GENETICS OF YIELD AND YIELD COMPONENTS IN FINGER MILLET (*Eleusine coracana Gaertn*) FOLLOWING GENERATION MEAN ANALYSIS

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Dedicated to the
Memory of my beloved
grand father

DEPARTMENT OF AGRICULTURAL BOTANY
UNIVERSITY OF AGRICULTURAL SCIENCES
BANGALORE

C E R T I F I C A T E

This is to certify that the thesis entitled "GENETICS OF YIELD AND YIELD COMPONENTS IN FINGER MILLET (Eleusine coracana Gaertn.) FOLLOWING GENERATION MEAN ANALYSIS" submitted in partial fulfilment of the requirements for the degree of MASTER OF SCIENCE (AGRICULTURE) in AGRICULTURAL BOTANY (PLANT BREEDING AND GENETICS) to the University of Agricultural Sciences, Bangalore, is a record of research work carried out by Mr. T. D. SHANKAR, under my guidance and supervision and that no part of the thesis has been submitted for the award of any other degree, diploma, associate-ship, fellowship or other similar titles.

(K. N. MALLANNA)
Plant Scientist (Ragi) Retd.

September 29 , 1982

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September 29, 1982

(T. D. SHANKAR)

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INTRODUCTION

I INTRODUCTION

Ragi or Finger Millet (Eleusine coracana Gaertn.) is one of the most important staple food crops of Southern States of India specially Karnataka, Andhra Pradesh, Tamil-Nadu and Maharashtra. Its cultivation extends from Southern plains to the foot hills of Himalayas across a wide range of agroclimatic conditions covering fifteen States in India. In Africa, places surrounding Lake Victoria, Sri Lanka and Nepal are the other countries which grow finger millet.

Among the millets, ragi ranks fourth after Pearl-millet (Pennisetum), Foxtail millet (Setaria italica), and Proso millet (Panicum miliaceum), which accounts for 8 per cent of the area and 11 per cent of production in the world. In India ragi stands second only to Pearl-millet and is cultivated on an area of about 25 lakh hectares with an annual production of about 22 lakh tonnes. Karnataka is the major ragi growing State with an area of 10.73 lakh hectares producing 9 lakh tonnes (Anonymous, 1980). This crop plays an important role in the nutrition of the poor and hard working people, living in the dry regions because of its high sustaining nutritive value, which provides fair amounts of protein, carbohydrates, fat and minerals specially calcium with an average amount of 0.34 per cent on whole seed basis (Kurien et al., 1959).

It has been established that in any breeding programme the information on the genetic architecture of polygenic systems governing the economic characters like yield and yield contributing attributes, their nature and extent of association among them is of paramount importance. Such information in this crop specially by utilising the segregating generations is lacking because of the difficulty in effecting crosses, as its flowers are very small and over crowded besides the very narrow time gap between anthesis and fertilization.

To have a clear understanding of the inheritance of yield factors biometrical methods like factorial methods, diallel analysis (Jinks and Hayman, 1953; Hayman, 1954 and Jinks, 1954) and generation mean analysis (Jinks and Jones, 1958; Hayman, 1958 and Gamble, 1962) have been largely adopted.

The present study comprises of two finger millet crosses with the parents contrasting for many characters with established yield potential. These were drawn from the All India Co-ordinated Millets Improvement Project and the Ragi Research Section of the University of Agricultural Sciences, Bangalore. The F_1, F_2 and F_3 populations of these crosses, generated as a part of the breeding programme of Ragi Research Section of the University, have been utilised in this study. The parents PES 172,

HR 23A (pistil: parents) being green in colour and HR 344, MR 5-6 (pollen parents) being purple pigmented were used in the crossing. The crosses were made with the idea of combining earliness of PES 172 and MR 5-6 with the yield potential of HR 344 and HR 23A. Nine characters viz., plant height, days to flowering, days to maturity, number of productive tillers per plant, number of fingers per ear, finger length, ear weight per plant, straw weight per plant and grain yield per plant, which have bearing on the yield were considered in the present study with the following objectives:

1. Estimation of the heritability, genetic advance, and
2. To determine type of gene action for yield and yield contributing characters, which would throw light on the effectiveness of selection procedures that may be followed in this crop.

REVIEW OF LITERATURE

II REVIEW OF LITERATURE

Eleusine coracana Gaertn. is a tetraploid species with a basic chromosome number 'nine' and known to have been originated from Eleusine indica (Mehra, 1962). It belongs to the tribe Paniceae, group chlorideae and family Poaceae.

Africa and India are considered as two independent centres of origin (Vavilov, 1951 and Krishnaswami, 1951), while Byrne (1957) and Mehra (1963 a&b) supported African origin of this crop. However, Hilu et al., (1979) threw more light on African origin quoting archaeological evidence which was lacking so far.

The information on the genetic variability, heritability and inheritance is an important pre-requisite for planning of any breeding programme. Such information in this crop is restricted only to studies on the genetic variability utilizing limited number of genotypes, while information on the extent of genetic variability is that could be exploited utilizing the segregating generations is very scanty owing to the difficulty in effecting crosses due to very minute flowers which are not easily amenable for emasculation. A limited information is available on the extent of variability, nature of inheritance and heritability of different yield attributes involving the segregating populations.

The present review is on the referred genetic parameters on the finger millet and other millets. For nature of gene action reference has been cited on other crops, with high degree of inbreeding (Wheat and Rice).

2.1.1 Genetic variability

The availability of right type of genetic variations for quantitative characters is a pre-requisite for promotion of breeding objectives.

RAGI (*Eleusine coracana* G.)

Mahadevappa and Ponnaiya (1965) highlighted the characters which have got direct bearing on yield through formulation of a discriminant function. They suggested number of ear bearing tillers, number of fingers and weight of straw per plant contribute to the yield and they could be considered for selection programme.

Kempanna and Thirumalachar (1968) reported significant variation for number of tillers, grain bearing area, and yield of which variation for number of tillers being the most influenced by environment based on the study of eighteen cultivars selected from divergent geographical regions.

Narasimha Rao and Pardasarathi (1968a) reported high genotypic co-efficient of variation for grain yield, plant height, peduncle length and panicle weight, least for stalk diameter. They also found greater phenotypic variance for the characters plant height, leaf number, tiller number and grain yield which indicated the effect of environment on these characters.

Patnaik (1968) reported high phenotypic co-efficient of variation for grain yield and plant height through his study involving fifty six early maturing genotypes on ten yield contributing characters. Among the characters, number of tillers and grain density showed greater phenotypic co-efficient of variation than heading date, plant height and finger number.

Chaudhari and Acharya (1969) in their study on genetic variability and path co-efficient analysis involving forty seven varieties reported high genotypic and phenotypic co-efficient of variability for the characters, namely productive tillers, grain weight of main ear, length of main ear, seed and straw yield.

Ahlu-Walia et al.(1970) reported that number of tillers per plant and number of ears had higher co-efficient of variation in their study on a collection of 3500 genetic stocks and reported that weight of main ear and of the grain in main ear were the most important ones.

Dhagat et al. (1972) studied correlation and genetic variability in twenty varieties selected from different parts of the country and observed high genotypic co-efficient of variation for grain weight, length of main ear, tiller number and low for yield.

Mahudeswaran and Murugesan (1973) in a study on twenty varieties observed high genotypic co-efficient of variation for grain yield, straw yield and number of productive tillers.

Patnaik and Jain (1973) reported higher genotypic co-efficient of variation for the number of days to maturity and grain yield in their study on eighteen early varieties for seven characters.

Goud and Lakshmi (1977) found wide phenotypic and genotypic variation for number of tillers, ear weight and grain yield per plant amongst the five characters studied on thirtythree varieties.

Mallanna et al. (1978) in a diversity assessment and pattern of variation in the world collection finger-millet comprising 1064 accessions collected from diverse geographic regions, reported considerable genetic variability for yield contributing characters such as plant height, days to 50 per cent flowering, grain bearing area, number of fingers, number of tillers, plant yield, ear weight and blast resistance.

Swamynath (1978) reported wide variation for the fifteen characters namely grain yield, number of productive tillers, plant height, last internode length, finger length, finger number, number of florets, finger width, number of spikelets, number of grains, ear weight, fodder weight, 1000 grain weight, days to 50 per cent flowering and days to maturity studied in 175 African collections.

