

**A COMPARATIVE STUDY OF THE
CONTRIBUTION OF BIOMETRIC CHARACTERS
ON YIELD IN
DESSERT AND CULINARY
VARIETIES OF BANANA**

BY
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THESIS

Submitted in partial fulfilment of the
requirements for the degree of

Master of Science (Agricultural Statistics)

Faculty of Agriculture

Kerala Agricultural University

Department of Statistics

COLLEGE OF VETERINARY & ANIMAL SCIENCES

Mannuthy, Trichur.

DECLARATION

I hereby declare that this thesis entitled "A COMPARATIVE STUDY OF THE CONTRIBUTION OF BIOMETRIC CHARACTERS ON YIELD IN DESSERT AND CULINARY VARIETIES OF BANANA" is a bonafide record of research work done by me during the course of research and the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship, or other similar title, of any other University or Society.


Hassanly,
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CERTIFICATE

**Certified that this thesis, entitled
"A COMPARATIVE STUDY OF THE CONTRIBUTION OF BIOMETRIC
CHARACTERS ON YIELD IN DESSERT AND CULINARY VARIETIES
OF BANANA" is a record of research work done
independently by Sri. Vijayaraghava Kumar, under my
guidance and supervision and that it has not
previously formed the basis for the award of any
degree, fellowship or associateship to him.**

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ACKNOWLEDGEMENT

With a deep sense of gratitude I acknowledge the valuable help of Dr. K.C. George, Associate Professor, Department of Agricultural Statistics, College of Horticulture and Major Advisor, under whose guidance this work has been carried out.

I am deeply indebted to Dr. P.U. Surendran, Professor, Department of Statistics, College of Veterinary and Animal Sciences, Dr. T.V. Viswanathan, Associate Professor, Plantation Crops, College of Horticulture and Sri. M.P. Abdul Rasak, Assistant Professor, Department of Statistics, College of Veterinary and Animal Sciences for their valuable suggestions given to me as members of the Advisory Committee.

This work owes much to Dr. N. Krishnan Nair, Professor, Agricultural Botany, College of Agriculture, Vellayani for his valuable help in the preparation of the data and to Sri. R. Balakrishnan Anon, Assistant Professor, Department of Statistics, College of Agriculture, Vellayani for the help given to me in the statistical analysis of the data.

I am thankful, to the other members of the Department of Agricultural Statistics Sri. P.V. Prabhakaran, Associate Professor and Sri. V.K.G. Unnithan, Assistant Professor, Department of Agricultural Statistics, College of Horticulture for their help rendered in the conduct of the work.

I am thankful to Dr. Simon Daniel my friend Sri. Ramesh B. Nair, Sri. Hariharan. V, and Sri. Jacob Thomas, M. my fellow scholars for their timely help in carrying out the research works.

I record my thanks to Dr.M.Krishnan Nair, Dean, College of Veterinary and Animal Sciences for the facilities provided for the research.

I am grateful to the Kerala Agricultural University for the fellowship awarded to me during the course of research works.

Thanks are also due to Sri. Hareendran. G and Sri. Muralidhara Karnavar. M.K, Typists, Kerala Agricultural University for typing of the manuscripts.

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D E D I C A T E D

T O

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INTRODUCTION

I N T R O D U C T I O N

Bananas were used as a food for man even before history began to be written. The cruises of Alexander the great found the banana growing in India in 327 B.C. No doubt it was growing in India even before that time.

Banana grows in many parts of Asia, South America, France, Australia and East Africa. India is having the second position in the world of production of banana and is cultivated in more than two lakh hectares. (Anon, 1981). Kerala, Tamil Nadu, Karnataka, Andhra Pradesh, Maharashtra, Orissa, Bihar and West Bengal are the important banana growing states in India. Kerala stands first among these states with an area of 13,518 hectares and a production of 171,493 tonnes. (Anon, 1981).

The banana plant cannot be considered as a real tree because there is no wood in the stem rising above the ground. The leaves growing very close together one inside the other constituting the stem of the plant. The leaves spreading out at the top of this stem usually are from 2.5 to 3.5 m long, about 5 m wide and there will be 25 to 30 such leaves on a matured plant. They are so spread out and rise in the air that the banana

plant looks like a palm tree. The fully grown plant is of 2.5 to 4 m high and stem is of 20 to 30 cm thick. Depending on the variety the girth ranges from 60 to 90 cm. The inflorescence appears about 9 to 10 months after planting of the banana plant. The stalk turns down and grows downwards while the small bananas from the stalk first point downwards and then they turn and point upwards. They are ready to harvest by about three months after flowering. The size of the plant and the size of the bunch of fruit depend on the climate and the kind of soil in the place where the plant grows. Deep and rich soil and warm moist climate is suitable for the growth of this plant. The banana grows well in the moist tropical areas of Kerala. The bunches in which the banana grows are called hands and the number of these hands ranges from 9 to 16. The number of separate fruits (called fingers) ranges from 12 to 25 in these hands. The weight of the hands ranges from 500 to 1500 gm.

Apart from the biometric characters mentioned above viz. girth, number of leaves, weight of fingers, number of fingers and number of hands measurements of the other biometric characters like weight of hands,

weight of bunch, length of fruit, thickness of fingers and number of roots also were taken for analysis. The observations were collected from a wide range including both dessert and culinary varieties. Fifty six varieties of dessert type and thirty varieties of culinary type were taken which include almost all the varieties cultivated in Kerala.

Since the demand of this fruit in the international market is increasing any aim for improving the yield of this fruit is not in vain. Systematic planning and breeding scheme is needed for its improvement in quality and in quantity. The yield is influenced not only by the genetical factors but also to a great extent by the environmental factors. Thus it is essential to find out the yield component of different characters and their associations with one another. The direct and indirect effects produced, by the relationships of the characters can be projected by making use of the correlation studies and also by the application of the method of path-coefficients. The phenotypic genotypic and environmental correlations can be used to exploit the relation between the various biometric characters in the different varieties.

The preliminary phases of analysis of a plant are normally based on search for and study of correlations.

This is true in the case of humans also. The use of phenotypic, genotypic and environmental correlations and the application of path coefficient analysis can be exploited to a great extent in this aspect. A knowledge of the inter relationships among the records of the different traits or the different biometric characters will help the procedures in the simultaneous improvement of the traits. By a study of the nature of their association it is possible to suggest a suitable selection procedure. The path coefficient which is the standardised partial regression coefficient is used to measure the direct influence of one variable upon another and permits the separation of the correlation coefficient into components of direct and indirect effects. Since a cause and effect relationship is always incorporated with this method, the yield (effect) can be well analysed by the plant dimensions (causes). Also the variations produced on the yield by the environmental changes can be determined by this analysis as the yield component of the plants are measured at different times. Thus by deleting the complex algebraic methods involved in the usual breeding procedures, a regular breeding system can be evolved by the application of Prof. Sewal Wright's technique of path analysis.

Very little work has been done towards banana crops with regard to correlation studies and path coefficient analysis. The present study is based on the data on the experiment conducted at the Banana Research Farm, Kannara, on different dessert and culinary varieties on different morphological characters. Thus the investigations made under the present study are

(i) To find the phenotypic, genotypic and environmental correlations in dessert and culinary varieties of banana and perform the path coefficient analysis in these two varieties. Then based on the results obtained make a comparative study of the contribution of the various biometric characters on the yield in both the varieties.

(ii) To construct a discriminant function to discriminate the various varieties and compare the genetic advance through discriminant function with the genetic advance through straight selection, based on the biometric characters in the two type of banana varieties.

(iii) To suggest a proper method of selection based on the path coefficient analysis for the various biometric characters of the dessert and culinary varieties of bananas.

REVIEW OF LITERATURE

REVIEW OF LITERATURE

The scientific breeding of bananas have been started by about 1922 at different parts of the world, and the first report is from the Imperial College of Tropical Agriculture, England. They gave due importance to varieties like *Musa acuminata* and *Musa balbisiana* which were mainly used for the needs of export trades (Simmons, 1954). In India works were begun to undertake only recently and some isolated studies of a few varieties were made. So, in this study a comprehensive comparison of the different varieties and different characters is made based on the modern statistical tools of analysis giving weight to later developments. A review of the papers based on which the present study made is given below.

2.1 GENERAL NOTES ON BANANA

Amarsingh (1960) classified bananas into five varieties. The important ones are varieties for consumption as such (Dessert bananas) and varieties used only after cooking (Culinary bananas). The other three varieties are used for making chips, jam and powders. The yields of these varieties vary depending on cultural practices. Hand managed

banana plantations were productive for 10 to 15 years where as mechanically cultivated plantations yields only for 5 to 6 years.

Simmonds (1954) used the leaf area ratios and discriminant function analysis to distinguish the 'Robusta' clone in a mixed planting. The results are not significant and about 10 per cent of the plants were misidentified. Further the total number of fingers in the bunch is directly proportional to the number of hands and he got a regression equation of the form $F = a + bH$; F is the number of fingers and H is the number of hands. The constants 'a' and 'b' were such that $-5 \geq a \geq -60$ and $-1 \leq b \leq 15.3$ depending on the variety.

2.2. COMPARATIVE STUDY OF BIOMETRIC CHARACTERS

MEASUREMENT OF CORRELATIONS

Karl Pearson (1857 - 1936) developed the formula of 'correlation coefficient' which is used to measure the intensity or degree of relationship between two variables. Later Spearman used this simple correlation coefficient to give a plausible explanation to a single pair of variables and it lead him into difficulties when there was a system of variables having consistency throughout.

So, when studying correlations the nature of the population must be clearly understood because the magnitude of the correlation can be influenced by the choice of individuals upon which the observations were taken (Dewey and Lu, 1939).

Searle (1955) obtained informations on the type of variations in the available genetic material and part played by environment on the expression of plant characters by using a general linear model. He broke the phenotypic variability into heritable and non heritable components. Genetic parameters such as genetic coefficient of variation, genetic advance were computed to evaluate the genotypic variability in different quantitative characters.

Wright (1968) reported that the general size of the characters is affected by both genetic and environmental reasons. So in interpreting set of correlations among morphological measurements the genetic correlations and sequential residuals can be made use of except in the case of self correlations.

2.2.1. Phenotypic Correlations

According to Falconer (1969) a phenotypic correlation is the correlation between records of two traits on the same plant (animal) and is

usually estimated by the product moment correlation statistic. Phenotypic correlations are estimated directly whereas the genetic correlations are derived from covariance analysis between the relatives.

2.2.2. Genetic Correlations

The genetic correlation is the correlation between a plant's (animal's) genetic value for one trait and the same plant's (animal's) genetic value for the other trait (Searle, 1955). Two methods of estimating genetic correlation between two traits are commonly used. One procedure utilizes estimates of within subclass covariances as described by Hazel (1943). Estimates of the group variance and covariance components for two characters from an analysis of within and between groups of relatives was used in the other method suggested by Varvick and Henderson (1951). In an example they used the between and within analysis of sib or half sib analysis.

Varvick and Henderson (1951) also proves that in Hazel's method the genetic model described assumes a random mating population where gene effects approximate to a four variate normal distribution. If selection is applied to the population then the parameters will

probably change and the model also considers effect due to linkage sexual or cytoplasmic differences.

2.2.3. Environmental Correlations

The environment generally affects an individual in all its parts and functions. The correlation between environmental effects (including errors) is denoted as the environmental correlation of any two traits (Searle, 1955). Even though the phenotype includes the genotype, a phenotypic correlation less than that of a genotypic correlation is explained as a result of a negative environmental correlation in the records of the two traits.

Srivastava and Das (1973) used the genetic correlation and discriminant function to brassica components. The association of plant characters which is statistically determined by correlation coefficient is useful as a basis for selecting desirable strains. Genotypic correlations were helpful in the construction of selection indices and it permits the prediction of correlated responses. They further permits the evaluation of the relative influence of various characters on yield.

Yield components were studied by Chaudhury *et al.*, (1973) in rice by genetic variability and correlation measures. They have been that genotypic variance was very high for grain number. The higher estimates of genotypic variances further indicated that variation owing to genetic causes is higher than that owing to non genetic factors. A high genotypic variance and heritability value combined with a greater genetic advance for grain number indicated that selection for this character would be effective for yield improvement.

