypes in eight clusters based on Eucledean's distance

4.4.3 Cluster analysis

The extent of genetic diversity among the 60 genotypes studied was assessed and the results are presented hereunder.

4.4.3.1 Grouping of genotypes into various clusters

Sixty genotypes were grouped into eight clusters using the Ward's minimum variance procedure (Anderberg, 1993) and the distributions of the genotypes into different clusters are presented in figure 4.6.

The 60 genotypes were grouped into eight clusters. The distribution of genotypes into eight clusters is presented in Table 4.14. Among all the clusters, cluster V was the largest containing fifteen genotypes followed by cluster I and IV with ten genotypes, cluster VII with seven genotypes, cluster III with six genotypes, cluster VI with five genotypes, cluster VIII with four genotypes and cluster II with two genotypes. This random distribution of genotypes indicated absence of parallelism between geographical and genetic diversity. The mutual relationship between clusters is represented diagrammatically (Fig.-4.7) by taking average intra- and inter- cluster Euclidean^2 distances.

4.4.3.2 Average intra- and inter- cluster Euclidean^2 distance values

The average intra- and inter- cluster Euclidean^2 distance were estimated based on Ward's minimum variance and are presented in the Table 4.15.

By Ward's method, the 60 genotypes were grouped into eight clusters. Of the eight clusters formed, cluster VI has minimum intra cluster Euclidean^2 distance value of 94.60 followed by cluster VIII (119.77), cluster V (126.27), cluster IV (133.85), cluster III (134.22), cluster VII (136.75), cluster I (142.38) and cluster II (352.39).The inter cluster Euclidean^2 distances varied from 200.61 (between cluster III and cluster IV) to 4495.79 (cluster II and VIII).

Cluster I was closest to cluster IV (302.03) followed by cluster III (398.20) and farthest from cluster VIII (2644.82) followed by cluster VII (1996.65).

Cluster II was nearest to cluster I (460.10) followed by cluster IV (938.07) and farthest from cluster VIII (4495.79) followed by cluster VII (3497.55).

Cluster III was closest to cluster IV (200.61) followed by cluster V (291.97) and farthest from cluster VIII (1314.79) followed by cluster VII (895.84).

Cluster IV was nearest to cluster III (200.61) followed by cluster I (302.03) and farthest from cluster VIII (1632.31) followed by cluster VII (1062.35).

Cluster V was closest to cluster VI (245.11) followed by cluster III (291.97) and farthest from cluster II (2014.18) followed by cluster I (920.27).

Cluster VI was nearest to cluster VII (204.84) followed by cluster V (245.11) and farthest from cluster II (3027.35) followed by cluster I (1577.77).

Table 4.14.Clustering pattern of 60 finger millet genotypes by Ward's minimum variance method.

Cluster No	No. of genotypes	Name of genotypes
I	10	GE-361,INDAF-5,GE-636,GE-4764,GE-2078,GE-2723,GE 2672,GE-2737,GE-145,GE-844
II	3	GE-258,GE-2127,GE-666
III	6	GE-5257,MR-6,GE-4999,GE-4842,GE-492,GE-3225
IV	10	GE-1074,GE-3775,GE-2931,HR-911,GE-3140,GE-3521,GPU-45,GE-1126,GE-5159,GE-995
V	15	GE-1680,GE-1274,GE-3689,GPU-26,GE-667,GE-3090,GE-4437,GE-1298,GE-4440,GPU-67, GE-225,GPU-66,L-5,GE-4976,GE-4707
VI	5	GE-3266,GPU-28,GE-4736,GE-3067,GE-1746
VII	7	GE-2811,GE-4777,GE-3986,GE-1673,GE-2073,GE-3099,GPU-48
VIII	4	GE-4798,GE-506,GE-2963,GE-3453