Genetic variability in segregating populations:

Shanthappa (1979) in an "Inheritance studies in Eleusine coracana G. crosses" reported high variability for plant height, productive tillers per plant, ear weight and harvest index and also found that there is a significant association between these characters for the yield. This happens to be the first effort made in knowing inheritance involving crosses.

FOXTAIL MILLET (Setaria italica Beauv.)

Gian Singh (1966) observed wide range of variation for the different characters. The GCV and PCV were high for yield per plant and low for ear girth and days taken to ear.

Sandhu et al. (1974) reported high genetic co-efficient of variation for grain yield and secondary tillers per plant, medium for primary tillers per plant,

plant height, ear length and low for days to flowering, days to maturity and 1000 grain weight.

Chinnaswamaiah (1975) reported considerable genetic variability for different characters like yield, tiller number, etc.

Gill and Randhawa (1975) found substantial variability for the characters namely days to heading, maturity, grain weight, plant height and tiller number.

Vishwanath (1977) observed wide variation for the characters namely, grain yield, number of productive tillers, plant height, early vigour, days to 50 per cent flowering, days to maturity, panicle length, panicle breadth, density of seeds, panicle weight, 1000 grain weight, straw yield and harvest index. High GCV was reported for number of productive tillers followed by straw and grain yield.

LITTLE MILLET (*Panicum miliare*)

Abhinash Yadav and Srivastava (1976) reported the highest genetic co-efficient of variation for straw yield, grain yield and number of panicles per plant.

2.1.2 Heritability and genetic advance

The knowledge of heritability to a Plant Breeder is an important tool as it indicates the extent to which the improvement is possible through selection (Liang and Walter, 1968). The heritability is used to know the relative degree to which a character is transmitted from parent to offspring. The broad sense heritability refers to the functioning of the whole genotype as a unit and is used in contrast with environmental effects. The narrow sense heritability largely includes only the average effects of genes transmitted additively from parent to progeny (Weber and Murthy, 1952).

Lush (1940) classified heritability into two types viz. (i) Broad sense heritability concerning the proportion of genotypic variance which would include additive, dominance and epistatic effect of all the genes and (ii) Narrow sense heritability is the fixable proportion caused only by additive gene action in relation to total variance.

Comstock and Robinson (1952) highlighted importance of broad sense heritability indicating that it is not only additive gene action which is responsible for the phenotypic expression but also epistatic gene action which is influenced by environment.

RAGI (Eleusine coracana G.)

Kempanna and Thirumalachar (1968) reported high heritability coupled with high genetic advance for grain yield per plant.

Narasimha Rao and Pardasarathi (1968a) reported high heritability for plant height, peduncle weight, panicle length, finger number per ear, low for grain yield, stalk diameter, tiller number and panicle length. The plant height and panicle length showed high genetic gain indicating that in plant breeding a character having high heritability coupled with high genetic gain is very helpful for selection.

Patnaik (1968) reported high heritability values for seed size, heading date, plant height; moderate values for finger length and yield; low for number of tillers, number of fingers and density of grain.

Chaudhari and Acharya (1969) found higher heritability values for straw yield, plant height, number of fingers per ear, seed yield and length of main ear and high genetic advance for straw yield.

Dhagat et al. (1972) found high heritability for days to 50 per cent flowering, length of main ear, number of tillers and plant height, medium values for grain weight and number of fingers, low for grain yield per plant and 1000 grain weight. Genetic advance was high for days to 50 per cent maturity and plant height.

Mahudeswaran and Murugesan (1973) observed high heritability values for plant height, straw yield and 1000 grain weight coupled with high genetic gain.

Patnaik and Jain (1973) reported that the days to maturity had high heritability coupled with high genetic advance. They suggested that this character could be improved through selection.

Setty et al. (1974) reported high estimates of heritability accompanied by high estimate of genetic advance as a percentage of mean for grain yield. Other yield components, namely days to heading, plant height, tiller number, number of leaves, number of fingers, finger length, number of spikelets and peduncle length had only moderate heritability. However, the predicted gain was high with regard to grain yield only, suggesting the additive gene action and hence genetic improvement in grain yield could be effected through selection.

Goud and Lakshmi (1977) reported high heritability for the characters plant height and number of fingers whereas the tiller number though had moderate heritability was associated with higher genetic grain.

Swamynath (1978) reported moderate heritability values for yield and yield characters. However, grain yield and number of tillers had moderate heritability with high genetic advance indicating the possibility of improvement through selection.

Heritability and genetic advance in segregating population:

Shanthappa (1979) reported through his studies involving two finger millet crosses, high heritability and genetic advance for plant height, straw weight and grain weight, medium for ear weight, and number of tillers and low for other characters.

FOXTAIL MILLET (**Setaria italica** Beauv)

Gian Singh (1966) reported high heritability values for number of days to flowering, plant height and ear length while ear girth per plant showed relatively low heritability. Estimates of genetic gain was fairly high for grain yield.

Sandhu et al.(1974) reported high heritability estimates for grain yield, secondary tillers per plant and medium for tillers per plant, ear length, days to maturity and 1000 grain weight. Expected genetic advance for grain yield was high.

Chinnaswamaiah (1975) reported considerable genetic variability for different characters. Moderate heritability was reported for grain yield, tiller number and plant height.

Gill and Randhawa (1975) observed high heritability for days to heading, days to maturity, grain weight, plant height, and tiller number, low for ear girth and grain yield. Genetic gain was high for tiller number, grain yield, 1000 grain weight, days to heading and plant height.

Vishwanath (1977) observed high heritability for days to 50 per cent flowering and days to maturity. Moderate to low heritability coupled with high genetic advance was observed for number of productive tillers, density of seeds, panicle length which indicated the effectiveness of improvement through selection.

Nagarajan and Prasad (1980) found high heritability coupled with high genetic advance expressed as per cent of mean for straw yield, grains per branch, productive tillers and number of branches.

LITTLE MILLET (*Panicum miliare*)

Abhinash Yadav and Srivastava (1976) reported high heritability estimates for straw yield, grain yield

and number of panicles per plant coupled with high genetic gain which indicate that these characters could be improved by selection.

2.1.3 Nature of Gene Action

Several methods are available to estimate the genetic components of variation in the segregating generations. In the present study, the parents and three generations viz., P_1, P_2, F_1, F_2 and F_3 of two crosses have been utilized to estimate gene effects by following the model suggested by Hayman (1958).

The studies on genetical aspects especially concerning biometrics of quantitative characters are very sparse in this crop. Therefore, the review has been done on other related highly self-pollinated crops (wheat and rice) having similar breeding behaviour.

WHEAT (*Triticum aestivum*)

Baier (1973) reported additive gene action for plant height in a study while Singh *et al.* (1973) additive gene action for the characters plant height, days to flowering, number of tillers.

Balakrishna Rao et al. (1973) opined that only additive gene action controls the character, number of tillers per plant.

Gill et al. (1974) and Paroda (1974) reported that plant height was controlled by additive gene action.

Nanda et al. (1974) in a diallel analysis study observed that additive gene action controlled the plant height, days to flowering and number of tillers.

Edwards et al. (1976) reported that additive gene action controlled number of fingers and plant height and also suggested that they could be improved through selection in early generation whereas heading date reported to be controlled by additive and dominance gene effects which could be improved if delayed untill the later generations.

Padilla et al. (1972) reported tiller number was controlled by additive gene action.

Bhuller et al. (1977) in their study on diallel analysis of P_1, P_2, F_1 to F_5 generations in wheat crosses reported days to maturity was under the influence of additive gene action, indicating that conventional methods of breeding would improve that character.

RICE (*Oryzae sativa*)

Ceccarelli *et al.* (1973) in their study reported additive gene action was found to control plant height and heading time.

Sivasubramanian and Madhava Menon (1973a and b) in a diallel analysis of rice found that the character plant height was controlled by the action of partially dominant gene while additive gene action controls the tiller number.

Tripati *et al.* (1973) indicated additive, dominance as well as epistatic gene action for the character number of tiller number.

Satyanarayanaiah and Reddi (1973) in their study with F_1 and F_2 generations reported dominant gene action for days to flowering, plant height and similar results were reported for plant height by Dzyuba (1976).

Kaleque and Eunus (1975) in a diallel study reported over dominance for plant height and days to flowering.