Katiyar *et al.*, (1974) measured the amount of advance by selection in Indian mustard. The genetic advance and heritability estimates are evaluated for about 50 varieties. The genotypic variance was calculated as $G.V. = \frac{Y - E}{N}$; V the varietal mean square, E the error mean square, and N is the number of replications. A wide range of phenotypic variation was obtained for all the six characters studied. High genetic advance was found for plant height and yield per plant but low values were observed for the days from flowering to maturity, number of secondary and primary branches.

The informations on the available genetic material and part played by environment on plant characters was studied by Bhatnagar and Sharma (1970) in barley.

The phenotypic variability was broken into heritable and non heritable components. High heritability values (in the broad sense) and high percentage of genetic advance were obtained for characters like length of peduncle, length of ear and seeds per ear indicating that there is a scope for improvement of these characters by selection.

Nehendra Singh and Singh R.K. (1973) in an experiment with barley, has seen that generally phenotypic and genotypic correlation coefficients are greater than the environmental correlations. In some cases like correlation of plant height with ear weight, effective tillers with yield per plant, ear length with effective tillers and number of spikelets per ear with yield per plant, they were of the same magnitude also. So grain yield as a complex character, selection based on simple correlations cannot yield to desirable results and to study the contribution of different components independently, it is essential to get the direct and indirect effects of each of the component to yield.

2.3 ANALYSIS OF PATH COEFFICIENTS

The theory of path coefficient was first established by Wright (1921, 1934, 1960 and 1968).

The most important application of path analysis is the working out of genetic consequences of mating systems. This method as powerful and flexible was immediately very popular among geneticists still less so among professional statisticians. It was much later that its usefulness became gradually and generally appreciated (Li, 1956).

In this method all the variables are assumed to be linearly related and whenever the relationship is non linear the approximate result is obtained by adopting some linear transformations to make it linear (Wright, 1968). It is a multivariate analysis dealing with a closed system of variables that are linearly related (Li, 1955). The more we know of the true relationships among the variables the more meaningful will be the result of path analysis (George, 1981).

Kauptherne (1957) has illustrated three main applications of path coefficients. They were (1) To study the consequences of a number of linearly related forces, on their resultant in a cause and effect system. (2) To examine the feasibility of a pattern of causal forces in estimating the path coefficients of paths between forces whose direct results cannot be

measured and (3) in making clear, what can be deduced from a set of correlation coefficients.

2.3.1. Applications of Path analysis

According to Wright (1934), this method is based on the construction of a qualitative diagram in which the variables whether actually measured or not are represented as additively and completely determined by more remote ones, until an array of ultimate factors is arrived at. All correlations among them were assumed to be known.

Dewey and Lu (1959) used the path analysis to study the components of wheat grass production, by taking six biometric characters. Because of the mutual associations between the characters they are either positively or negatively correlated. As the number of characters under study were increased and the correlation tables were used, the indirect associations became more complex, less obvious and somewhat perplexing. At this point the path analysis provides an effective means of understanding direct and indirect causes of associations, and permits a critical examination of the specific forces acting, and measures the relative importance of each causal factor.

2.3.2. Mathematical Theory of Path Analysis

A path coefficient is the standardized (partial) regression coefficient and as such it measures the direct influence of one variable upon another. The correlation coefficients can be splitted into components of direct and indirect effects by the use of it (Li, 1956).

Since a cause and effect relation exists among these variables in this system the actual work is to construct a diagram by assigning directions to the causal system and then estimating the amount of influences along these directions based on the experimental evidences (George, 1961). Double arrowed lines are usually used to indicate correlation and single arrowed lines to indicate path coefficients.

From the papers of Wright (1934, 1960 & 1968) the basic mathematical equations of this method may be elucidated as follows.

Consider the total yield, Y which is correlated to a number of characters X_1, X_2, \dots, X_n and R where R includes all the residuals. The linear relationship assumed can be expressed as $Y = C_0 + C_1 X_1 + C_2 X_2 + \dots + C_n X_n + R$ and the C_i 's known as partial

regression coefficients except the one pertains to the residual were estimated by the method of least squares. Wright defines them as "path regression coefficients". The C_1 's measure the contribution that the X_1 's make directly to Y . If this measures the contribution in an absolute sense its value can be used in the analysis of other populations.

Now standardizing the variables (by putting $X_i = \frac{X_i - \bar{X}_i}{\sigma_i}$ the path coefficients $P_i = \frac{C_i \sigma_i}{\sigma_y}$ will be obtained which has got greater convenience in analysis.

Thus $Y = P_1 X_1 + P_2 X_2 + \dots + P_n X_n$ (then all standard deviations reduces to 1) so that the correlation coefficient r_{yq} may be estimated as the product moment statistic

i.e. $r_{yq} = \frac{1}{n} \sum Y X_q = \sum P_i r_{iq}$. This is the basic equation in path analysis.

In the above analysis the residual factors are treated as uncorrelated with the represented factors, even though it may be known or suspected that the dependent variable is correlated with the latter through paths other than those represented.

So the effects due to residual factors may be ^(P_n)

estimated by taking another factor X_q such that $r_{X_1q} = 0$.

Thus $r_{YX_1} = P_1 + P_2 r_{12} + \dots + P_n r_{1n}$ and when X_q becomes Y then $r_{Yq} = P_1 r_{Y1} + P_2 r_{Y2} + \dots + P_n r_{Yn} + P_u^2 = 1$

i.e. $1 = P_u^2 + \sum_j P_j r_{Yj}$ and this equation is helpful in the estimation of residual factors.

Malhotra and Jain (1972) made a study to measure the direct and indirect effect of certain characters on grain yield in barley by the method of path analysis. Only 1000 grain weight and grains per ear had direct positive effect on seed yield. The direct effect of these characters was even more than the respective correlations, because of the negative associations among them. Ultimately they resulted in negative indirect effects.

Malhotra et al. (1972) used the correlation and path coefficient analysis in Soybean. Randomised block design with 3 replications was used. From the analysis of variance characters having significant difference among strains were selected. Partial regression and path coefficient analysis revealed

that the pods per plant is the most important yield contributing character.

To assess the influences and ascertain their reliability in planning, an experiment was conducted in green by Phandis *et al.* (1970). Randomised block with 3 replications and 45 varieties were used. The genetic simple correlation coefficient between all the possible combinations of the variables were worked out. The path analysis shown that yield was directly influenced by the seed weight followed by the number of seeds and number of pods per plant.

Partial regression analysis was done between yield and morphological characters by Venkata Rao *et al.* (1973) in tobacco. The genotypic variances and covariance matrices were used to estimate the path coefficients. Very low correlation was obtained for regression of bright leaf yield with yield indicating that the causal scheme is not tight. Hence, path analysis was not given for bright leaf yield as it may not give much valid informations.

2.4. DISCRIMINANT FUNCTION FOR PLANT SELECTIONS

To discriminate between individuals belonging to two different populations a discriminant function was

proposed by Fisher (1936). But its application for plant selection was first described by Smith (1939).

Fisher (1936) defined a function $Z = b_1 X_1 + b_2 X_2 + \dots + b_n X_n$ where X_1, X_2, \dots, X_n are different variables measured and b_1, b_2, \dots, b_n are the weighing coefficients. The weights b_1 are determined in such a manner that the ratio of the variance between the populations to the variance within the populations is maximised. This maximisation procedure leads to a set of simultaneous equations which will provide the b_1 values.

Smith (1939) points out that in selecting for characters such as yield differences due to genotypes are very largely masked by non heritable variations such as those due to soil locations. Therefore when breeding works are done in plants, selection for yield must be done on the basis of general vigour, number of clumps, size of spike etc. which can be believed as associated with corresponding genes. But there is no basis for giving more or less weight to certain characters depending on the extent to which they really indicate a concentration of genes for yield. The method of approach is the development of a discriminant function that will indicate the genotypic value of a plant or line for

selection by representing the genotype of the plant by a function of the form $U = a_1 X_1 + a_2 X_2 + \dots + a_n X_n$. In this function the value of the expected genotype of the original characters X_1, X_2, \dots, X_n is taken and the weights a_1, a_2, \dots, a_n depend on the economic values of the corresponding characters.

Singh and Chaudhary (1977) constructed a discriminant function for plant selection. The relative importance of the different characters is used in deciding the weights. The above equation $U = a_1 X_1 + a_2 X_2 + \dots + a_n X_n$ representing the genotypes of the characters was expressed as $Y = b_1 X_1 + b_2 X_2 + \dots + b_n X_n$ by making use of the phenotypic values. The b_i values are derived in such a manner that the regression for Y on U will be maximum. The selection of phenotype will then ensure a maximum concentration of desired genes in the plants or lines selected.

Coulden (1959) describes some rules in assigning weights for the genotypes. Disregarding the proportional economic values of the characters they are weighted equally. Since the means of the characters differs, equal weights are obtained by putting $a_1 = \frac{1}{\bar{X}_1}$, $a_2 = \frac{1}{\bar{X}_2}$ etc. When there is fair knowledge of the

economic values of the characters the weights are assigned by modifying the above method. If the relative values of X_1 , X_2 and X_3 are in the ratio 2:1:3 we take $a_1 = \frac{2}{X_1}$, $a_2 = \frac{1}{X_2}$ and $a_3 = \frac{3}{X_3}$.

But in many practical situations the assigning of weights is more arbitrary and the breeder selects those plants showing desirable characters, like number of tillers, to get more yield. In the present analysis the discriminant function as well as the genetic advance through discriminant function are estimated based on the criterion suggested by Fisher.

2.5. SELECTION MODELS

The first major selection experiment was begun at the Illinois Experiment Station in 1936 and was for the oil and protein content of maize (corn) grains. It was continued for several decades and the results were reported by Winter (Thompson and Thoday, 1979).

The discriminant functions are constructed based on the genotypic performance of the individuals. But the selection indices are used for the discrimination of good genotypes from undesirable ones on the basis of phenotypic values itself.

If $G_1, G_2 \dots G_n$ are the genotypic values the genetic worth 'H' is defined as (Smith, 1936)

$$H = a_1 G_1 + a_2 G_2 + \dots + a_n G_n \quad ; \quad a_1, a_2, \dots, a_n$$

takes values according to the economic importance. Similarly a function 'I' based on the phenotypic performance is defined as $I = b_1 P_1 + b_2 P_2 + \dots + b_n P_n$ where b_1, b_2, \dots, b_n are estimated such that the correlation between H and I must be maximum. Then from such a function it is possible to select varieties based on the phenotypic values itself.

Singh and Chaudhary (1977) suggests a selection criterion for calculating the index values for each of the individual varieties. The Phenotypic and Genotypic variance covariance matrices were made linearly related and economic values were taken as unity. The expected genetic gain also can be calculated from this index when the selection differential 'S' and the intensity of selection 'i' are known.

Robinson *et al.* (1954) gives a note on the factors to be considered in assigning weights to characters. (1) The phenotypic variance and covariance between each of the characters to be involved (2) The genotypic variance and covariances (3) The relative

economic values of the several characters are to be considered for the proper evaluation of the ultimate product. When the phenotypic and genotypic correlations differ in magnitude selection for one of the characters would result in greater changes in the other character than would be expected if the genotypic correlations were assumed equal to the phenotypic correlation. (They have obtained such a result with ears per plant and plant height, and ears per plant and yield in an experiment with corn). In such cases the assumption is that the difference indicated between genotypic and phenotypic correlations are true differences and not due to sampling variances alone.

2.5.1. Restricted Selection

Kempthorne and Hordisag (1959) give another approach in selection in which changing the arithmetic means of 'r' out of 'p' characters while the means of remaining (p - r) characters is kept unchanged. In this case the problem of index construction is done by maximising the correlation between I and H subject to the condition that the genetic gain G is zero. Thus by using Lagrangian Multipliers they obtained a solution (set of selection indices under

restricted selection) by solving an expression of the form

$$b = \left\{ I_{pp} - P^{-1} G C (C' G P^{-1} G C)^{-1} C' G \right\} P^{-1} G a$$

where I_{pp} is an identity matrix of order p .

P The phenotypic dispersion matrix

G The genotypic dispersion matrix

a The vector of economic weights (in which all the elements are equal to 1) and

C is a coefficient matrix which depends on the number of restricted characters.