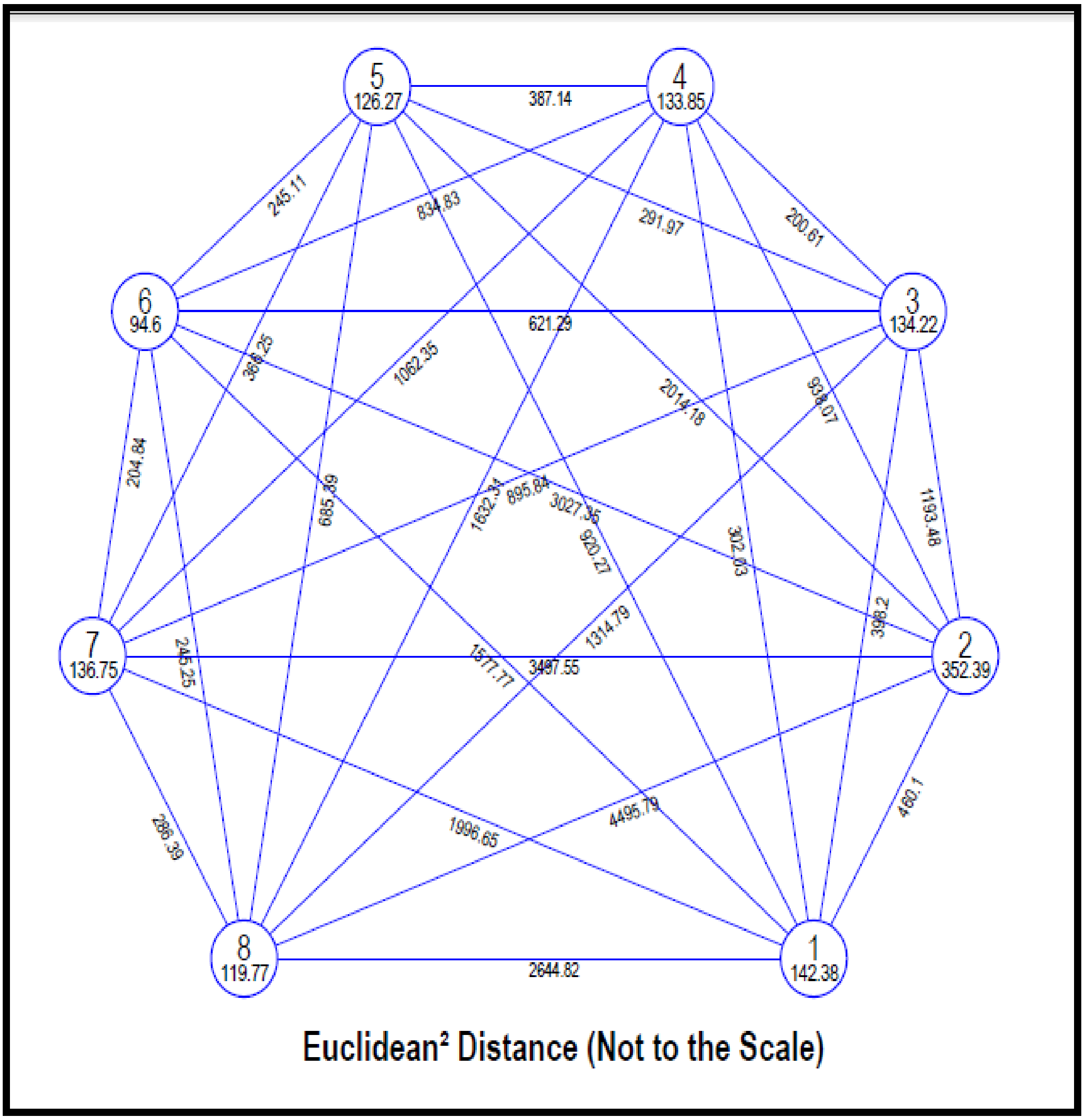

Fig 4.7. **Intra-and inter-cluster distance of 60 finger millet genotypes in eight clusters based on Euclidean^2 values.**

Table 4.15. Average intra (diagonal) and inter-cluster Eucledian^2 values among eight clusters in 60 finger millet genotypes.

Cluster number	I	II	III	IV	V	VI	VII	VIII
I	142.384	460.096	398.203	302.03	920.269	1577.771	1996.649	2644.823
II		352.393	1193.481	938.068	2014.179	3027.347	3497.545	4495.791
III			134.224	200.607	291.97	621.285	895.844	1314.789
IV				133.845	387.135	834.828	1062.354	1632.306
V					126.268	245.114	366.246	685.386
VI						94.602	204.844	245.252
VII							136.747	286.393
VIII								119.774

Cluster VII was closest to cluster VI (204.84) followed by cluster VIII (286.39) and farthest from cluster II (3497.55) followed by cluster I (1996.65).