Li (1975) observed both dominance and additive gene action for plant height and finger length with only dominance for the number of fingers.

Singh and Nanda (1976) in their study found that the number of panicles was controlled by partial dominance while in a parallel study they also reported additive and dominance gene action for panicle number. The panicle length was found to be controlled mostly by dominant gene action.

Shailaja (1980) in the study "Inheritance of quantitative traits and exploitation of male sterility" reported additive gene action and complementary epistasis for plant height, length of panicle, days to flowering and days to maturity.

MATERIAL AND METHODS

III MATERIAL AND METHODS

3.1.1 MATERIAL

The experimental material consisted of two parents designated as P_1 and P_2 and three generations viz., F_1, F_2 and F_3 of the two finger millet crosses namely, PES 172 x HR 344 and HR 23A x MR 5-6, generated as a result of breeding work at the Ragi Research Section of the University. The salient features of the parents used for the crossing programme are:

i) PES 172

A pure line selection made in Pantnagar, tested in the All India Co-ordinated trial and released for cultivation. It is high tillering, synchronous, dwarf, early maturing, [illegible]. green type with short semi-compact ears and possesses high stability for yield.

ii) HR 344

It is a stabilized line developed in the Ragi Research Section through hybridization between PR 202 and IE 927 (African). It is medium tall, moderately tillering, synchronous, purple pigmented, medium late in maturity with medium to long semi-compact tip incurved ears.

iii) HR 23A

It is a line developed in the Ragi Research Section from the cross between TAH 60-6 and Indaf-1. It is tall, medium tillering, green, late maturing with long tip incurved ears.

iv) MR 5-6

It is a selection from the local genotype, "Gangur-2". It is an early maturing, purple, shy-tillering, medium tall with medium long open ears.

3.1.2 METHODS

The seeds of parents, their F_1, F_2 and F_3 were sown in raised nursery beds and 24 days old seedlings were transplanted in the field at the Main Research Station of the University of Agricultural Sciences, Hebbal, Bangalore, during summer 1980, by following the Randomized Complete Block Design with three replications. The crop was grown under irrigated conditions and recommended agronomic practices were followed during the crop growth period.

The different generations were designated as suggested by Mather (1949) as follows and formed genetic group-1.

PES 172 (O+)	..	P_1
HR 344 (O♂)	..	P_2
PES 172 x HR 344	..	F_1
F_1 selfed	..	F_2
F_2 selfed	..	F_3

The same pattern of symbolization has been used for the other cross as well.

3.1.3 LAYOUT

Each replication consisted of five rows of each of the parent, one row of F_1s, five rows of F_2s and three rows each of twenty F_3 families planted with a spacing of 22.5 cm between rows and within the line spaced 9 cm apart. Ten plants in each of the parent, ten plants in each of F_1s, fifty plants in each of two F_2s and eighty plants in each of F_3 (four plants per F_3 progeny) populations were tagged. Observations on the nine characters taken for study were recorded on these plants and were used for analysis. The same procedure was adopted to the Genetic Group-2.

3.1.4 METHOD OF RECORDING OBSERVATIONS

The procedure of recording observations is given below:

1. **Plant height**

   The plant height was measured from the base of the plant/ ground level to tip of earhead and expressed in centimetre.

2. **Days to 50% flowering**

   The number of days taken from the date of sowing to 50% anthesis in the primary earhead.

3. **Days to maturity**

   The number of days taken from sowing to harvesting based on seed development and hardness with simultaneous turning of stem to straw colour.

4. **Number of productive tillers**

   The number of basal (primary) tillers bearing earheads counted at maturity.

5. **Number of fingers**

   The number of fingers on main earhead were counted at maturity.

6. **Finger length**

The length of the finger measured from the base of the finger excluding the thumb at maturity, expressed in centimetre.

7. **Ear weight**

The earheads in each plant were harvested at the base and the total weight was recorded in gms. after drying.

8. **Straw weight**

The total weight of the straw per plant was determined after complete sundrying. As ragi is grown for dual purpose, straw is having immense value for cattle feed in drier parts fetching very remunerative price.

9. **Grain yield**

The dried earheads per plant were threshed separately and the total weight was recorded in gms.

3.2.0 STATISTICAL ANALYSIS

The parameters viz., standard error, heritability (broad sense), genetic advance, genetic advance (per cent over mean), co-efficient of variation (PCV and GCV), scaling test and gene effects were estimated for nine characters studied in two finger millet crosses, as given below:

3.2.1 Standard Error

The generation-wise population means and variances were calculated from the observations of individual plants according to Hayman (1958). The standard error of the population mean was calculated as

$$S.E. = \sqrt{\frac{\text{Variance of population}}{\text{Total number of plants}}}$$

3.2.2 Heritability

Heritability is the ratio of genotypic variance to the phenotypic variance and it was estimated by following the procedure suggested by Weber and Murthy (1952).

$$\text{Heritability of character} = H = \frac{V_{F_2} - V_E}{V_{F_2}} \times 100$$

where, V_{F_2} = Total F_2 variance observed for the character

V_E = Environmental variance

$$= \frac{(V_{P_1} + V_{P_2} + V_{F_1})}{3}$$

= Average variance of non-segregating generations.

It is presumed in this method that the environmental variance based on non-segregating generations is equivalent to environmental variance in the segregating populations.

3.2.3 Genetic Advance

Genetic advance was calculated as per the method suggested by Johnson, et al.(1955).

$$GA = H \times K \times P$$

where, H = Heritability co-efficient,

K = selection differential (2.06 at 5 per cent level) as predicted by Lush (1948).

P = Phenotypic standard deviation of the character.

3.2.4 Genetic Advance (Per cent over mean)

$$GA \text{ (Per cent over mean)} = \frac{GA}{\bar{X}} \times 100$$

where, $\bar{X}$ = F_2 mean for the character.

3.2.5 Co-efficiemt of variation

3.2.5.1 Phenotypic Co-efficient of variation

It indicates the total variation existing for a character in the segregating population and it was calculated by formula suggested by Burton (1952).

$$P.C.V. = \frac{\sqrt{\text{Phenotypic variance of } F_2}}{\bar{X}} \times 100$$

3.2.5.2 **Genotypic co-efficient of variation**

It indicates the genetic variation existing in a character and it was calculated by the formula suggested by Burton (1952).

$$G.C.V. = \frac{\sqrt{\text{Genotypic variance of } F_2}}{\bar{X}} \times 100$$

Here, $\bar{X} = \bar{F}_2$ mean for the character was considered for the calculation purpose.

3.2.6 **Scaling Test**

The 'D' Scaling test suggested by Mather (1949) and Hayman and Mather (1955) was employed to detect the presence of epistasis using the formula

$$D = 4\bar{F}_3 - 2\bar{F}_2 - \bar{P}_1 - \bar{P}_2$$

where, $\bar{P}_1$, $\bar{P}_2$, $\bar{F}_2$ and $\bar{F}_3$ are the mean values of respective generations. The variance in respect of scaling test employed was worked out as follows:

$$V_D = 16V(\bar{F}_3) + 4V(\bar{F}_2) + V(\bar{P}_1) + V(\bar{P}_2)$$

Now, the $SE_{(D)} = (V_D)^{\frac{1}{2}}$ and $t_{(D)} = \frac{D}{SE_{(D)}} = \frac{D}{(V_D)^{\frac{1}{2}}}$

The calculated values of 't' are compared with 1.96 and 2.57 which are the tabulated values of 't' at 5 per cent and 1 per cent level of significance.