They have also showed that when there is no restriction (when the C matrix is not using) this expression reduces to the previous case i.e. unrestricted selection index.

2.5.2. General Selection

Hanson and Johnson (1957) have introduced the concept of general selection indices by combining two populations and it was applied on Soybean populations by Caldwell and Weber (1965). The ' b_1 ' values were obtained from pooled information of various populations. These ' b_1 ' values are used to obtain a correlation factor for the phenotypic and genotypic variance and covariances and then a new set of (corrected) ' b_1 ' is developed.

The relative efficiency of general selection indices against specific ones are tested by Singh (1975). He has shown that they are as efficient as specific indices. But when it is used for selecting individuals from a population other than the one tested its efficiency is reduced to a great extent.

MATERIALS AND METHODS

MATERIALS AND METHODS

The present study was based on the crop raised at the University Research Farm, Kanneer, during the last two years. The plants were grown in randomized blocks of 3 replications and the number of different varieties chosen in the two sets i.e dessert and culinary sets were 56 and 30. All the treatments given to these two sets were quite uniform. Within each set of plants the application of manure fertilizers and chemicals, irrigation and other management practices were managed time to time so that there is uniformity in all respects. The different morphological characters measured from these plants were given below:

- (1) Height
- (2) Girth
- (3) Number of leaves
- (4) Weight of hands
- (5) Weight of fingers
- (6) Number of fingers
- (7) Length of fingers
- (8) Thickness of fingers
- (9) Number of hands
- (10) Number of fingers per hand
- (11) Length of Peduncle

(12) Number of roots and

(13) The yield (weight of bunches)

In the dessert varieties it was possible to get only an incomplete set of observations in regard to the twelfth character, viz. Number of roots. So it became difficult to include this character into study as the observations on many varieties were lacking and hence only the remaining 12 were taken for the entire analysis. However all the 13 were included in the culinary varieties.

3.1. Varieties Selected

The dessert bananas included five different groups. They were Kunnan, Kadali, Poovan and Miscellaneous. Seven varieties were obtained from Kunnan, 7 from Poovan, 6 from Kadali, 15 from dwarf and 21 from the Miscellaneous (Total 56). Thirty different varieties were included in the culinary group. The different varieties of the two groups along with their genotype is given below.
(Musa sapientum is represented by AA and Musa balbisiana by BB)

Dessert Bananas:**I. Kunnan group**

	Genotypes
(1) Nendra Kunnan	AAB
(2) Pay Kunnan	AAB
(3) Valiya Kunnan	AB
(4) Kodupilla Kunnan	AAB
(5) Thala Kunnan	AAB
(6) Peecha Kunnan	AAB
(7) Adaka Kunnan	AAB

II. Poovan Group

(1) KHR 1/75	AAB
(2) KHR 2/75	AAB
(3) Rasthali	AAB
(4) Tangate	AAB
(5) Njalipoovan	AB
(6) Ayirunka Poovan	AAB
(7) Poovan	AAB

III. Kadali group

(1) Cheekadali	AAA
(2) Red banana	AAA
(3) Ambala Kadali	AA
(4) Vadakan Kadali	AA
(5) Chakara Kadali	AAB
(6) Kanni Kadali	AAB

IV. Dwarf Varieties

(1) Mons Marie	AAA
(2) Annt Sagar	AAA
(3) Robusta	AAA
(4) Peddapacha Arathi	AAA
(5) Giant Cavendish	AAA
(6) Vather	AAA
(7) Harichal	AAA
(8) High Gate	AAA
(9) Greenichal	AAA
(10) Sapumal amamolu	AA
(11) Mauritius	AAA
(12) Dwarf Cavendish	AAA
(13) Prinkhal	AAA
(14) Locatan	AAA
(15) Vamanteli	ABA

V. Miscellaneous

(1) Prebon	AAA
(2) Naethnan	AAB
(3) Pachashingan	AAA
(4) Sirupani	AA
(5) Chingan	AA
(6) Pillan	AB
(7) Pacha Madan	AAB
(8) Sirumalai	AAB

(9) Chirupunchi	ABB
(10) Charupadathi	ABB
(11) Thiruvananthapuram	ABB
(12) Ladies finger	AB
(13) Nendra Padathi	ABB
(14) Pirija	ABB
(15) Rodja	ABB
(16) Chinali	ABB
(17) Krishna Venzai	ABB
(18) Sira	AAA
(19) Virupakshy	ABB
(20) Kadjiradij	AAA
(21) Adakken	AB

In the case of culinary bananas 30 varieties were grown from which measurements on 13 characters were taken. The different varieties were listed below:

(1) Hallabaksha	ABB
(2) Nangunthi Royan	ABB
(3) Jama	ABB
(4) Mylenid Samed	ABB
(5) Couria	ABB
(6) Erachi Venzai	AA
(7) Noodi	ABB
(8) Annabarian	ABB

(9) Samsi	ABB
(10) Pising monk	ABB
(11) Poyimann	ABB
(12) Moy mannan	ABB
(13) Alakkal	ABB
(14) Raina	ABB
(15) Kugge	ABB
(16) Malai Menthon	ABB
(17) Sambrai Menthon	ABB
(18) Nalla mentha	ABB
(19) Menthon	ABB
(20) Kanchikola	ABB
(21) Asyhabhalla	ABB
(22) Pochabantha bathosa	ABB
(23) Karibantha	ABB
(24) Ashamenthon	ABB
(25) Kapur	AAB
(26) Valha	ABB
(27) Chetty	ABB
(28) Moyvannan	AAB
(29) Vannan	AAB
(30) Mannan	AAB

3.2. ANALYSIS OF VARIANCE AND COVARIANCE

The varietal difference among the characters could be studied by the construction of various analysis

of variance tables. Total there were 12 ANOVA for the 12 characters of the dessert varieties and 13 for the culinary varieties.

The analysis of covariance table may be used to compare the varietal differences among the characters. (All together there will be 12 $C_2 = 66$ ANCOVA tables in the dessert varieties and 13 $C_2 = 78$ tables in culinary varieties). The phenotypic, genotypic and environmental variance and covariances could be obtained from this analysis of variance and covariance tables. As an example the ANOVA and ANCOVA tables for the first two characters height and girth will have the following form. The tables for the other varieties were similar to this.

Character 1 (height) ANOVA

Source	df	SS	MSS	F
Replications	$r-1$	$(r-1) R_q$	R_q	R_q/E_q
Varieties	$v-1$	$(v-1) V_q$	V_q	V_q/E_q
Error	$(r-1)(v-1)$	$(r-1)(v-1)E_q$	E_q	
Total	$rv-1$	$(rv-1) T_q$	T_q	

Character 2 (Girth) ANOVA

Source	df	SS	MSS	F
Replications	$r-1$	$(r-1) R_2$	R_2	R_2/E_2
Varieties	$v-1$	$(v-1) V_2$	V_2	V_2/E_2
Error	$(r-1)(v-1)$	$(r-1)(v-1) E_2$	E_2	
Total	$rv-1$	$(rv-1) T_2$	T_2	

The analysis and computation will follow the same pattern of a randomized block design both in the ANOVA and ANCOVA tables. The part of the ANCOVA table between the above two characters may be written in following way.

Characters 1 x 2 ANCOVA

Source	df	SP	MSP
Replications	$r-1$	$(r-1) PR$	PR
Varieties	$v-1$	$(v-1) PV$	PV
Error	$(r-1)(v-1)$	$(r-1)(v-1) PE$	PE
Total	$rv-1$		PT

In the present analysis the degrees of freedom for replications is $(r-1) = 2$ and the varietal degrees of freedom $(v-1)$ of the dessert and culinary varieties were 55 and 29 respectively.

3.3. COMPUTATION OF CORRELATION COEFFICIENTS

The phenotypic, genotypic and environmental variance and covariance matrix (dispersion matrix) was constructed from the above analysis of variance and covariance tables.

i.e Taking expectations we will obtain the variances as

$$\left. \begin{aligned} E (K_1) &= \sigma e_1^2 \\ E (K_2) &= \sigma e_2^2 \\ \text{and } E (PE) &= \sigma e_1 e_2 \end{aligned} \right\} \dots (1)$$

where σe_1^2 and σe_2^2 are the environmental variances of the first and second character and $\sigma e_1 e_2$ is the environmental covariance between them.

The environmental correlation (r_e) between them will be equal to $r_e = \frac{\sigma e_1 e_2}{\sqrt{\sigma e_1^2 \times \sigma e_2^2}}$ and may be

estimated as $\frac{PE}{\sqrt{E_1 \times E_2}}$

Similarly if we take the expectation of mean squares due to varieties

$$\begin{aligned}
 E(V_1) &= r \sigma_{E_1}^2 + \sigma_{e_1}^2 \\
 E(V_2) &= r \sigma_{E_2}^2 + \sigma_{e_2}^2 \\
 \text{and } E(PV) &= r \sigma_{E_1 E_2} + \sigma_{e_1 e_2}
 \end{aligned}
 \quad \left. \vphantom{\begin{aligned} E(V_1) \\ E(V_2) \\ \text{and } E(PV) \end{aligned}} \right\} \dots(2)$$

Where $\sigma_{E_1}^2$ and $\sigma_{E_2}^2$ are the genotypic variances and $\sigma_{E_1 E_2}$ is the genotypic covariance between the two characters.

From the two sets of equations (1) and (2) the genotypic variances and covariances may be estimated as

$$\begin{aligned}
 \sigma_{E_1}^2 &= (V_1 - E_1)/r \\
 \sigma_{E_2}^2 &= (V_2 - E_2)/r \\
 \text{and } \sigma_{E_1 E_2} &= (PV - PE)/r
 \end{aligned}$$

∴ The genotypic correlation may now be obtained as

$$r_g = \frac{\sigma_{E_1 E_2}}{\sqrt{\sigma_{E_1}^2 \times \sigma_{E_2}^2}} \quad \text{and its estimate will be}$$

$$\frac{PV - PE}{\sqrt{(V_1 - E_1) \times (V_2 - E_2)}}$$

The phenotypic variance and covariance of each character will be the sum of the corresponding genotypic

and environmental variances and covariances, the expression for phenotypic correlations was

$$r_p = \frac{\sigma_{E_1 E_2} + \sigma_{e_1 e_2}}{\sqrt{(\sigma_{E_1}^2 + \sigma_{e_1}^2) \times (\sigma_{E_2}^2 + \sigma_{e_2}^2)}} \quad \text{and was}$$

estimated as
$$\frac{rV + (r-1)PE}{\sqrt{(V_1 + (r-1)E_1) \times (V_2 + (r-1)E_2)}}$$

3.4. HERITABILITY VALUES

Heritability in the broad sense is the ratio of the genotypic to the phenotypic variances

$$\text{i.e. } h^2 = \sigma_G^2 / \sigma_P^2$$

In practice the predicted value of h^2 will hold for several generations, even though it will valid, in theory for one generation. As it is clear from the definition, the h^2 value will lie between 0 and 1 and those characters having high heritability will have the h^2 value nearer to one.

3.5. ANALYSIS OF PATH COEFFICIENTS

The direct and indirect effect of various morphological characters on yield can be studied by path coefficient analysis. The genotypic correlation coefficient of the characters is used in the computation of path coefficients. The linear model assumed is of the form $Y = X_1 + X_2 + \dots + X_n + R$ where Y is the

yield, X_1, X_2, \dots, X_n are the morphological characters having significant influence on yield and R represents the residual effects caused by the remaining characters.

3.5.1. Selection of important characters

The genotypic correlation matrix was first computed by the formula discussed. Those characters having (statistically) insignificant correlations with yield were removed from further analysis. The linear model is assumed with regard to the characters having significant influence on yield and of course, the influence due to the other characters will come in the estimates of residual effects.

3.5.2. Computation of path coefficients

The path values were computed from the linear model $Y = X_1 + X_2 + \dots + X_n + R$. Taking correlations of the character X_1 with yield Y we get.

$$r_{X_1Y} = \frac{\text{Covariance } (X_1, Y)}{\sqrt{\text{Var } (X_1) \times \text{Var } (Y)}}$$

$$= \frac{\text{Cov } (X_1, X_1 + X_2 + \dots + X_n + R)}{\sqrt{\text{Var } (X_1) \times \text{Var } (Y)}}$$

$$= \frac{\text{Cov } (X_1, X_1) + \text{Cov } (X_1, X_2) + \dots + \text{Cov } (X_1, X_n) + \text{Cov}(X_1, R)}{\sqrt{\text{Var } (X_1) \times \text{Var } (Y)}}$$

Since X_1 and R were assumed to be independent the covariance and the correlation between them will be reduced to zero.