Cluster VIII was closest to cluster VI (245.25) followed by cluster VII (286.39) and farthest from cluster II (4495.79) followed by cluster I (2644.82).

Results of cluster analysis based on PCA scores were compared with the results of the principal component analysis on a visual aid in desecrating clusters in the 2D and 3D scattered diagrams. The genotypes falling in same cluster were present closer to each other in scattered diagram.

Hari Krishna *et al.* (2005) and Jaya Lakshmi (2007) studied the utilization of principal component analysis combined with clustering of Ward's method in genetic divergence studies in finger millet.

4.4.3.3 Cluster means

Cluster means were computed for the 10 characters studied on pooled basis and are presented in Table 4.16.

Cluster I registered second high mean value for grain yield plant^{-1} (23.34).

Cluster II recorded high mean value for finger length (9.907). While low mean was recorded for days to 50% flowering (55.33), number of fingers ear^{-1} (5.30), number of grains panicle^{-1} (2036.76), seed protein % (6.41) and grain yield plant^{-1} (19.25).

Cluster III recorded high mean value for days to maturity (120.17). While low mean was recorded for test weight (2.64).

Cluster IV recorded low mean values for days to maturity (95.30) and finger length (8.36).

Cluster V registered low mean value for plant height (100.79) and number of productive tillers (4.92).

Cluster VI recorded highest mean value for number of grains panicle^{-1} (2505.48), test weight (3.31) and grain yield plant^{-1} (24.88).

Cluster VII recorded high mean values for number of productive tillers days to 50% (5.36) and number of fingers ear^{-1} (7.12).

Cluster VIII recorded high mean values for days to 50% flowering (74.75), plant height (115.87) and seed protein % (10.65).

Thus, cluster VI and VIII showed high mean values for most of the yield contributing traits like number of grains panicle^{-1} (2505.48), test weight (3.31), grain yield plant^{-1} (24.88), days to 50% flowering (74.75), plant height (115.87) and seed protein % (10.65). So the genotypes from cluster VI (GE-3266, GPU-28, GE-4736, GE-3067 and GE-1746) and cluster VIII (GE-4798, GE-506, GE-2963 and GE-3453) can be used for finger millet yield improvement programme.

Table 4.16. Mean values of eight clusters estimated by Ward's minimum variance method from 60 finger millet genotypes

Cluster Number	Days to 50% Flowering	Days to Maturity	Plant Height	Number of Productive Tillers	No. of Fingers ear^{-1}	Finger Length	Number of Grains panicle^{-1}	Test Weight	Seed Protein %	Grain Yield plant^{-1}
I	65.167	109.967	103.402	5.033	6.320	8.819	2362.791	2.933	7.327	23.335
II	**55.333**	101.111	109.131	5.144	**5.300**	**9.907**	**2036.755**	2.857	**6.406**	**19.250**
III	64.167	**120.167**	107.619	5.206	7.161	9.280	2236.521	**2.640**	8.428	21.526
IV	61.800	**95.300**	103.333	5.117	6.230	**8.362**	2328.454	2.937	8.174	22.624
V	60.956	108.289	**100.793**	**4.924**	6.769	8.938	2213.073	3.182	9.220	21.786
VI	67.667	118.667	114.005	5.167	6.400	8.898	**2505.480**	**3.309**	9.885	**24.878**
VII	60.952	95.952	107.151	**5.362**	**7.124**	9.655	2196.671	2.844	10.260	21.701
VIII	**74.750**	119.917	**115.873**	5.308	7.117	9.352	2436.975	3.301	**10.653**	23.302

Note: Bold figures indicate minimum and maximum values

4.4.4 Comparative study of both D^2 analysis, principal component analysis and cluster analysis

The grouping or clustering pattern using the D^2 analysis, principal component analysis and cluster analysis were compared and the implications are discussed here.

All the three methods of grouping revealed a single concept of non-correspondence of genetic divergence and geographic diversity. In D^2 analysis, the intra-and inter-cluster distances are low while in the cluster analysis the distances are high. This is same with the utilization of correlation matrix in principal component analysis derived from covariance matrix. This standardization made the principal component analysis to support the cluster analysis.