3.2.7 Estimation of gene effects

The estimates of various gene effects and interactions were worked out as suggested by Hayman (1958). The notations for the various gene effects used in this study were as follows:

Gene effects	Notations of Hayman (1958)
Mean	$\hat{m}$
Additive	$\hat{d}$
Dominance	$\hat{h}$
Additive x additive	$\hat{i}$
Dominance x dominance	$\hat{l}$

The estimates of $\hat{m}$, $\hat{d}$, $\hat{h}$, $\hat{i}$ and $\hat{l}$ are worked out using the following equations:

$$\hat{m} = \bar{F}_2$$

$$\hat{d} = \frac{\bar{P}_1 - \bar{P}_2}{2}$$

$$\hat{h} = \frac{4\bar{F}_1 + 12\bar{F}_2 - 16\bar{F}_3}{6}$$

$$\hat{i} = \bar{P}_1 - \bar{F}_2 + (\tfrac{1}{2})(\bar{P}_1 - \bar{P}_2 + h) - 1/4\,l$$

$$\hat{l} = \frac{16F_3 - 24F_2 + 8F_1}{3}$$

The variances in respect of the different gene effects were calculated as follows:

$$V_m = V\bar{F}_2$$

$$V_d = 1/4\ (V\bar{P}_1 + V\bar{P}_2)$$

$$V_h = \frac{16V\bar{F}_1 + 144V\bar{F}_2 + 256V\bar{F}_3}{36}$$

$$V_i = V\bar{P}_1 + V\bar{F}_2 + 1/4(V\bar{P}_1 + V\bar{P}_2 + V_h) + \frac{1}{16}V_l$$

$$V_l = \frac{256\bar{F}_3 + 576V\bar{F}_2 + 64V\bar{F}_1}{9}$$

The standard error of different gene effects were computed as follows:

$$SE_m = (V_m)^{\frac{1}{2}}$$

$$SE_d = (V_d)^{\frac{1}{2}}$$

$$SE_h = (V_h)^{\frac{1}{2}}$$

$$SE_i = (V_i)^{\frac{1}{2}}$$

$$SE_l = (V_l)^{\frac{1}{2}}$$

The 't' test was employed to test the significance of these estimates both at 1 per cent and 5 per cent level of significance.

$$t_m = \frac{m}{SE_m}$$

$$t_d = \frac{d}{SE_d}$$

$$t_h = \frac{h}{SE_h}$$

$$t_i = \frac{i}{SE_i}$$

$$t_l = \frac{l}{SE_l}$$

The calculated 't' values are compared with 1.96 and 2.57 which are tabulated values at 5 and 1 per cent level of significance.

EXPERIMENTAL RESULTS

IV EXPERIMENTAL RESULTS

Phenotypic and genotypic co-efficient of variation and quantitative inheritance of nine characters namely, plant height, days to 50 per cent flowering, days to maturity, number of productive tillers per plant, number of fingers per ear, finger length, ear weight per plant, straw weight per plant and grain yield per plant were studied in finger millet by utilizing the parents and three generations viz., P_1, P_2, F_1, F_2 and F_3 as suggested by Hayman (1958), and phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) after Burton (1952).

The results are presented character-wise under following headings:

1. Population means and variance.
2. Genetic variability, heritability and genetic advance.
3. Scaling test.
4. Estimation of gene effects.

4.1 Population means and variances

Generation means, standard error and variance of parents and three generations (P_1, P_2, F_1, F_2 and F_3) of the two finger millet crosses namely PES 172 x HR 344, HR 23A x MR 5-6 in respect of nine characters studied are presented in Table 1.

Table 1 : Generation means with their standard errors and variances for different characters in two genetic groups.

Generations	1. Plant height		2. Days to 50% flowering		3. Days to maturity	
	Mean ± SE	Variance	Mean ± SE	Variance	Mean ± SE	Variance
	1. GENETIC GROUP-1 (PES 172 x HR 344)					
P_1	66.56 ± 0.42	5.62	76.37 ± 0.35	3.55	115.40 ± 0.20	1.25
P_2	77.66 ± 0.52	8.16	86.73 ± 0.42	5.44	120.76 ± 0.28	2.50
F_1	83.06 ± 0.57	10.06	84.86 ± 1.30	11.77	118.86 ± 0.43	5.60
F_2	70.78 ± 0.63	59.62	79.59 ± 0.58	50.89	111.48 ± 0.41	25.85
F_3	79.00 ± 0.43	45.60	82.88 ± 0.47	40.54	110.61 ± 0.26	17.63
	2. GENETIC GROUP-2 (HR 23A x MR 5-6)					
P_1	80.40 ± 0.43	5.70	87.06 ± 0.32	3.06	120.66 ± 0.28	2.42
P_2	80.46 ± 0.53	8.50	79.40 ± 0.49	7.30	115.00 ± 0.42	5.00
F_1	79.10 ± 0.72	15.64	81.56 ± 0.82	19.98	114.46 ± 0.59	10.51
F_2	71.07 ± 0.62	57.70	73.35 ± 0.53	42.66	109.32 ± 0.32	15.71
F_3	84.35 ± 0.53	47.76	82.59 ± 0.35	28.18	112.18 ± 0.23	12.83

Contd.

Table 1 (contd).

Generations	4. Number of productive tillers per plant		5. Number of fingers per ear		6. Finger length	
	Mean ± SE	Variance	Mean ± SE	Variance	Mean ± SE	Variance
	1. GENETIC GROUP-1 (PES 174 x HR 344)					
P_1	3.70 ± 0.14	0.72	6.13 ± 0.17	0.88	4.80 ± 0.11	0.37
P_2	3.50 ± 0.17	0.88	6.46 ± 0.18	0.95	5.90 ± 0.14	0.50
F_1	4.80 ± 0.20	1.20	6.97 ± 0.20	1.25	6.47 ± 0.17	0.81
F_2	3.50 ± 0.11	1.95	6.70 ± 0.36	19.22	5.77 ± 0.09	1.34
F_3	3.90 ± 0.08	1.65	6.73 ± 0.22	11.65	6.63 ± 0.07	1.22
	2. GENETIC GROUP-2 (HR 23A x MR 5-6)					
P_1	3.00 ± 0.16	0.82	6.86 ± 0.17	0.91	7.03 ± 0.15	0.68
P_2	2.73 ± 0.55	0.93	7.23 ± 0.19	1.08	6.85 ± 0.17	0.85
F_1	4.20 ± 0.20	1.29	4.20 ± 0.31	2.58	6.31 ± 0.20	1.25
F_2	3.50 ± 0.11	1.85	6.13 ± 0.28	11.56	6.25 ± 0.10	1.68
F_3	3.82 ± 0.08	1.43	6.80 ± 0.18	8.01	7.85 ± 0.70	1.29

Contd.

Table 1 (contd)

Generations	7. Ear weight per plant		8. Straw weight per plant		9. Grain yield per plant	
	Mean ± SE	Variance	Mean ± SE	Variance	Mean ± SE	Variance
	1. GENETIC GROUP-1 (PES 174 x HR 344)					
P_1	23.00 ± 0.66	13.43	27.53 ± 0.72	15.60	19.00 ± 0.46	6.45
P_2	28.00 ± 0.80	19.45	34.96 ± 0.91	25.08	23.00 ± 0.40	4.90
F_1	32.00 ± 1.00	30.50	42.00 ± 1.27	49.15	28.00 ± 0.64	12.48
F_2	25.87 ± 0.81	99.50	33.35 ± 0.87	116.31	20.86 ± 0.75	84.91
F_3	26.74 ± 0.55	75.62	38.54 ± 0.58	82.05	22.50 ± 0.54	72.54
	2. GENETIC GROUP-2 (HR 23A x MR 5-6)					
P_1	29.00 ± 0.70	15.00	32.90 ± 0.79	18.65	20.66 ± 0.38	4.29
P_2	21.25 ± 0.54	8.65	27.76 ± 0.59	10.54	16.93 ± 0.49	7.32
F_1	34.90 ± 0.97	28.50	41.86 ± 1.07	34.45	28.80 ± 0.82	20.56
F_2	20.03 ± 0.74	82.95	25.70 ± 0.85	109.31	20.35 ± 0.65	62.80
F_3	23.40 ± 0.54	70.05	35.00 ± 0.59	85.60	20.97 ± 0.49	54.68

4.1.1 Plant height

Genetic Group-1 (PES 172 x HR 344)

The parents differed for plant height and the mean height of F_1 was higher than either of the parents whereas the F_2 mean value was in between the parental values while the mean height of F_3 families was higher than F_2 but less than F_1. Minimum variance was in the parent No.1 (P_1) followed by parent No.2 (P_2) and F_1. The maximum variance was in F_2 with a decline in F_3.

Genetic Group-2 (HR 23A x MR 5-6)

The parents and F_1 did not differ much for plant height while F_2 had slightly lower mean than the parents and F_1 and F_3 showed slightly higher value.

Similar trend as in Genetic Group-1 was observed for P_1, P_2, F_1, F_2 and F_3 variances.