So the correlation between X_1 and Y can be written as

$$r_{x_1y} = \frac{\sigma_{X_1}}{\sigma_Y} + r_{x_1x_2} \frac{\sigma_{X_2}}{\sigma_Y} + \dots + r_{x_1x_n} \frac{\sigma_{X_n}}{\sigma_Y}$$

But according to the definition of path coefficients;

$$\frac{\sigma_{X_1}}{\sigma_Y} = P_{y.x_1} = P_1, \text{ the path coefficient of } X_1 \text{ to } Y$$

$$\frac{\sigma_{X_2}}{\sigma_Y} = P_{y.x_2} = P_2, \text{ the path coefficient of } X_2 \text{ to } Y$$

⋮

$$\frac{\sigma_{X_n}}{\sigma_Y} = P_{y.x_n} = P_n, \text{ the path coefficient of } X_n \text{ to } Y$$

$$\text{Thus } r_{x_1y} = P_1 + r_{x_1x_2}P_2 + \dots + r_{x_1x_n}P_n \quad (1)$$

Hence the correlation between X_1 and Y is partitioned into 'n' different components, viz. P_1 , the direct effect of X_1 on Y , and the (n-1) products of the form $r_{x_1x_i}P_i$ which estimates the indirect effects of X_1 to Y through the remaining (n-1) causes, X_i ($i = 2 \dots n$) .

Similarly the correlations of the remaining characters X_2, \dots, X_n with Y can be written as

$$r_{xy} = P_1 r_{x_1x_2} + P_2 + \dots + P_n r_{x_nx_2} \quad (2)$$

$$r_{xy} = P_1 r_{x_1x_3} + P_2 r_{x_2x_3} + \dots + P_n r_{x_nx_3} \quad (3)$$

⋮

$$r_{xy} = P_1 r_{x_1x_n} + P_2 r_{x_2x_n} + \dots + P_n \quad (n)$$

By matrix equations these n simultaneous equations could be represented as

$$\begin{bmatrix} r_{xy} \\ r_{xy} \\ \vdots \\ r_{xy} \end{bmatrix} = \begin{bmatrix} 1 & r_{x_1x_2} & \dots & r_{x_1x_n} \\ r_{x_2x_1} & 1 & \dots & r_{x_2x_n} \\ \vdots & \vdots & \ddots & \vdots \\ r_{x_nx_1} & r_{x_nx_2} & \dots & 1 \end{bmatrix} \times \begin{bmatrix} P_1 \\ P_2 \\ \vdots \\ P_n \end{bmatrix}$$

i.e. $A = B C$ (may) and the path values (vector C) could be obtained as $C = B^{-1} A$

3.5.3. Determination of residual effects

The residual effect will be estimated by considering the correlation of Y with Y itself. As in the case of the above 'n' simultaneous equations,

$r_{yy} = 1 = P_1 r_{x_1y} + P_2 r_{x_2y} + \dots + P_n r_{x_ny} + h^2$ where h will represent the residual effect.

Thus $h^2 = 1 - \sum P_i r_{x_iy}$ is used to determine the residual effects.

The model used above does not depend on any assumption of normality of the variables or on the nature of the correlations. Hence the correlation between any two variables which are not having any reciprocal interaction can be expressed as the sum of contributions pertaining to the paths by which one may trace from one to the other in the diagram without passing through any variable twice in the same path.

3.5.4. Direct and indirect effects

By multiplying the correlation matrix B by the path values the direct effects and the effects through the remaining characters (indirect effect) can be determined. A table of the direct and indirect effects may be constructed which will be useful for further selection.

3.6. DISCRIMINANT FUNCTIONS

With the help of a discriminant function, it would be possible to say whether a plant or the

pregny belongs to a high yielding or low yielding group (discrimination of good genotype). The problem involved in the discriminant function analysis is the construction of a function of the form

$Z = b_1 X_1 + b_2 X_2 + \dots + b_n X_n$ where X_1, X_2, \dots, X_n are the variables measured and b_1, b_2, \dots, b_n are the corresponding weights. Since the relative importance of the different characters (found to have significant correlation with yield) is not known in calculating the discriminant function all of them have given equal weights.

Smith's (1936) method of arriving at the discriminant function is the maximization of the correlation between genetic worth and phenotypic performance of the various characters.

i.e. $r(H, I)$ must be maximum, where the genetic worth $H = a_1 G_1 + a_2 G_2 + \dots + a_n G_n$; G_1, G_2, \dots, G_n are the genotypic values of individual characters and a_1, a_2, \dots, a_n where weight given according to their relative economic importance and the phenotypic performance I of the character is defined as $I = b_1 P_1 + b_2 P_2 + \dots + b_n P_n$ where b_1, b_2, \dots, b_n are the solutions to be obtained

to fit the desired function and P_1, P_2, \dots, P_n are the phenotypic values.

After maximising $F(H, I)$ the set of simultaneous equations obtained were of the form

$$b_1 t_{11} + b_2 t_{12} + \dots + b_n t_{1n} = a_1 G_{11} + a_2 G_{12} + \dots + a_n G_{1n}$$

$$b_1 t_{21} + b_2 t_{22} + \dots + b_n t_{2n} = a_1 G_{21} + a_2 G_{22} + \dots + a_n G_{2n}$$

⋮

$$b_1 t_{n1} + b_2 t_{n2} + \dots + b_n t_{nn} = a_1 G_{n1} + a_2 G_{n2} + \dots + a_n G_{nn}$$

where G_{ij} is the genotypic and t_{ij} is the phenotypic covariance between the i^{th} and j^{th} character.

But as the assigned values of a_j were same (equal to 1) the right hand side of the above set of equations would be simply the sum of the genotypic covariances of each character.

$$\text{So by matrix notation } bT = Ga = \sum_j G_{1j}$$

from which the b_j values may be solved out and the discriminant function Z could be fitted.

3.6.1. The genetic advance and genetic gain

The genetic advance or the expected improvement by selection was calculated from the expression of

$$\text{genetic worth, } H = a_1 G_1 + a_2 G_2 + \dots + a_n G_n$$

The genetic advance was defined as the expected value of the difference between the genetic worth and its mean i.e. $E (H - \bar{H})$.

When the intensity of selection is fixed at a certain per cent level say $q\%$ and if 'Z' is the ordinate of the normal probability curve at the $q\%$ intensity of selection then $E (H - \bar{H}) = \frac{Z}{q} Nv^{\frac{1}{2}}$ where Z is the regression coefficient of I on H and V is the variance of H.

The maximum value of the genetic advance is obtained when $Nv^{\frac{1}{2}}$ is maximised by using Lagrangean Multipliers, and the expression will be reduced to

$$Nv^{\frac{1}{2}} = \sqrt{\sum_i \sum_j a_j b_i c_{ij}}$$

This method of arriving at the genetic advance using a_j and b_i is called the genetic advance calculated through discriminant function. For the convenience of calculation it can be expressed as

$$GA = \frac{Z}{q} \sqrt{K \sum_i b_i A_i} \quad \text{where } A_i = \sum_j a_j c_{ij}$$

and K is a constant usually equal to 1

When $a_j = b_i$ the genetic advance through straight selection will be obtained as follows:

$$GA = \frac{Z}{q} \left(\sum_i \sum_j a_i a_j c_{ij} \right) / \sqrt{\sum_i a_i a_j c_{ij}}$$

The percentage genetic gain due to selection through discriminant function over straight selection can now be found as

$$\left\{ \frac{G A \text{ (through discriminant function)}}{G A \text{ (through straight selection)}} - 1 \right\} \times 100$$

This is also called as the per cent gain in efficiency by discriminant function compared to straight selection.

3.6.2. Selection indices for individual varieties

Based on the discriminant function values (b_1) index values can be determined for all of the individual varieties. By using these values the different varieties may be arranged on the order of their merit and it would be possible to select the best 5% or 10% and further breeding programmes can be made based on them.

The method of obtaining index values was suggested by Singh and Chaudhary (1977). For the 'n' varieties calculate the mean of the (three) replications corresponding each of the 'n' biometric characters. Then the index or score for the i^{th} variety V_i is estimated as the product $V_i = \sum X_{ij} b_j$ where ' b_j ' are the 'n' discriminant function values and X_{ij} is

the mean of the observation corresponding to the j^{th} character of the i^{th} variety.

The equation $V_i = \sum_j X_{ij} b_j$ can be conveniently illustrated by matrix notations as

$$\begin{bmatrix} V_1 \\ V_2 \\ \vdots \\ V_n \end{bmatrix} = \begin{bmatrix} X_{11} & X_{12} & \dots & X_{1n} \\ X_{21} & X_{22} & \dots & X_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ X_{n1} & X_{n2} & \dots & X_{nn} \end{bmatrix} \times \begin{bmatrix} b_1 \\ b_2 \\ \vdots \\ b_n \end{bmatrix}$$

3.7. RESTRICTED SELECTION

Kempthorne and Hering (1959) has indicated a method of studying the changes in the arithmetic means of 'r' out of 'n' characters while the remaining (n-r) is kept unchanged. As before the selection index in this case also is constructed by maximising the correlation between I and H (phenotypic performance and genetic worth) but subject to a condition that the genetic gain of the restricted character is zero. The derived expression for 'b₁' (selection indices) values in this case is

$$b = \left\{ I_{nn} - P^{-1}CC (C'G P^{-1}CC)^{-1} C'G \right\} P^{-1} Ca$$

where b is the vector of b_i values

I_{nn} is a unit $n \times n$ matrix

P is the phenotypic and G is the genotypic
dispersion matrix.

a is the vector of economic characters, as

in previous case this vector is $a = (1 \ 1 \ \dots \ 1)$

C is the coefficient matrix which depends on
the restricted characters i.e

In single restriction case,

Character 1, say X_1 only is restricted

$$C = (1 \ 0 \ \dots \ 0)$$

Character 2, say X_2 only is restricted

$$\text{then } C = (0 \ 1 \ 0 \ \dots \ 0)$$

If two characters X_1 and X_2 are restricted
simultaneously then

$$C = \begin{bmatrix} 1 & 0 & 0 & \dots & 0 \\ 0 & 1 & 0 & \dots & 0 \end{bmatrix} \text{ and so on.}$$

When C is chosen in this manner the genetic
advance of the restricted characters will reduce to
zero. (Obviously when there is no restriction, this
expression will be reduced to the previous form).

3.7.1. Genetic advance in restricted selection

When one character is restricted the genetic advance in the individual characters is obtained by the following formula.

Let the genetic advance of X_1 be A_1

$$\text{then } \begin{bmatrix} A_1 \\ A_2 \\ \vdots \\ A_n \end{bmatrix} = \begin{bmatrix} G_{11} & G_{12} & \dots & G_{1n} \\ G_{21} & G_{22} & \dots & G_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ G_{n1} & G_{n2} & \dots & G_{nn} \end{bmatrix} \times \begin{bmatrix} b_1 \\ b_2 \\ \vdots \\ b_n \end{bmatrix} \times \frac{1}{\sqrt{a'Gb}}$$

3.7.2. Rules regarding selection

The restricted selection can be applied only after analysing the behaviour of the morphological characters under study. The behaviour of these characters can be viewed by the path coefficient analysis, and correlation studies, which were already discussed.

1. When the total correlation and the direct effect are of the same sign and are of nearly equal magnitude then it can be assumed that the total

correlation is mainly explained by the direct effect and the rest indirect effects cancels each other. In such cases an individual selection is beneficial.

2. When the total correlation is positive and the direct effect is negative then simultaneous selection or individual selection without any restriction must be practiced. If we put any restriction the genetic gain will be reduced.

3. When total correlation is negative and the direct effect is positive then simultaneous selection with restriction on negatively contributed characters should be employed. If individual selection is made then the end result will be negative.