Mahalanobis' D^2 statistic and Jackson's principal component analysis are tools for analysing multivariate data. PCA confirms the group constellations obtained by D^2 analysis. It determines the effective number of axis of differentiation primary and secondary or so based on number of canonical vectors. The advantage of PCA over D^2 analysis is that it reduces the dimensionality of the data set by creating significant principal components which contributed towards maximum variability of the genotypes. The largest element (absolute value) in each vector constitutes the greatest contributor for divergence. In PCA, standardization of data makes attributes to contribute equally towards the divergence studies irrespective of the units taken.

The principal component analysis sorted only significant principal components out of the total 10 attributes. The contribution of the main characters for variance easily identified by the characters loaded on the PC_1 with high loading values.

D^2 analysis grouped the 60 finger millet genotypes into eight clusters, whereas Ward's method also grouped them into eight clusters. In D^2 analysis, cluster I is the largest with 24 genotypes followed by cluster II (24 genotypes), cluster III (seven genotypes) and cluster IV,V,VI,VII and VIII (one genotype each), Whereas in Ward's method, the cluster V is the largest comprising of 15 genotypes followed by cluster I and IV (ten genotypes each), cluster VII (seven genotypes), cluster III (six genotypes), cluster VI (five genotypes), cluster VIII (four genotypes) and cluster II (three genotypes).

The pattern of distribution of genotypes into different clusters was at random. Furthermore, the two clustering methods grouped differently and clustering pattern for genotypes are not same. There was no solitary cluster formed in Ward's minimum variance method, where as in D^2 analysis cluster IV, V, VI, VII, VIII represent solitary clusters due to absence of intra cluster distance indicating that genetic diversity was the outcome of several factors along with geographic diversity. Hence, the selection for hybridization should be more based on genetic diversity rather than geographic diversity.

Ward's minimum variance dendrogram (cluster analysis) created sub-group within a cluster, so relative position of the genotypes within the clusters can be determined by seeing the dendrogram distance. In case of D^2 analysis, only the intra-cluster distance can be known but not the genotypes relative position in the respective cluster.

Chapter V

SUMMARY AND CONCLUSIONS

The present investigation was carried out during *kharif* 2012 at Agricultural College Farm, Bapatla, with 60 genotypes of finger millet (*Eleusine coracana* (L.) Gaertn).

The mean, genetic variability, heritability, genetic advance as per cent of mean, genetic divergence, character association and the magnitude of direct and indirect effects of yield component traits on finger millet grain yield were studied for 10 characters *viz.,* days to 50% flowering, days to maturity, plant height (cm), number of productive tillers, number of fingers ear $^{-1}$, finger length (cm), number of grains panicle^{-1}, test weight, seed protein% and grain yield plant^{-1}.

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating the presence of variability in the material studied.

Narrow difference between the phenotypic and genotypic coefficients of variation indicates least role played by environment on these characters. Moderate to high variability and high heritability coupled with high genetic advance as per cent of mean was observed for days to 50% flowering, days to maturity, plant height, number of fingers ear^{-1}, finger length, number of grains panicle^{-1}, test weight, seed protein % and grain yield plant^{-1} indicating the predominance of additive gene action and hence direct phenotypic selection is useful with respect to these traits.

High heritability coupled with moderate genetic advance was observed in case of number of productive tillers plant^{-1} indicating the role of additive and non-additive gene action. This trait might be exploited through heterosis breeding, cyclic hybridization, biparental mating and diallel selective mating systems.

Correlation studies indicated that the traits viz., days to 50% flowering, days to maturity, number of grains panicle^{-1} and test weight had positive significant association with grain yield plant^{-1} and the trait number of productive tillers had negative significant association with grain yield plant^{-1}.

The path analysis indicated that number of fingers ear^{-1}, number of grains panicle^{-1}, test weight and seed protein % had positive direct effect on grain yield plant^{-1}. The correlation and path analysis clearly represent that direct selection based on these attributes may be helpful in evolving high yielding varieties of finger millet.

The results of multivariate analysis indicated the presence of considerable genetic divergence among the 60 genotypes studied. The 60 genotypes were grouped into eight clusters in case of D^2 analysis and also eight clusters through Ward’s minimum variance method and clearly indicated that the genetic diversity and geographical diversity were not related.