4.1.2 Days to 50 per cent flowering

Genetic group-1:

The parents differed much for days to flowering. The mean flowering date for F_1 was in between parents and more than either F_2 or F_3. However, the F_2 mean was less than late maturing parent (P_2) and that of F_3 was slightly more than F_2 mean.

Highest variance for flowering date was shown in F_2 progeny and with decline in the F_3. The variance in the P_1, P_2 and F_1 was minimum.

Genetic group-2:

In the cross HR 23A x MR 5-6, the male parent (MR 5-6) was earlier in flowering than P_1 (HR 23A) with a mean flowering date of 79.40 and 87.06 respectively. The flowering time for F_1 was between the parents and that of F_2 was less than either of the parents.

As in the genetic group-1 variance of flowering date was high for F_2 followed by F_3, F_1 and parents.

4.1.3 Days to maturity

Genetic group-1:

The mean days to maturity in F_1 was between the parents and that of F_2 was less than the parents as well in F_3 but less than F_2.

F_2 progeny showed the highest variance next in order being F_3 and minimum in F_1, P_2 and P_1.

Genetic group-2:

The mean values for days to maturity were similar to flowering date except for F_3 which was higher than F_2. in contrast to genetic group-1.

Regarding variance the behaviour was very close to that of genetic group-1.

4.1.4 Number of productive tillers

Genetic group-1:

With respect to mean tiller number parents did not show much of a difference. The F_1 showed slightly higher mean tiller number than the parents while in case of F_2 and F_3 it was similar to the parents.

The variance of F_2 was highest and lowest in the parents. The variance of F_3 was less than F_2 and more than F_1.

Genetic group-2:

The mean tiller number showed difference between parents, highest mean value being recorded in F_1. The F_2 value was more than the more tillering parent (P_1), and mean tiller number of F_2 was similar to F_3.

As in the genetic group-1, the value for variances for parents and generations bore the same trend.

4.1.5 Number of fingers

Genetic group-1:

The parents for the character did not show much of a difference. The F_1 value was slightly more than P_2

with little more finger numbers. The mean finger for F_2 and F_3 was close to F_1.

Variance was similar to other characters i.e. F_2 showing the highest followed by F_3.

Genetic group-2:

The difference between parents for mean number of fingers was observed compared to genetic group-1. The F_1 mean was less than the parents while that of F_2 and F_3 were more close to that of parent (P_1).

The variance for F_2 was highest followed by F_3.

4.1.6 Finger length

Genetic group-1:

The mean length of finger in F_1 was higher than either of the parents though difference between the parents for the same character was not marked.

F_2 mean value was similar to P_2 (parent with longer finger length). The F_3 mean was in close proximity to F_1.

The variance for the above character was similar to that of other characters so far dealt with.

Genetic group-2:

The difference for finger length between the parents was appreciable; P_1 (HR 23A) being longer than P_2 (MR 5-6) while F_1 mean finger length was slightly less than (MR 5-6) whereas the F_2 mean for the same character was less than both the parents but very close to F_1. F_3 value was higher (7.85 cm) falling near the mean of P_1 (HR 23A).

The values of variance were similar to that of other characters.

4.1.7 Ear weight

Genetic group-1:

The parents differed considerably for the ear weight per plant. The mean weight of F_1 was higher than the parents. The F_2 was in between the parents. There was an increase in the value of F_3 and F_2.

The variance for F_2 was very high for the character and F_3 value for the same was slightly less than F_2 but more than F_1 and parents.

Genetic group-2:

The difference between parents for ear weight was marked. The F_1 value for the same was very much higher

than the parents, F_2 mean was close to that of P_2 (MR 5-6). The value for the F_3 was more than F_2 but less than F_1.

The F_2 variance for the ear weight per plant was higher than F_3 showing high values whereas variance in P_1, P_2 and F_1 was minimum.

4.1.8 Straw weight

Genetic group-1:

The difference between parents for straw weight was clear and marked. P_2 parent (HR 344) recording higher mean than P_1 (PES 172) parent. The mean straw weight of F_1 was highest, the mean weight of F_2 was more than P_1 and different to the parent (P_2) was marginal. F_3 values for the character was more than F_2 but less than F_1 in both the crosses.

The variance for this character in F_2 was very high next in order were the values of F_3 which was considerably less than that of F_2.

Genetic group-2:

The values for F_1, F_2 and F_3 in relationship with the parents were similar to that of genetic group-1, whereas in this group the mean value of P_2 was less than P_1. The difference between parents was pronounced.

The variance for parents and F_1s was relatively high for this character in both the crosses.

4.1.9 Grain yield

Genetic group-1:

The difference between parents for the grain weight was appreciable. The F_1 value for the same character was much higher than the parents while the F_2 mean yield per plant was more than the lesser yielding plant (P_1) and less than the P_2, whereas there was an increase in per plant yield in F_3.

The values for the variance of this character were similar to that of other characters i.e. F_2 variance was higher than F_3 and next in order to that of F_1, P_1 and P_2.

Genetic group-2:

F_1 value for grain yield was very much higher than the mean yield of parents. F_2 and F_3 values for the same character were close to the P_1 parent (HR 23A) but more than P_2 (MR 5-6). The variance was similar in trend to other characters.

There was a marked difference between the parents for all the three characters namely, ear weight, straw weight, and grain yield. The trend of results were similar for all

Table 2. Genetic variability for the different characters in two crosses of finger millet.

Sl. No.	Parameters	Plant height	Days to 50% flowering	Days to maturity	No. of productive tillers per plant	No. of fingers per ear	Finger length	Ear weight per plant	Straw weight per plant	Grain yield per plant
				1. GENETIC GROUP-1 (PES 172 x HR 344)						
1	Phenotypic variance	59.62	50.89	25.85	1.95	19.22	1.34	99.50	116.31	84.91
2	Genotypic variance	51.67	43.97	22.73	1.02	18.20	0.78	78.38	86.37	76.97
3	Environmental variance	7.95	6.92	3.12	0.93	1.02	0.56	21.12	29.94	7.94
4	P.C.V.	10.90	8.96	4.56	38.89	65.43	20.06	38.55	32.33	44.17
5	G.C.V.	10.15	8.33	4.27	28.89	63.67	13.52	34.22	27.86	42.05
6	Heritability	86.66	86.40	87.93	60.66	94.69	58.20	78.77	74.25	90.94
7	Genetic Advance(GA)	13.67	12.63	9.11	1.60	8.48	1.37	20.66	16.44	17.08
8	GA (% over mean)	19.32	15.87	8.16	45.88	126.56	23.81	79.73	49.29	81.89
				2. GENETIC GROUP-2 (HR 23A x MR 5-6)						
1	Phenotypic variance	57.70	42.66	15.71	1.85	11.56	1.68	82.95	109.31	62.80
2	Genotypic variance	47.75	32.54	9.53	0.84	10.03	0.75	65.56	88.09	52.07
3	Environmental variance	9.94	10.12	5.97	1.01	1.52	0.92	17.38	21.21	10.72
4	P.C.V.	10.68	8.90	3.62	38.85	55.46	20.70	45.43	40.66	38.92
5	G.C.V.	9.72	7.77	2.82	26.18	51.66	13.85	40.42	36.52	35.46
6	Heritability	82.76	76.29	60.66	45.22	86.82	44.84	79.04	80.59	82.92
7	Genetic advance(GA)	12.83	3.76	4.98	1.26	6.02	1.17	14.82	17.23	13.38
8	GA (% over mean)	18.05	5.14	4.55	36.20	98.20	18.79	73.99	67.04	65.78

these characters and found to be related with each other. Mean value of F_1 was highest and next in order are F_3 and F_2. The P_1, P_2 and F_1 had lowest variances while the highest variance was in F_2 followed by F_3 generation.

4.2 Genetic variability, heritability and genetic advance

Genetic group-1:

The phenotypic and genotypic variances were high for the characters straw weight, ear weight and grain yield per plant and moderate for plant height, days to flowering, days to maturity and number of fingers per ear, low for number of productive tillers and finger length.

The environmental variance was high for straw weight, ear weight, grain yield and days to 50 per cent flowering and plant height. The finger length, number of productive tillers and number of fingers exhibited low environmental variance. The PCV was high for number of fingers per ear followed by grain yield, number of productive tillers, straw weight and it was medium for finger length, plant height and days to 50 per cent flowering and low for days to maturity. Similar trend was observed in case of GCV also except little lower GCV in case of productive tillers per plant.