3.8. GENERAL SELECTION INDICES

(BY COMBINING BOTH DESSERT AND CULINARY VARIETIES)

The concept of combined selection indices was introduced by Hanson and Johnson (1957). These indices are specific to a particular population. The pooled information from all the varieties were used to obtain the ' b_1 ' values. These ' b_1 ' values were used to obtain correction factors for the phenotypic and genotypic variance and covariances of the characters and a new set of ' b_1 ' values could be developed.

The characters having significant influence on yield (measured by path analysis) in both dessert and culinary varieties were chosen in the construction of this index. Combining the observations two new phenotypic and genotypic matrices were constructed. As before, assuming the relation $P b = G a$, (P , pooled phenotypic matrix and G , the pooled genotypic matrix), the b_i values were solved out.

The corrected estimates of ' b_i ' values are obtained from the equation $\sum \sum b_i C_k P_{ijk} = \sum \sum a_i D_k G_{ijk}$ where P_{ijk} and G_{ijk} are the phenotypic and genotypic dispersion matrices of the i^{th} population, C_k and D_k are the correction factors of the phenotypic and genotypic covariances of each matrix respectively.

The C_k and D_k values are calculated as follows:

Define

$$A_{ik} = \sum_j a_j G_{ijk}$$

$$B_{ik} = \sum_j b_j P_{ijk}$$

$$\text{Then } C_i = V_i / (V_{pi})^{1/2} \quad \text{where } V_i = \sum b_i A_i$$

$$\text{and } D_i = 1 / (V_{pi})^{1/2} \quad V_{pi} = \sum b_i B_i$$

Estimation of corrected ' b_i ' values: Since we have two populations k takes values 1 and 2. The

corrected estimates of b say b' were calculated by the relation $Ab' = C$ or $b' = A^{-1}C$ and the matrices A and C were worked out as follows:

$$A = \begin{bmatrix} G_1 P_{111} + G_2 P_{112} & G_1 P_{121} + G_2 P_{122} & \dots & G_1 P_{1n1} + G_2 P_{1n2} \\ \vdots & \vdots & \ddots & \vdots \\ G_1 P_{n11} + G_2 P_{n12} & G_1 P_{n21} + G_2 P_{n22} & \dots & G_1 P_{nn1} + G_2 P_{nn2} \end{bmatrix}$$

$$C = \begin{bmatrix} R_1 \\ R_2 \\ \vdots \\ R_n \end{bmatrix}$$

where

$$R_1 = a_1 D_1(G_{111} + G_{121} + \dots + G_{1n1}) + a_2 D_2(G_{112} + G_{122} + \dots + G_{1n2})$$

$$R_2 = a_2 D_1(G_{211} + G_{221} + \dots + G_{2n1}) + a_2 D_2(G_{212} + G_{222} + \dots + G_{2n2})$$

\vdots

$$R_n = a_n D_1(G_{n11} + G_{n12} + \dots + G_{nn1}) + a_2 D_2(G_{n12} + G_{n22} + \dots + G_{nn2})$$

The general selection index may be written as $I = \sum h_1 X_1$. It's efficiency has been tested by Singh (1974) and found that they were as efficient as the specific indices, when they were used to select individuals from the populations tested. But they were not as efficient in selection from an outside set of varieties.



RESULTS

RESULTS

To get a general information on the morphological characters, the mean of these characters along with the standard error is presented in table 1. The mean values were higher in the culinary varieties in all characters except number of fingers and number of fingers per hand. The average per plant yield also is much higher (1.76 kg) in the culinary varieties.

The analysis of variance tables and part of the analysis of covariance tables were calculated (Appendix I & II). The varietal differences were highly significant among all characters in both dessert and culinary varieties. From the analysis of covariance tables the phenotypic, genotypic and environmental correlations were calculated (presented in tables 2 and 3). The environmental correlations were less than the phenotypic and genotypic correlations in many combinations. The genotypic and phenotypic correlations of all the characters with yield were positive. Number of fingers per hand had shown a negative environmental correlation (-0.0365) in dessert varieties. In culinary varieties number of leaves (-0.1104) and number of fingers per hand (-0.1236) had shown negative environmental correlations with yield.

The heritability values (in the broad sense) were given in table 4. Characters like height, weight of fingers, thickness of fingers, and number of fingers per hand and yield per plant were highly heritable in both the varieties.

4.1. PATH COEFFICIENT ANALYSIS

4.1.1. Dessert varieties

In the dessert varieties 9 characters were found to have significant genetic correlations with yield at the 95% and 99% probability levels. These characters were taken for the path coefficient analysis. The characters and the path coefficients were

Characters	Path coefficients
1. Girth	-0.1951
2. Number of leaves	0.1479
3. Weight of hands	1.2050
4. Weight of fingers	-0.5301
5. Number of fingers	1.0238
6. Thickness of fingers	0.2718
7. Number of hands	0.2865
8. Number of fingers per hand	0.4340
9. Length of peduncle	0.3097 and
Residual h	0.4317

Fig. 1 gives the cause and effect relationship of yield (effect) and the above 9 characters (causes). The direct and indirect effect of these causes can be read from table 5. From this table it can be observed that the character 'weight of hands' had a positive direct effect of 1.2050 with yield. But it had no significant indirect effect through any other character. The 'weight of fingers' had a direct negative effect of -0.5305 on yield. But it is having an indirect positive contribution 1.1227 through the third character, 'weight of hands'. This means that the 'weight of fingers' can influence the yield through the 'weight of hands'. Another character capable of producing appreciable variation in yield is the 'number of fingers' with a direct effect of 1.0256. But it makes no significant influences through any other character except a small negative effect through 'number of hands'. Thus to increase the yield there must be an increase in the fingers.

Even though the 'thickness of fingers' cannot produce any significant direct effect, with yield, it can produce an indirect influence (1.0052) through the 'weight of hands'. Thus the weight of hands contributes

positively through the 'thickness of fingers'. The remaining characters such as 'number of hands', 'number of fingers' per hand' and 'length of peduncle' were not having any worth mentioning effect on yield except an indirect effect 0.9695 produced on yield by the 'number of fingers' through the 'number of hands'.

4.1.2. Culinary varieties

From the correlation matrix of the culinary varieties the following characters were selected on the basis of the significance of their genotypic correlations with the yield. These characters were taken for the path coefficient analysis. The characters and the path coefficients were

Characters	Path coefficients
1. Plant height	-0.0668
2. Girth	0.2052
3. Number of fingers	2.2744
4. Number of hands	-1.4896
5. Number of fingers per hand	0.6606
6. Length of peduncle	0.3725 and
Residual h	0.6387

The diagram of the cause and effect relationship between the yield (cause) and the above six characters

(effects) is as shown in Fig. 2 . The table 6 of the direct (diagonal) and indirect (off diagonal) effects of yield components on yield can be used for assessing the relative importance of the various characters.

From this table it can be observed that the 'number of fingers' is having the maximum direct contribution (2.2744) towards the yield, meaning thereby that as more the number of fingers' the yield is on the increase. But if we watch the indirect effects through the 'number of fingers', the 'number of hands' is having a retarding effect (-1.4272). Thus more the number of hands less will be the 'number of fingers', thereby decreasing the yield.

Another significant character is the 'number of hands' which is having a negative direct effect of (-1.4836. Thus when the 'number of hands' is more, the total yield decreases. But among the characters which are having indirect effect through the 'number of hands', the 'number of fingers' had the maximum positive indirect effect (2.2033). This is in agreement with the previous result. Thus it can be interpreted as to get maximum yield the number of fingers' must be maximum.

The 'number of fingers per head' is having a negative direct effect (-0.6606) on yield. But the

indirect effect through the total 'number of fingers' is positive (1.9096) and the indirect effect through the 'number of hands' is negative (-1.0479). Hence it can be interpreted as the yield was increased when 'number of fingers' is increased and it decreased when the 'number of hands' increased. Thus when the 'number of hands' increases the 'number of fingers per hand' decreases, bringing down a decrease in yield.

The three other significant characters were 'plant height, girth and length of peduncle'. The plant height had practically no effect on yield. The girth and length of peduncle were having a direct effect of 0.2052 and 0.3725 respectively. The indirect effect of these characters on yield was also unimportant. Only the length of peduncle is having positive effect of 1.1646 through the 'number of fingers' on yield. These characters were not having any worth significant contribution to yield.

4.2. DISCRIMINANT FUNCTION AND GENETIC ADVANCE

4.2.1. Selection in Genetic Variation

Using the characters girth (X_1), number of leaves (X_2) weight of hands (X_3) weight of fingers (X_4) number of fingers (X_5) thickness of fingers (X_6) number of

hands (X_7) number of fingers per hand (X_8) length of peduncle (X_9) and yield per plant (X_{10}), the discriminant function was fitted. (These characters had significant correlation with yield).

The fitted discriminant function was

$$Z = 2.4012 X_1 - 4.13 X_2 - 0.6545 X_3 + 8.9878 X_4 - 2.2901 X_5 \\ + 56.1297 X_6 + 37.4433 X_7 + 34.4781 X_8 - 2.0017 X_9 \\ + 35.5615 X_{10}$$

At 5% level of intensity of selection, the genetic advance was found to be 1025.8025 (through discriminant function). But at the same intensity the genetic advance through straight selection was found to be 1163.7709.

From the genetic advances calculated by the above two methods, the latter was a little superior to the former (the percentage gain in efficiency of discriminant function was only -6.72%), indicating that it is enough to select the characters by straight selection itself.

4.2.2. Selection in culinary varieties

In the culinary varieties the characters height (X_1) girth (X_2) number of fingers (X_3) number of hands (X_4) number of fingers per hand (X_5) length of

peduncle (X_6) and yield (X_7) were used in the construction of the selection index.

The fitted discriminant function was

$$Z = -0.8369 X_1 + 3.8736 X_2 + 2.3405 X_3 - 23.0606 X_4 \\ - 11.3156 X_5 + 2.8362 X_6 - 6.8963 X_7$$

The genetic advance through discriminant function for an intensity of selection of 0.05 probability level was calculated and was equal to 164.9822. In order to assess its superiority over direct selection, the genetic advance through straight selection was also worked out, and comes out to be 179.7731, showing there by a slight superiority of straight selection. Hence, as in the previous case, it is reasonable to recommend straight selection than selection through discriminant function.

4.3 SELECTION INDICES

The b_i values obtained from the discriminant function analysis were used in the construction of selection indices. The best varieties are the ones which had maximum score.

The index scores obtained for each variety is given in table 7 and 8 in the decreasing order of the index values.

4.4. RESTRICTED SELECTION INDICES

From the path coefficient analysis for dessert varieties it has been seen that in characters like height, girth, weight of hands, number of fingers per hand and number of hands, the total correlation with yield is positive and at the same time the direct effect is negative. In the other morphological characters the direct effect as such explains the total correlation. Hence in the dessert varieties an individual selection is beneficial rather than any selection with restriction.

In the case of culinary varieties the number of hands had a negative direct effect whereas the total correlation is positive. The direct effect caused by height is practically zero. The other characters to a great extent explains the total correlation by the direct effect itself. However, the restricted selection was applied to 'girth' (X_2) which had a direct effect, one-third of the total correlation. The index fitted was

$$I = -0.4627 X_1 - 0.0740 X_2 + 0.1649 X_3 \\ + 5.4340 X_4 - 0.8051 X_5 + 2.9406 X_6 - 0.9918 X_7$$

where X_1, X_2, \dots, X_7 were the characters included in the discriminant function analysis.

The expected genetic advance by restricted selection was also worked out. As expected, there is no gain in genetic advance by restricting girth. The number of fingers had the highest genetic advance by this restriction. The magnitude of genetic advance of various characters are as given

Characters	Genetic advance
X_1	4.235
X_2	-1.228
X_3	86.484
X_4	4.983
X_5	2.369
X_6	40.988
X_7	2.128

4.9. THE COMBINED SELECTION INDEX

The most general selection index was constructed by combining all the dessert and culinary varieties. The characters included in the construction of this index were height, girth, number of fingers, number of hands, number of fingers per hand, length of peduncle and yield per plant.

The pooled phenotypic and genotypic variances, covariance matrix was constructed for these characters.