By Mahalanobis’ D^2 statistic, it could be inferred that days to 50% flowering, days to maturity, number of fingers ear^{-1}, test weight and seed protein % contributed maximum towards genetic divergence. Based on intra-and inter-cluster distance, it is suggested to make crosses between the genotypes of clusters III (GE-4798, GE-506, GE-2963, GE-1746, GPU-48, GE-3099, GE -3453) and VII (GE-2127) or III (GE-4798, GE-506, GE-2963, GE-1746, GPU-48, GE-3099, GE -3453) and VIII (GE-666) or III (GE-4798, GE-506, GE-2963, GE-1746, GPU-48, GE-3099, GE -3453) and VI (GE-258) for evolving transgressive segregants for yield and yield components.

Principal component analysis identified four principal components (PCs), which contributed 74.71 per cent of cumulative variance. The significant factors loaded in PC_1 towards maximum genetic divergence were grain yield plant^{-1}, number of grains panicle^{-1}, days to 50% flowering, plant height, days to maturity and number of productive tillers. 2D and 3D graphs showed wide divergence between GE-666, GE-4842, GE-2723, GE-361 and GE-3521 signifying their usefulness in finger millet breeding to develop high heterotic hybrids.

Agglomerative cluster analysis revealed that wide genetic distance between the genotypes of clusters II (GE-258, GE-2127, GE-666) and VIII (GE-4798, GE-506, GE-2963, GE-3453) indicating their usefulness in the breeding programmes for finger millet yield improvement.

The genotypes GE-2127, GE-666, GPU-48, GE-4798, GE-506, GE-2963 and GE-3453 showed maximum inter-cluster distance in Mahalanobis’ D^2 analysis, principal component analysis and cluster analysis. So they can be exploited for the development of heterotic hybrids in future breeding programmes.

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* Original not seen

Note: The pattern of literature cited above is in accordance with the guidelines for thesis presentation Acharya N.G. Ranga Agricultural University, Rajendranagar, Hyderabad-30.

Appendix A. Weekly meterological data recorded at Agricultural College, Bapatla during the cropping period (11-07-2011 to 08-12-2011)-*kharif*, 2012.

Standard week	Date and month weekly	Mean Temperature (^{0}C)		Mean Relative Humidity (%)		Rainfall (mm)	Number of rainy days
		Max	Min	A.M	P.M		
33	06 Aug - 12 Aug, 2012	34.8	25.2	77.0	65.1	1.4	4
34	13 Aug - 19 Aug, 2012	35.8	25.4	78.3	56.6	2.4	3
35	20 Aug – 26 Aug, 2012	34.9	25.6	82.3	71.3	1.9	3
36	27 Aug – 02 Sep, 2012	34.9	26.0	75.0	72.0	0.1	2
37	03 Sep – 09 Sep, 2012	34.2	26.8	79.4	71.4	11.3	4
38	10 Sep – 16 Sep, 2012	35.0	26.6	75.3	55.7	0.01	1
39	17 Sep – 23 Sep, 2012	34.1	25.0	82.1	79.7	16.9	4
40	24 Sep – 30 Sep, 2012	34.0	24.5	86.7	82.9	2.1	3
41	01 Oct – 07 Oct, 2012	31.4	24.5	87.6	71.3	12.9	5
42	08 Oct – 14 Oct, 2012	34.3	23.8	78.7	64.3	0	0
43	15 Oct – 21 Oct, 2012	32.2	23.2	86.9	74.3	0.7	1
44	22 Oct – 28 Oct, 2012	32.0	23.1	88.0	72.9	9.5	4
45	29 Oct – 04 Nov, 2012	30.0	22.7	87.0	83.9	17.7	2
46	05 Nov – 11 Nov, 2012	31.1	23.1	88.9	70.1	20.0	2
47	12 Nov – 18 Nov, 2012	29.7	16.8	81.6	57.1	0	0
48	19 Nov – 25 Nov, 2012	31.2	22.3	86.3	77.6	0.3	1
49	26 Nov – 02 Dec, 2012	30.5	19.4	91.1	70.4	0	0
50	03 Dec – 09 Dec, 2012	30.6	20.7	89.0	74.3	0	0
TOTAL						**97.2**	**39**
MEAN						**5.40**	**2.2**