High heritability was noticed for the character number of fingers per ear followed by grain yield per plant, moderate heritability estimates for days to maturity, days to 50 per cent flowering, ear weight, straw weight, number of tillers and finger length. The genetic gain was high for number of fingers per ear followed by grain yield and ear weight per plant, medium for straw weight, number of productive tillers per plant and low for remaining characters.

The number of fingers per ear had high heritability coupled with high genetic advance followed by grain yield and ear weight per plant. The genetic advance for days to maturity and other remaining characters was found to be low.(Table 2).

Genetic group-2:

In this group, for all the above referred parameters similar results were obtained except the straw weight per plant which had high heritability coupled with little high genetic gain in contrast to genetic group-1.

4.3 Scaling test

'D' scaling test was applied to all the characters as this estimate would throw some light on the presence or absence of non-allelic gene interactions and results of the test are presented in Table 3.

Table 3. Results of 'D' Scaling test for the nine characters in two genetic groups of finger millet crosses.

Sl. No.	Characters	PES 172 x HR 344	HR 23A x MR 5-6
		D ± SE	D ± SE
1	Plant height	30.29** ± 2.26	34.30** ± 2.28
2	Days to 50% flowering	9.27** ± 2.27	17.20** ± 1.86
3	Days to maturity	-16.68** ± 1.38	-11.58** ± 1.23
4	Number of productive tillers per plant	1.40** ± 0.44	1.35** ± 0.45
5	Number of fingers per plant	0.93 ± 1.14	0.85 ± 0.95
6	Finger length	4.28 ± 0.38	5.02** ± 0.42
7	Ear weight per plant	8.22** ± 2.59	7.29** ± 2.76
8	Straw weight per plant	24.97** ± 3.14	29.94** ± 3.09
9	Grain yield per plant	6.28** ± 2.72	6.79** ± 2.43

** : Significant at 1 per cent level of confidence.

The scaling test was found significant for most of the characters studied in both the genetic groups except for number of fingers per ear. In the genetic group-1, finger length was also found insignificant.

4.4 Estimation of gene effects

The first degree parameters pertaining to the effects due to additive (d), dominance (h) and epistatic gene action (i and l) were estimated for the nine important characters in two genetic groups of finger millet following Hayman (1958) and results are presented along with standard errors in Table 4a and 4b.

4.4.1 Plant height

Genetic group-1 (PES 172 x HR 344)

All the four gene effects viz. additive (d), dominance (h), additive x additive (i) and dominance x dominance (l) were found to be operating for this character.

Additive (d), dominance (h), additive x additive(i) and dominance x dominance (l) were highly significant.

Significant negative dominance (-82.40) and positive dominance x dominance (76.58) indicated duplicatory type of epistasis. Dominance gene effect was negative and of high magnitude.

Table 4(a): Gene effects with their standard errors for nine characters in Genetic Group-1(PES 172 x HR 344) of finger millet cross.

Sl. No.	Characters	Genetic parameters					Type of epistasis ‡
		m	d	h	i	l	
1	Plant height	70.78 ± 0.63	-5.55** ± 0.33	-82.40** ± 1.76	-70.11** ± 1.86	76.58** ± 5.68	Duplicatory
2	Days to 50% flowering	79.59 ± 0.58	5.18** ± 0.27	- 5.18** ± 1.92	-18.93** ± 1.98	31.60** ± 6.32	Duplicatory
3	Days to maturity	111.48 ± 0.41	-2.68** ± 0.17	7.24** ± 1.12	1.10 ± 1.17	15.04** ± 3.65	Complementary
4	Number of productive tillers/plant	3.50 ± 0.11	1.95** ± 0.11	- 0.20 ± 0.33	- 1.20** ± 0.38	5.60 ± 1.06	Duplicatory
5	No. of fingers per ear	6.70 ± 0.36	2.90** ± 0.12	0.10 ± 0.58	- 0.90 ± 0.93	0.88 ± 3.15	Complementary
6	Finger length	5.77 ± 0.08	-0.55 ± 0.08	- 1.82** ± 0.28	- 4.04** ± 0.32	6.45** ± 0.93	Duplicatory
7	Ear weight per plant	25.87 ± 0.41	-2.50** ± 0.52	1.76 ± 1.82	- 9.73** ± 1.84	20.98** ± 5.18	Complementary
8	Straw weight perplant	33.35 ± 0.87	-3.71** ± 0.58	- 8.07** ± 2.49	-26.25** ± 2.72	50.74** ± 8.20	Duplicatory
9	Grain yield per plant	20.86 ± 0.75	-2.00 ± 0.30	1.58 ± 2.13	61.71** ± 2.22	-269.12** ± 6.87	Duplicatory

‡ Note: i) h^+l^+ or h^-l^- : Complementary epistasis. (ii) h^+l^- or h^-l^+ : Duplicatory epistasis.

Gene effects: m = Mean, d = Additive, h = Dominance, i = additive x additive, l = dominance x dominance

Table 4(b): Gene effects with their standard errors for nine characters in Genetic Group-2 (HR 23A x MR 5-6) of finger millet cross.

Sl. No.	Characters	Genetic parameters					Type of epistasis ‡
		m	d	h	i	l	
1	Plant height	71.00 ± 0.61	0.10 ± 0.34	-30.06** ± 1.78	-29.5 ** ± 1.89	92.24** ± 5.80	Duplicatory
2	Days to 50% flowering	73.35 ± 0.35	3.83** ± 0.29	-19.16** ± 1.52	- 9.83** ± 1.64	71.17** ± 5.14	Duplicatory
3	Days to maturity	109.32 ± 0.32	5.83** ± 0.25	- 4.20** ± 0.97	13.83** ± 1.07	28.96** ± 3.27	Duplicatory
4	Number of productive tillers/plant	3.50 ± 0.10	0.13** ± 0.28	0.41 ± 0.33	- 0.93** ± 0.46	3.09** ± 1.06	Complementary
5	Number of fingers per ear	6.13 ± 0.28	-0.18 ± 0.12	- 3.07** ± 0.77	1.38 ± 0.83	-1.57 ± 2.59	Complementary
6	Finger length	6.25 ± 0.10	0.09 ± 0.11	- 4.22** ± 0.31	- 1.33 ± 0.37	7.79** ± 1.06	Duplicatory
7	Ear weight per plant	20.00 ± 0.74	3.87** ± 0.44	0.92 ± 2.16	- 1.12 ± 2.36	57.72** ± 7.09	Complementary
8	Straw weight per plant	25.70 ± 0.85	2.27** ± 0.49	-15.36** ± 2.44	-21.74** ± 2.60	95.36** ± 8.09	Duplicatory
9	Grain yield per plant	20.35 ± 0.65	1.86** ± 0.31	4.51** ± 1.92	- 1.76 ± 2.00	24.77** ± 6.23	Complementary

‡ Note: i) h^+l^+ or h^-l^- : Complementary epistasis. (ii) h^+l^+ or h^-l^+ : Duplicatory epistasis

Gene effects: m = Mean, d = Additive, h = Dominance, i = Additive x Additive, l = Dominance x Dominance

Genetic group-2 (HR 23A x MR 5-6)

In this genetic group, dominance (h), additive x additive (i) and dominance x dominance (l) was found to be operating in governing this character as they are highly significant. Dominance x dominance (l) epistatic effect was positive and had higher magnitude in contrast to genetic group-1 but the epistasis was of duplicate type as in the case of group-1.

4.4.2 Days to 50 per cent flowering

Genetic group-1:

All the four gene effects namely, additive (d), dominance (h), additive x additive (i) and dominance x dominance (l) were highly significant controlling the days to 50 per cent flowering.

Highly significant positive effects of dominance x dominance (l) epistatic effect and significant negative dominance (h) effect indicate the duplicatory type of interaction which may control this trait.

Genetic group-2:

Similar trend as in case of genetic group-1 was observed with respect to gene effects and epistasis for days to maturity in genetic group-2 also.

4.4.3 Days to maturity

Genetic group-1:

Only three types of gene effects viz., additive (d), dominance (h) and dominance x dominance (l) were found to be governing the days to maturity.