As in the case of the previous selection index the uncorrected set of index values 'b₁' for these varieties were obtained by solving the equations P b = G a, and the b values obtained were given below

Y ₁	0.9207
Y ₂	0.7300
Y ₃	0.8286
Y ₄	3.3246
Y ₅	1.625
Y ₆	0.925
Y ₇	0.7391

These uncorrected 'b₁' were used to obtain a new set of corrected 'b₁' values.

The general selection index obtained by using these b₁ values was $I = b_1 X_1 + b_2 X_2 + \dots + b_n X_n$

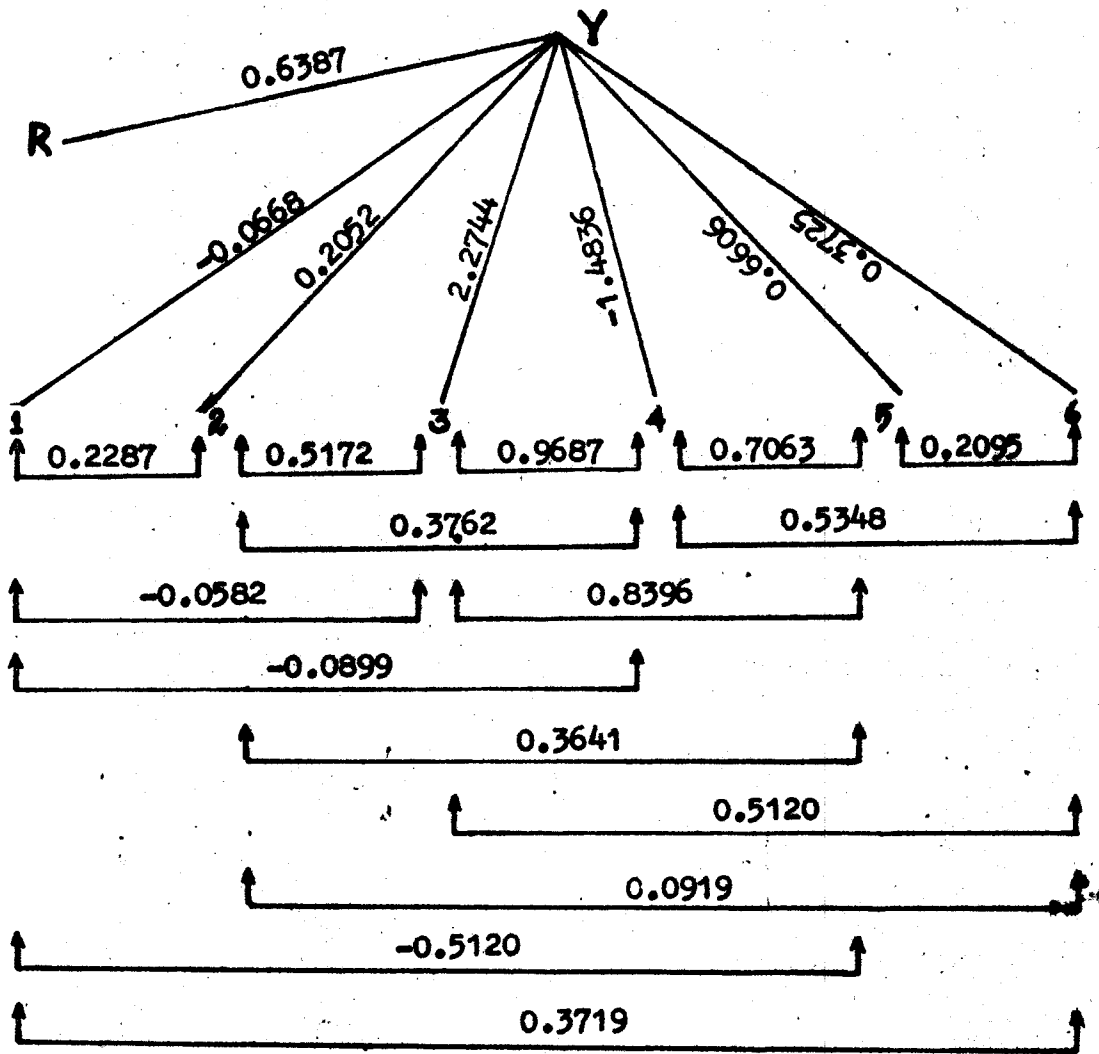
i.e $I = 1.5117 X_1 - 3.013 X_2 + 0.8427 X_3 + 1.4302 X_4 + 1.4954 X_5 - 0.0771 X_6 + 16.6048 X_7$

The expected genetic advance through the combined selection index also was worked out. At 5% intensity of selection it seems to be equal to 194,830, whose value was near to the genetic advances in the culinary varieties.

Table 1. Means along with standard errors of morphological characters in dessert and calisaya varieties of bananas

Sl. No.	Morphological characters	Dessert varieties	Calisaya varieties
1.	Height (cm)	262.369 \pm 4.194	301.111 \pm 3.483
2.	Girth (cm)	68.720 \pm 0.697	74.167 \pm 0.534
3.	Number of leaves	29.679 \pm 0.214	31.244 \pm 0.200
4.	Weight of hands (g)	1087.663 \pm 39.026	1232.492 \pm 53.448
5.	Weight of fingers (g)	78.914 \pm 2.933	100.762 \pm 5.002
6.	Number of fingers	119.123 \pm 3.481	114.833 \pm 6.081
7.	Length of fingers (cm)	14.063 \pm 0.239	14.334 \pm 0.327
8.	Thickness of fingers (cm)	10.242 \pm 0.148	12.495 \pm 0.484
9.	Number of hands	8.288 \pm 0.207	8.211 \pm 0.342
10.	Number of fingers per hand	14.276 \pm 0.176	13.844 \pm 1.499
11.	Length of peduncle (cm)	79.327 \pm 1.413	82.402 \pm 2.130
12.	Number of roots	226.444 \pm 4.862	227.844 \pm 5.088
13.	Yield per plant (kg)	10.161 \pm 0.283	11.191 \pm 0.367

Fig. 2 THE CAUSE AND EFFECTS RELATIONSHIP IN CULINARY VARIETIES



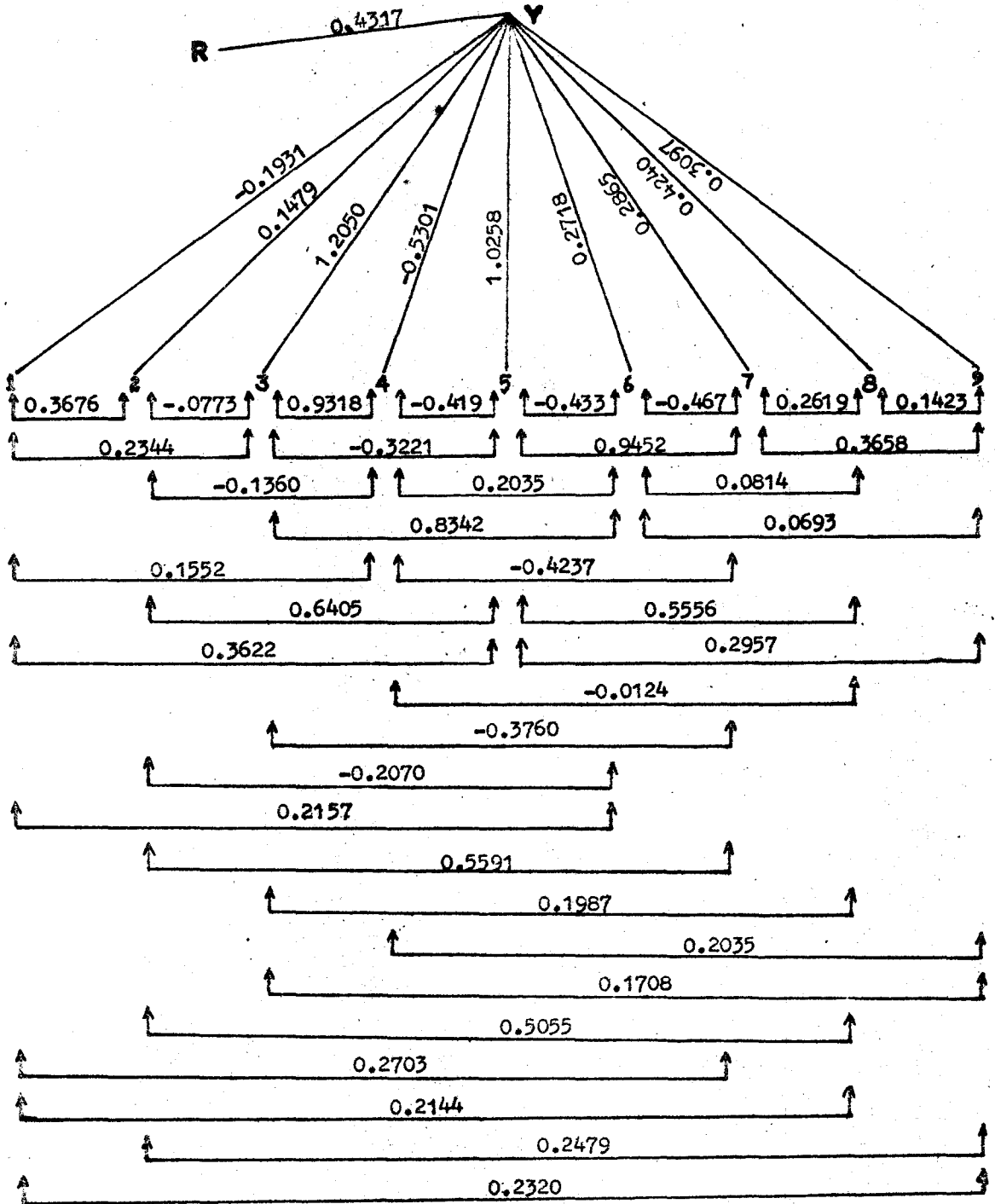
**DIAGRAM OF QUANT AND
EFFECT RELATIONSHIP**

CULINARY VARIETIES

Characters

- 1. Plant height**
- 2. Girth**
- 3. Number of fingers**
- 4. Number of heads**
- 5. Number of fingers
per head**
- 6. Length of peduncle and
individual h**

Fig. 1 THE CAUSE AND EFFECTS RELATIONSHIP IN DESSERT VARIETIES



**DIAGRAM OF CAUSE AND
EFFECT RELATIONSHIP**

DESSERT VARIETIES

Characters

1. Girth

2. Number of leaves

3. Weight of hands

4. Weight of fingers

5. Number of fingers

6. Thickness of fingers

7. Number of hands

**8. Number of fingers
per hand**

9. Length of peduncle and

Residual h

Table 4. The morphological characters and heritability values (Broad sense)

Sl. No.	Morphological characters	Desert varieties	Culinary varieties
1.	Height	0.9349	0.6559
2.	Girth	0.7424	0.3805
3.	Number of leaves	0.5800	0.5025
4.	Weight of hands	0.9870	0.9775
5.	Weight of fingers	0.9190	0.9287
6.	Number of fingers	0.8974	0.9849
7.	Length of fingers	0.9667	0.9877
8.	Thickness of fingers	0.9410	0.8590
9.	Number of hands	0.3632	0.4348
10.	Number of fingers per hand	0.9152	0.8590
11.	Length of peduncle	0.8726	0.9849
12.	Number of roots	..	0.8452
13.	Yield per plant	0.9328	0.9469

Table 6. Path coefficient analysis of yield in culinary varieties of banana

Characters	EFFECT THROUGH						Correlation with yield
	Height	Girth	Number of fingers	Number of hands	Number of fingers per hand	Length of peduncle	
Height	-0.0668	0.0469	-0.1323	0.1333	0.3383	0.1305	0.4079
Girth	-0.0132	0.2052	1.1764	-0.5382	-0.2405	0.0342	0.6018
Number of fingers	0.0039	0.1061	2.2744	-1.4370	-0.5247	0.1907	0.5833
Number of hands	0.0060	0.0772	2.2053	-1.4836	-0.4667	0.1992	0.5354
Number of fingers per hand	0.0342	0.0747	1.9096	-1.0479	0.3891	0.0780	0.3891
Length of peduncle	-0.0248	0.0168	1.1630	-0.7935	-0.1384	0.3725	0.5992

Table. 7 Index scores calculated to the dessert varieties

Sl. No.	Number of variety	Variety	Index values
1.	III (1)	Cheshadali	3905.9222
2.	III (2)	Red banana	3522.7911
3.	IV (6)	Wather	3455.8294
4.	V (20)	Radjiradj	3070.6095
5.	IV (9)	Gros michel	2987.1248
6.	II (6)	Ayiranta poovan	2883.3278
7.	IV (3)	Neelata	2637.4647
8.	II (2)	K N R 2/75	2597.8311
9.	IV (11)	Mouritas	2578.6420
10.	V (9)	Chirapuzhi	2563.3178
11.	V (16)	Chinalli	2556.4642
12.	IV (8)	High gate	2540.1158
13.	V (17)	Krishna veshai	2577.2673
14.	IV (13)	Prishabel	2537.0418
15.	IV (5)	G O	2531.6300
16.	I (2)	Poy banana	2466.3291
17.	V (18)	Sira	2419.2423
18.	IV (14)	Laatan	2343.1192
19.	V (13)	Nendra padathi	2332.1677
20.	IV (4)	Pedapasha Arathi	2328.4197
21.	IV (12)	DS	2315.2437
22.	V (3)	Pacha chingan	2310.3016

Sl. No.	Number of variety	Variety	Index Scores
23.	I (3)	Valiya kunnan	2264.3328
24.	IV (13)	Vernana keli	2249.3530
25.	V (13)	Redja	2231.1677
26.	I (4)	Kudapilla kunnan	2212.4117
27.	V (14)	Piriya	2211.4147
28.	II (7)	Poovan	2181.3618
29.	II (5)	Kjali poovan	2176.1866
30.	V (7)	Pacha nadan	2170.9613
31.	V (1)	Prohan	2133.1122
32.	II (1)	K N R 1/76	2117.8738
33.	V (19)	Viroopakshy	2113.2077
34.	V (12)	Lodjas finger	2100.1747
35.	I (1)	Neendra kunnan	2094.2332
36.	II (4)	Vadakkon kadali	2077.3729
37.	IV (2)	Aart sagar	2071.4806
38.	IV (7)	Harishal	2061.9707
39.	III (3)	Asbala kadali	2022.0883
40.	V (10)	Cherapadathi	2009.1154
41.	V (11)	Thiruvananthapuram	2003.6196
42.	II (4)	Teengate	1987.2314
43.	III (5)	Chokara kadali	1978.3737
44.	I (6)	Poocha kunnan	1925.2331

Sl.No.	Number of variety	Variety	Index values
45.	IV (10)	Sapumiahamsalu	1901.1067
46.	III (6)	Kanni kadali	1893.3965
47.	V (21)	Adukkan	1892.3430
48.	I (5)	Then kunnan	1891.1887
49.	V (8)	Sirumalai	1833.8472
50.	II (3)	Rasthali	1827.2975
51.	IV (1)	Mons marie	1789.7906
52.	V (2)	Maathman	1734.4195
53.	V (5)	Chingan	1668.1114
54.	V (4)	Sikugani	1530.1041
55.	I (7)	Adoka kunnan	1482.3459
56.	V (6)	Pilian	1281.4228

Table 8. Index scores calculated to the culinary varieties

Sl.No.	Number of variety	Variety	Index values
1.	11	Poy kanna	369.8479
2.	26	Valha	292.7515
3.	10	Pisangawak	257.6200
4.	1	Hallabekha	220.4529
5.	21	Ashybabkha	160.3663
6.	3	Jana	153.0936
7.	7	Bodi	147.4012
8.	4	Hyleneid Sewai	120.0772
9.	17	Sambhani Nonbhan	109.5643
10.	8	Kumbhani	104.7319
11.	29	Vanna	103.1346
12.	14	Baina	100.7719
13.	24	Ashenbhan	98.7974
14.	5	Couria	92.5401
15.	2	Kangani Bayan	91.7367
16.	12	Neymannan	91.5654
17.	13	Alubhal	90.9500
18.	25	Kapur	88.5664
19.	6	Krachi Vashai	80.0808
20.	18	Hallabantha	79.2298
21.	20	Kandrikola	74.0716

Sl.No.	Number of variety	Variety	Index values
22.	28	Kay vanna	58.5080
23.	27	Gatty	55.5875
24.	15	Kingoo	54.3330
25.	9	Sawai	53.0961
26.	30	Kanna	40.5867
27.	22	Pachabanthabathosa	39.9705
28.	16	Kali ^a nathan	32.2522
29.	19	Kanhan	25.3942
30.	23	Karibatha	20.0199

DISCUSSION

D I S C U S S I O N

In the present study data on 12 characters of the 56 dessert varieties and 13 characters of the 39 culinary varieties were taken. From the table (1) of means and standard errors of these two groups, it was found that the mean values were more or less higher in the culinary varieties in most of the characters. The average yield obtained from culinary varieties was also little more than that of the dessert varieties.

The analysis made in the present study were based on different methods and formulae obtained from different statistical publications. Even though a number of papers were available in literature dealing with the path coefficient and discriminant function analysis, they were usually done in the cereals or vegetable crops. Thus it became difficult to compare the present results with any other work previously done, as the results of the vegetable crops were certainly vary from that of human plants.

The analysis of variance tables for all the characters were worked out (Appendix 1 & 2) in both the groups. It was found that all the characters were highly significant in both type of varieties.

51. STUDIES ON THE DESSERT VARIETIES

In the dessert varieties 9 characters, girth, number of leaves, weight of hands, weight of fingers, number of fingers, thickness of fingers, number of hands, number of fingers per hand and length of peduncle were found to have significant genetic correlations with yield. Hence, they were selected for the study of path coefficient analysis. A diagram of cause and effect relationship for these characters was also drawn (Fig. 1).

From the table of path coefficient analysis on dessert banana varieties (table 5), the direct (diagonal) and indirect (off diagonal) effects and the correlation with yield of the different selected characters was found and it has been seen that the weight of hands had a positive direct effect with yield. But it had no significant indirect effect through any other character. The weight of fingers had a direct negative effect on yield. But it was having an indirect positive effect through the weight of hands. This may be explained as that the weight of fingers can influence the yield through the weight of hands. Another character capable of producing significant variation in yield was the number of fingers. Hence, we can reasonably believe that

the increase of fingers will result in the increase of yield. The thickness of fingers was unable to produce any significant direct effect. But it could produce an indirect influence on yield through the weight of hands. Hence, the weight of hands could increase the yield through the thickness of the fingers also. All the other characters such as number of hands, number of fingers per hand, and length of peduncle were not having any worth mentioning effect on yield.

In the second stage of study on the dessert type varieties of banana a discriminant function was fitted, for the contributing characters girth, number of leaves, weight of hands, weight of fingers, number of fingers, thickness of fingers, number of hands, number of fingers per hand, length of peduncle and yield. The genetic advances through discriminant function and through straight selection were found. Comparing these two genetic advances, it was seen that straight selection is slightly superior than that of the discriminant function. Hence in the dessert varieties it is enough to adopt the direct selection.

As a third step of study selection indices for all the 56 varieties were worked out. The best 5

selected on the basis of their performance were (selected on the basis of the index scores given in table 7) (1) Chankadali, (2) Red Banana, (3) Wether, (4) Rajjiradi and (5) Greenishel and last five with feeble performance were (1) Pillan, (2) Adika Kunnan, (3) Simpani, (4) Chingan and (5) Harthman.

Another result that has been obtained from the path coefficient analysis and rules regarding selection is that in the dessert varieties there is no necessity to adopt a restricted selection.

5.2. STUDIES ON THE CULINARY VARIETIES

Only the six characters plant height, girth, number of fingers, number of hands, number of fingers per hand and length of peduncle have got significant genetic correlation with yield and these six characters were included in the path coefficient analysis. As in the previous case the diagram (Fig. 2) of the cause and effect relationship was drawn and indirect effects of each the characters through others was determined.

In the dessert varieties, 'the weight of hands' had the maximum influence on yield but in culinary varieties the character for maximum yield is number of fingers, by its highest direct effect. But this

character had a retarding influence on yield through the number of hands. Thus the increase in the number of hands can decrease the number of fingers, and the yield. (The direct effect through number of hands is also negative). However, it had a very high positive indirect effect through number of fingers. Another important character is number of fingers per hand which is also had a weak negative direct effect, but this character also produces a high indirect effect through the number of fingers. Thus to get maximum yield the number of fingers must be maximum. The other characters height, girth and length of peduncle had a minor direct effect to yield except in the case of peduncle which had an appreciable indirect effect through the number of fingers.

For the computation of discriminant function also the above six characters and yield were chosen. The genetic advance was calculated at 5% intensity of selection but as in the previous case its value was slightly less than the genetic advance through straight selection. Hence, in the culinary varieties also it is enough to adopt direct selection.

The individual selection scores were calculated for 30 culinary varieties. The best 3 among them

depending on their performance was (1) Poy Kuman, (2) Valha, (3) Pisingmak, (4) Nolla bontha and (5) Ashyabhusa and the worst among them were (1) Karibontha, (2) Nankhan, (3) Malai Nonthan, (4) Pachabonthabhosaa (5) Namman.

The restricted selection index was also fitted by putting restriction on the character 'girth' with the restriction that it's genetic advance is zero. Then genetic advances of these characters after restriction was found and it showed that there was maximum genetic advances for number of fingers followed by number of fingers per hand and number of hands.

5.3. COMBINED SELECTION INDEX

The dessert and culinary varieties were used as the two populations for the construction of this index. Since, the characters were selected by considering their effect in influencing the yield of both the groups simultaneously, it became necessary to omit the weight of hands and weight of fingers which were important in the case of dessert bananas. The genetic advance calculated through this index in this case also was very near to the genetic advance of the culinary varieties.

SUMMARY

S U M M A R Y

The present study has been undertaken with a view to analyse the effect of different morphological characters on yield in dessert and culinary varieties of bananas.

The plants grown in the University Banana Research Farm, Kannara were used for the study. The data were collected from 26 dessert and 30 culinary varieties. Measurements on 12 biometric characters viz. height, girth, number of leaves, weight of hands, weight of fingers, number of fingers, length of fingers, thickness of fingers, number of hands, number of fingers per hand, length of peduncle and yield were taken for the analysis. Data on another character 'number of roots' also was used in culinary varieties but it has been seen that this character had a very weak correlation with yield and thus it was omitted from the analysis made later.

In the preliminary study of morphological characters the 'mean' values of all the characters were calculated and found that they were more or less high in the culinary varieties, except in the case of number of fingers and number of fingers per hand. The yield also is higher by about 1.8 kg in culinary varieties. All the characters were found to have significant

varieties among varieties also. The phenotypic and genotypic correlations of the characters have shown that in the dessert varieties all the characters had positive genotypic and phenotypic correlation with yield, and only number of fingers per hand had a negative environmental correlation (which is very near to zero). In the culinary varieties also number of fingers per hand and number of leaves were shown negative environmental correlation but at the same time all of them have shown positive genotypic and phenotypic correlation with yield.

The path coefficient analysis in the dessert varieties has shown that 'weight of hands' is the character having maximum direct influence on yield. The weight of fingers also indirectly affects the yield through 'weight of hands'. The number of fingers also influences the yield directly, but it had no indirect effect through any other characters.

In the culinary varieties 'the number of fingers' is the character having maximum direct contribution to yield. But it had a high retarding influence through the number of hands. Moreover, the number of hands had a direct negative effect on yield

and at the same time an indirect positive effect through number of fingers. The number of fingers also had an indirect positive effect through the number of hands. An appreciable indirect effect can be noticed through the number of fingers, made by the length of the peduncle. It can be concluded that when the number of hands increases the number of fingers per hand decreases and hence it will bring down the yield.

The discriminant function was fitted for both the varieties. The characters for discriminant analysis were selected based on the significance of their genotypic correlation with yield. In dessert varieties girth, number of leaves, weight of hands, weight of fingers, number of fingers, thickness of fingers, number of hands, number of fingers per hand, length of peduncle and yield were used. In culinary varieties, height, girth, number of fingers, number of hands, number of fingers per hand, length of peduncle and yield were used in the construction of discriminant functions.