Dominance x dominance (l) was highly significant and positive with higher magnitude (15.04) followed by dominance (7.24) indicating the complementary type of epistasis.

Genetic group-2:

Additive (d), dominance (h), additive x additive (i) and dominance x dominance (l) were found to control the days to maturity as they are highly significant.

Dominance x dominance (l) epistasis which was positive and of higher magnitude (28.96) in contrast to negative dominance (4.20) explains the duplicatory epistasis as compared to genetic group-1.

4.4.4 Number of productive tillers

Genetic group-1:

Additive (d), additive x additive (i) and dominance x dominance (l) were found significant and known to govern the character number of productive tillers per plant.

The positive and high magnitude dominance x dominance (l) with negative lower magnitude dominance (h) indicated the duplicatory epistasis.

Genetic group-2:

Similar gene effects as in genetic group-1 were found to control number of productive tillers per plant but the epistasis was found to be complementary as h and l are found to operative in the same direction and are additive in this group.

4.4.5 Number of fingers

Genetic group-1:

Only the additive (d) component was significant and known to govern the number of fingers per plant, while all other three gene effects were insignificant.

The dominance (h) and dominance x dominance (l) were found to operate in the same direction with additive effect indicating the complementary epistasis.

Genetic group-2:

In this group, only dominance (h) which was negative and significant was found to govern the character number of fingers per ear.

The epistasis was complementary as in the case of genetic group-1 but with negative values both in magnitude and direction for h and l effects.

4.4.6 Finger length

Genetic group-1:

Dominance (h), additive x additive (i) and dominance x dominance (l) effects were significant and found to be operating in governing the finger length.

The significant positive dominance x dominance (l) with negative dominance (h) effect indicated the duplicate type of interaction.

Genetic group-2:

In this group, dominance (h) and dominance x dominance (l) were significant in contrast to genetic group-1. Dominance x dominance (l) was significant and of higher magnitude coupled with negative dominance as in the case of genetic group-1 shows duplicatory epistasis operating for finger length.

4.4.7 Ear weight

Genetic group-1:

The three gene effects additive (d), additive x additive (i) and dominance x dominance (l) were known to operate for this character as they were highly significant.

Among the gene effects dominance x dominance (l) had higher effect and this with positive dominance (h) indicated complementary epistasis.

Genetic group-2:

Only additive and dominance x dominance (l) were significant for the above character in the genetic group-2. As in case of other characters dominance x dominance (l) had positive and high magnitude indicating the epistasis was complementary type.

4.4.8 Straw weight

Genetic group-1:

All the four gene effects additive (d), dominance (h), additive x additive (i) and dominance x dominance (l) were significant for this character namely straw weight.

Higher magnitude positive dominance x dominance (l) with negative dominance (h) showed duplicatory interaction.

Genetic group-2:

The same type of gene effects both in magnitude and direction were observed for the character straw weight per plant.

4.4.9 Grain yield

Genetic group-1:

Only the epistatic gene actions namely additive x additive (i) and dominance x dominance (l) were significant for the grain yield per plant.

As in case of other characters dominance x dominance (l) had higher magnitude but with negative sign showing the duplicatory action.

Genetic group-2:

In this group additive (d) gene effect was also found significant in addition to other two epistatic effects, showing the complementary type.

In general, among the nine characters studied most of them were controlled by more than one kind of gene effects except the finger numbers per ear and finger length which were controlled by only additive and dominance respectively. The character grain yield per plant was controlled by epistatic gene interactions namely additive x additive and dominance x dominance which caused complexicity in selecting this character for breeding programme specially for improvement in yield by selection procedures.

DISCUSSION

V DISCUSSION

An understanding of the mode of inheritance of complex quantitative traits like yield and yield attributes is indispensable for formulating effective selection procedure to improve the yield potential in any crop breeding programme. The estimates of gene effects will help in understanding the genetic potentiality of the populations. There are several biometrical methods which could be adopted to estimate the genetic parameters utilizing segregating generations. Generation mean analysis is one such method followed for estimation of gene effects (Hayman, 1958). Apart from this, further information on the extent of influence of environment (i.e. heritability) on different yield attributes is yet another important factor to know the level of improvement that could be achieved through selection in segregating populations.

Even though, the five generation mean analysis pose a difficulty in separating the additive genetic component (d) from the epistatic component additive x dominance (j), Hayman (1958) pointed out that when d and j are fully correlated, they cannot be estimated separately but the best estimates of dominance (h), additive x additive (i) components are obtained.

An attempt in this direction has been made in finger millet by utilizing parents and three generation (P_1, P_2, F_1, F_2 and F_3) to estimate the genetic parameters governing the

nine important yield and yield attributes. The information on this line is very much lacking in finger millet because of the difficulties explained elsewhere in this thesis.

The population means and variances, genetic variability, heritability, genetic advance and estimates of gene effects for nine characters namely, plant height, days to 50 per cent flowering, days to maturity, number of productive tillers, number of fingers, finger length, ear weight, straw weight, and grain yield per plant are discussed below:

1. Plant height

Plant height did not show appreciable amount of variation as there was no significant difference between F_1 and their parents, indicating importance of additive (d) genetic effects governing this character. Sufficiently higher variability has been generated in the segregating generations F_2 and F_3, giving scope for selection. This is in confirmation with earlier study made in this crop by utilizing segregating populations (Shanthappa, 1979).

The increase in the mean and reduction of variance in the F_3 generation could be attributed to the effect of selection of F_2 generation in both the genetic groups. The high heritability for this character indicates the least effect of environment. This is in confirmation with earlier

reports (Patnaik, 1968; Chaudhary and Acharya, 1969; Dhagat et al., 1972; and Shanthappa, 1979). This further indicates scope for manipulating this character.

The 'D' scaling test, indicated the importance of epistatic gene effects apart from additive (d) and dominance (h) effects governing this character.

The estimates of genetic parameters utilizing the generation means revealed the importance of additive (d), dominance (h), as well as epistatic gene effects (i and l) controlling this character. However, in the genetic group-2 the insignificant additive effect (d) may be due to cancelling effects of the epistatic component (l) on the additive component of variation. It has further indicated that type of epistasis was duplicative in action. This is in conformity with earlier reports on wheat (Baier, 1973; and Padilla, 1972). However, the negative gene effects indicated their depressing effect on this character revealing that it is easier to reduce the plant height than the response when we try to increase the plant height, indicating possibilities of breeding for dwarfness in this crop.

2. Days to 50 per cent flowering

The absence of hybrid vigour in both the genetic groups indicated the importance of additive genetic component compared to dominance component. An appreciable amount of variability has been generated in the F_2 generation of the

genetic groups which could be subjected for selection to manipulate days to 50 per cent flowering. This is in confirmation with the earlier reports made by utilizing segregating populations of finger millet (Shanthappa, 1979).

The stability of this character as evidenced by high heritability gives sufficient scope for improvement. This confirms with earlier reports (Patnaik, 1968; Narasimha Rao and Pardasarathi, 1968a; Dhagat et al., 1972 and Shanthappa, 1979).

The 'D' scaling test indicates the presence of epistasis along with additive (d) and dominance (h) gene effects. All the four types of gene effects namely, additive (d), dominance (h), additive x additive (i) and dominance x dominance (l) were found to play an important role in governing this character. However, the significant positive additive (d) component clearly explains its major role in controlling this character, indicating that selection could be effective for this character. The duplicative epistasis present in this case explains involvement of genes having similar effects both in magnitude and direction but are non-additive in nature. This is in agreement with the earlier report on rice (Ceccarelli, 1973; Singh and Nanda, 1974 and Bhuller et al., 1977).

3. Days to maturity

A good number of segregants matured earlier than the late parents and this gives a scope of selecting for earliness to develop short duration lines. The high means coupled with low variances in the F_2 generations compared to F_3 in both the genetic groups indicates the effect of selection intensity in later generations.

The moderate heritability coupled with moderate genetic gain indicated that this character could be improved by selection to some extent. This is in agreement with earlier reports in finger millet (Patnaik, 1968; Dhagat et al., 1972; Patnaik and Jain, 1973) and in foxtail millet (Sandhu et al., 1974).

The 'D' scaling test indicated the days to maturity was controlled by both duplicate and complementary epistasis.

Although the three gene effects viz., additive (d), dominance (h) and epistatic effects were present, the higher magnitude of dominance x dominance (l), epistatic effect in the genetic group-1 indicate the least response to selection in this character, while it is moderately promising in genetic group-2 as the additive and additive x additive (i) components were major controlling factors. This is in confirmation with the earlier reports (Edwards et al., 1976; Padilla, 1972 and Bhuller et al., 1977) in wheat.

It could be summarised that both additive and non-additive effects play an important role in governing days to maturity.

4. Number of productive tillers

The F_1s possessed more productive tillers than either of the parents while F_2 mean was slightly lower than F_1 in both the genetic groups. The moderate variability generated in F_2 and F_3 showed the possibility of selection for this character at later stages of generation.

The moderate heritability coupled with moderate genetic gain indicate considerable environmental effect on this character. This is on par with earlier reports (Narasimha Rao and Pardasarathi, 1968a; Dhagat et al., 1972; Setty et al., 1974; Goud and Lakshmi, 1977 and Shanthappa, 1979).

The additive (d), additive x additive (i), dominance x dominance (l) effects were found to govern this character but dominance x dominance effect had larger effect indicating duplicatory epistasis in genetic group-1 and complementary epistasis in genetic group-2. The significant positive additive effect coupled with high significant dominance x dominance effect might be having cancelling effect on each others thus rendering selection ineffective for this character. This is in confirmation with earlier reports in wheat (Edwards et al., 1976; Tripati et al., 1973 and Dzyuba, 1976).

5. Number of fingers

High variability was generated in F_2 as compared to F_3 and this is on par with earlier reports (Narasimha Rao and Pardasarathi, 1968a; Ahluwalia, 1970; Shanthappa, 1979) in ragi and in little millet (Abhinash Yadav and Srivastva, 1976). The higher heritability coupled with high genetic gain indicated additive genetic effects (d) governing this character. The significant positive additive component is found to control the finger number in the genetic group-1 indicating that the selection is effective for this character and significant, negative dominance effect in genetic group-2 revealing its strong drepressing effect which is supported by the lower mean value of F_1.

6. Finger length

Considerable level of hybrid vigour was found in F_1 of the genetic group-1. However, there was no difference among generations in the genetic group-2. High variability was observed in F_2 as compared to F_3 generation in both the genetic groups. This is in agreement with the reports in finger millet (Narasimha Rao and Pardasarathi, 1968a; Dhagat, et al.,1972; Chaudhari and Acharya, 1969).

The presence of significant dominance x dominance (l) epistasis governing this character indicated that the selection may not be so effective. On the other hand the significant negative dominance effect (h) coupled with

significant positive dominance x dominance (l) epistasis in genetic group-2 indicated the cancelling effect of genes with dominance effect resulting in apparent increase due to selection for this character.

7. Ear weight

An appreciable amount of variation was observed for this character in both the genetic groups, indicating the importance of non-additive gene effects. This is further supported by the significant positive dominance x dominance (l) effects in both the groups.

Considerable amount of variability was generated both in F_2 and F_3 giving scope for selection. The moderate heritability coupled with moderate genetic gain for this character in both groups indicate the influence of environment on this character. This is in confirmation with the earlier report (Shanthappa, 1979) by utilizing segregating populations in finger millet.

8. Straw weight

Greater variation was observed in segregating populations than the parents. The F_1 value recorded, revealed that the importance of dominance effect (h) controlling this character in both the groups. The straw weight has moderate heritability with low genetic gain

indicating the difficulty in improvement. This agrees with the presence of all the four types of gene effects namely, dominance (h), additive (d), additive x additive (i), dominance x dominance (l) reflects on the complexicity of inheritance of this character. Among the genetic parameters, the influencing parameter viz., dominance x dominance (l) epistatic component makes the selection still complicated. The significant negative additive effect in the genetic group-1 supports the depressing effect of additive genes as plant height resulting in the poor straw yield.

9. Grain yield

An appreciable amount of variability was noticed for this character in both the crosses indicating the importance of dominance gene effect on this character. Ample variability has been generated in F_2 and F_3 in both the genetic groups. This agrees with earlier reports in ragi (Kempanna and Thirumalachar, 1968; Narasimha Rao and Pardasarathi, 1968a; Dhagat et al., 1973; Swamynath, 1978) and in foxtail millet (Sandhu et al., 1974; Chinnaswamaiah, 1975; Vishwanath, 1977).

The significant positive additive x additive (i) epistatic effect in the genetic group-1 coupled with significant negative dominance x dominance (l) effect reinforce the additive effects, thus indicating good selection response

while the significant positive dominance (h) and additive (d) effect coupled with significant dominance x dominance (l) effect makes the selection complicated in the genetic group-2.

In general, it could be concluded based on the present study that it is possible to make selection for the characters, resulting in the development of lines with early, good tillering and increased finger number which are the important yield attributes. However, the gene effects governing these yield characters may vary greatly from cross to cross, making it complicated to strongly pinpoint on any particular kind of gene action which further needs confirmation.

SUMMARY

VI SUMMARY

The present investigation was carried out utilizing the segregating generations of two crosses of finger millet (Eleusine coracana G.) viz., PES 172 x HR 344 and HR 23A x MR 5-6 to determine the genetic architecture through the estimation of heritability (broad sense), genetic advance and genetic parameters namely additive (d), dominance (h) and epistatic gene effects (i and l) for nine yield and yield attributes namely, plant height, days to 50 per cent flowering, days to maturity, number of productive tillers, number of fingers, finger length, ear weight, straw weight and grain yield per plant. Such studies involving segregating populations in finger millet are very scanty. Hence, the present study was undertaken during summer 1980, at the Main Research Station, University of agricultural Sciences, Hebbal, Bangalore.

The observations recorded in the parents and three generations (hereafter known as five generations) namely P_1, P_2, F_1, F_2 and F_3 with respect to the above mentioned characters were analysed by adapting generation mean analysis (Hayman, 1958). The results indicate that the F_1 values observed for days to maturity, number of productive tillers, and grain yield per plant were insignificant indicating the importance of additive genetic effects controlling these characters. The F_2 and F_3 generations recorded significantly higher variability in both the genetic groups revealing that

the selection could be applied to manipulate the characters. When the parents are contrasting for some or several characters the variances in F_2 would be high and decrease in F_3 will be usual observation showing that a few plants though not many are suitable for selection on the extreme sides and the selection for these characters is possible with the evolution of lines incorporating specific character.

The genotypic co-efficient of variability was the highest for number of fingers per ear in both the genetic groups followed by grain yield, ear weight and straw weight. The heritability was the highest for number of fingers per ear followed by grain yield, plant height and days to maturity indicating the moderate effect of environment on these characters, and could be effectively subjected to selection to manipulate them as required. The genetic advance as per cent of mean followed the similar trend as that of the heritability further strengthening their response on selection.

The 'D' scaling test was significant for most of the characters except finger number and finger length, indicating the possible role of epistasis in governing these characters. The absence of epistasis for finger number and finger length further reduced the complexity of selection programme in improving these characters depending on the nature of allelic interaction.

The first degree genetic parameters namely additive (d), dominance (h), additive x additive (i) and dominance x dominance (l) estimates for the nine yield and yield attributes revealed that days to 50 per cent flowering and number of productive tillers are governed by significant positive additive genetic effects in both genetic groups. However, the possibility of involvement of other type of gene effects are not ruled out as the other components were also found significant. The negative significant additive effects for plant height, days to maturity, ear weight and straw weight per plant in the genetic group-1 indicate the depressing effect on these traits, that the selection towards the reduced expression of these characters or negative selection is more beneficial, while significant positive additive effects for days to 50 per cent flowering, days to maturity, number of productive tillers, ear weight, straw weight and grain yield per plant in genetic group-2 indicate that selection could be effective in improving these characters to some extent though these characters are governed by other types of gene effects. It is interesting to note that days to maturity in genetic group-2 was controlled by significant positive additive (d) and additive x additive (i) effects indicating that it is easily amenable for improvement.

In general, it could be concluded based on the results of present study that it is possible to make selection for the characters, resulting in the development of lines with early and good tillering types with increased finger number which contribute to increase in yield. However, the gene effects governing these important characters may vary very greatly from cross to cross making it complicated to strongly pin-point on any particular kind of gene action. This needs further confirmation.

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*Originals not seen.