The genetic advances through discriminant function and through straight selection methods were also found in both the varieties. It has been seen that,

the genetic advance in the latter case is slightly superior to former indicating that it is enough we select the characters by straight selection itself for selections in both dessert and culinary varieties.

Index values were fitted for all the varieties taken for study. This indices can be used to select the best or worst varieties from among the different varieties.

Another result obtained is that in the dessert varieties there is no need to apply any restricted selection and an individual selection is beneficial. However, in the culinary varieties the genetic advance for the characters was calculated after applying restriction for girth. The character 'number of fingers' has got the maximum genetic advance.

A most general index also has been worked out by selecting those character significantly influencing the yield in both the type of bananas. The genetic advance of this combined selection index also was worked out. These indices and the path coefficients will give guide lines to select characters, which are of more contributing nature to yield.

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* Originals not referred.

**Appendix 1. Analysis of variance and covariances
in desert varieties.**

Analysis of variance tables

Source	df	Nos of characters		
		Height	Girth	Number of leaves
		(1)	(2)	(3)
Replications	2	995.2301	35.5236	3.375
Varieties	55	8549.4628**	204.4215**	16.2622**
Error	110	193.929	21.1965	3.2780

Source	df	Nos of characters		
		Weight of buds	Weight of fingers	Number of fingers
		(4)	(5)	(6)
Replications	2	3269.4079	132.3059	15.8750
Varieties	55	770116.1226**	4147.3949**	3904.6874**
Error	110	3372.1114	118.4618	132.4992

Source	df	Nos of characters		
		Length of fingers (7)	Thickness of fingers (8)	Number of hands (9)
Replications	2	0.6572	0.0574	0.3531
Varieties	55	22.8220 ^{**}	10.9735 ^{**}	21.2917 ^{**}
Error	110	0.0558	0.1245	0.4338

Source	df	Nos of characters		
		Number of fingers per hand (10)	Length of pedicels (11)	Yield per plant (12)
Replications	2	0.3535	22.2222	2.9422
Varieties	55	9.2234 ^{**}	222.2224 ^{**}	27.2224 ^{**}
Error	110	3.4021	22.7222	1.7222

Analysis of covariance tables

Source	df	Map of height with		
		Girth (2)	Number of leaves (3)	Weight of heads (4)
Replications	2	40.3330	-3.6429	-590.2352
Varieties	55	905.5134	170.7745	11002.0435
Error	110	13.9000	7.9965	49.0014

Source	df	Map of height with		
		Weight of fingers (5)	Number of fingers (6)	Length of fingers (7)
Replications	2	272.4607	121.0929	-1.7667
Varieties	55	204.6904	2023.2200	-305.9723
Error	110	17.4974	0.0007	-0.0691

Source	df	Map of height with		
		Thickness of fingers (8)	Number of heads (9)	Number of fingers per head (10)
Replications	2	-6.7302	-14.3590	8.0204
Varieties	55	36.0021	137.7409	113.1724
Error	110	-0.0335	0.2370	-1.1741

Source	df	Map of height with	
		Length of peduncle (11)	Yield per plant (12)
Replications	2	141.9040	-33.0631
Varieties	55	820.1279	159.0667
Error	110	0.5623	0.9942

Source	df	Map of girth with		
		Number of leaves (3)	Weight of hands (4)	Weight of fingers (5)
Replications	2	-10.8214	-338.2726	-33.2964
Varieties	55	19.9496	2017.9900	136.1328
Error	110	1.6119	39.6756	2.7781

Source	df	Map of girth with		
		Number of fingers (6)	Length of fingers (7)	Thickness of fingers (8)
Replications	2	-0.8214	-4.7798	-1.4548
Varieties	55	373.7795	-82.6018	9.8926
Error	110	3.4625	0.1584	0.2780

Source	df	Map of girth with	
		Number of hands (9)	Number of fingers per hand (10)
Replications	2	-2.8809	3.4548
Varieties	55	17.2382	17.6057
Error	110	0.5857	-0.2735

Source	df	Map of girth with	
		Length of peduncle (11)	Yield per plant (12)
Replications	2	4.7738	-6.9905
Varieties	55	28.5040	32.4591
Error	110	2.6738	0.5519

Source	df	Map of number of leaves with		
		Weight of hands (4)	Weight of fingers (5)	Number of fingers (6)
Replications	2	101.1000	12.9616	1.3661
Varieties	55	-236.4896	-29.9763	176.3106
Error	110	13.0821	2.2331	-2.9279

Source	df	Map of number of leaves with		
		Length of fingers (7)	Thickness of fingers (8)	Number of hands (9)
Replications	2	1.4895	0.3964	0.7768
Varieties	55	-7.0374	-2.6245	9.4591
Error	110	-0.0519	-0.1118	0.0425

Source	df	Map of number of leaves with		
		Number of fingers per hand (10)	Length of peduncle (11)	Yield per plant (12)
Replications	2	-1.0132	-0.2143	1.8830
Varieties	55	4.5748	26.6457	8.3966
Error	110	-0.1179	-1.2324	0.5049

Source	df	Map of weight of hands with		
		Weight of fingers (5)	Number of fingers (6)	Length of fingers (7)
Replications	2	247.2042	-19.8530	44.6908
Varieties	55	52180.1189	-21261.7025	2926.9670
Error	110	390.9501	153.9597	7.8535

Map of weight of hands with				
Source	df	Thickness of fingers (8)	Number of hands (9)	Number of fingers per hand (10)
Replications	2	15.0110	29.9324	-53.2203
Varieties	95	2412.4540	-1496.6068	423.1763
Error	110	6.3872	7.0300	5.4720

Map of weight of hands with			
Source	df	Length of peduncle (11)	Yield per plant (12)
Replications	2	-76.1887	72.6739
Varieties	95	4700.0921	3322.9940
Error	110	137.6085	56.2275

Map of weight of fingers with				
Source	df	Number of fingers (6)	Length of fingers (7)	Thickness of fingers (8)
Replications	2	40.2232	5.6737	-0.3138
Varieties	95	-2009.2794	233.2237	183.1876
Error	110	9.9193	0.9623	0.7086

Map of weight of fingers with			
Source	df	Number of hands (9)	Number of fingers per hand (10)
Replications	2	-0.9188	1.9019
Varieties	55	-122.2049	-1.4167
Error	110	0.5300	0.4742

Map of weight of fingers with			
Source	df	Length of peduncle (11)	Yield per plant (12)
Replications	2	40.0530	-2.2937
Varieties	55	411.4360	212.2853
Error	110	17.2097	7.9077

Map of number of fingers with				
Source	df	Length of fingers (7)	Thickness of fingers (8)	Number of hands (9)
Replications	2	0.5830	-0.6304	-1.3661
Varieties	55	-229.4520	-108.2220	331.0417
Error	110	1.9033	0.1336	3.2915

Source	df	Map of number of fingers with		
		Number of fingers per hand (10)	Length of peduncle (11)	Yield per plant (12)
Replications	2	0.4491	17.5089	-3.3402
Varieties	55	104.1844	708.2992	161.8517
Error	110	2.4092	23.1423	2.4290

Source	df	Map of length of fingers with		
		Thickness of fingers (8)	Number of hands (9)	Number of fingers per hand (10)
Replications	2	0.1750	0.5449	-0.4491
Varieties	55	10.7809	-12.3885	-3.2825
Error	110	0.0405	0.0813	0.0382

Source	df	Map of length of fingers with	
		Length of peduncle (11)	Yield per plant (12)
Replications	2	-0.1173	0.2362
Varieties	55	11.3590	7.2387
Error	110	0.2084	0.2402

Map of Thickness of fingers with			
Source	df	Number of hands (9)	Number of fingers per hand (10)
Replications	2	0.1788	-0.1636
Varieties	55	-6.9938	0.6500
Error	110	0.0340	0.0111

Map of thickness of fingers with			
Source	df	Length of peduncle (11)	Yield per plant (12)
Replications	2	-0.9333	0.4329
Varieties	55	7.3359	8.4478
Error	110	0.3691	0.2192

Map of number of hands with				
Source	df	Number of fingers per hand (10)	Length of peduncle (11)	Yield per plant (12)
Replications	2	-0.3300	-1.9792	0.8853
Varieties	55	2.3708	52.0885	9.9792
Error	110	-0.5146	1.0956	0.1639

Source	df	Map of number of fingers per hand with	
		Length of peduncle (11)	Yield per plant (12)
Replications	2	1.0521	-0.7967
Varieties	55	10.7225	5.9041
Error	110	0.2433	-0.0887

Source	df	Map of length of peduncle with	
		Yield per plant (12)	
Replications	2	-4.2307	
Varieties	55	103.9084	
Error	110	2.5257	

* Significant at 5% level

** Significant at 1% level

**Appendix 2. Analysis of variances and covariances
in culinary varieties**

Analysis of variance table

Source	df	Nos of characters		
		Height	Girth	Number of leaves
		(1)	(2)	(3)
Replications	2	1178.4110	42.2333	0.9111
Varieties	29	2519.4799 ^{**}	42.9402 ^{**}	7.3008 ^{**}
Error	58	374.9860	16.9113	1.8111

Source	df	Nos of characters		
		Weight of heads	Weight of fingers	Number of fingers
		(4)	(5)	(6)
Replications	2	1632.1818	34.2172	290.4330
Varieties	29	787609.4249 ^{**}	6004.2243 ^{**}	9294.2012 ^{**}
Error	58	655.0675	9.0009	100.4103

Source	df	Nos of Characters		
		Length of Fingers (7)	Thickness of Fingers (8)	Number of hands (9)
Replications	2	0.2819	0.8105	4.0440
Varieties	29	29.1062 ^{**}	49.1330 ^{**}	28.9877 ^{**}
Error	58	0.1400	0.2008	1.4996

Source	df	Nos of characters	
		Number of fingers per hand (10)	Length of peduncle (11)
Replications	2	0.6839	17.8068
Varieties	29	16.0432 ^{**}	1244.3571 ^{**}
Error	58	4.8506	4.0648

Source	df	Nos of characters	
		Number of roots (12)	Yield per plants (13)
Replications	2	99.4778	6.3688
Varieties	29	7070.5686 ^{**}	33.0735 ^{**}
Error	58	36.2479	1.9044

Analysis of covariance tables

Map of height with

Source	df	Girth (2)	Number of leaves (3)	Weight of hands (4)
Replications	2	271.5230	0.9510	92.2596
Varieties	29	86.4940	-38.2777	19348.2006
Error	58	27.3940	0.7540	43.5022

Map of height with

Source	df	Weight of fingers (5)	Number of fingers (6)	Length of fingers (7)
Replications	2	-15.5522	-574.4030	-5.0596
Varieties	29	1204.2255	-222.2019	43.4942
Error	58	1.0602	-23.4091	1.0734

Map of height with

Source	df	Thickness of fingers (8)	Number of hands (9)	Number of fingers per hand (10)
Replications	2	-14.6208	-64.9000	-23.5206
Varieties	29	120.9266	-23.2546	-22.9122
Error	58	0.7395	-2.0222	-1.9222

Map of height with				
Source	df	Length of peduncle (11)	Number of roots (12)	Yield per plant (13)
Replications	2	7.8538	145.6778	-24.5126
Varieties	29	616.1054	1264.2031	120.8682
Error	58	9.5539	4.7812	2.7486

Map of girth with				
Source	df	Number of leaves (3)	Weight of hands (4)	Weight of fingers (5)
Replications	2	-0.1667	99.7108	9.2215
Varieties	29	8.7241	-429.8410	-70.9771
Error	58	1.0985	-19.7665	1.0961

Map of girth with				
Source	df	Number of fingers (6)	Length of fingers (7)	Thickness of fingers (8)
Replications	2	-40.2700	0.1343	-0.9930
Varieties	29	273.8790	-19.7270	-5.1933
Error	58	-9.6632	-0.0988	0.1116

Source	df	Map of girth with		
		Number of hands (9)	Number of fingers per hand (10)	Length of palmole (11)
Replications	2	-9.1330	-3.2178	10.0900
Varieties	29	10.7069	6.2547	18.9351
Error	58	-0.2028	-0.5413	0.8677

Source	df	Map of girth with	
		Number of roots (12)	Yield per plant (13)
Replications	2	44.7300	0.3050
Varieties	29	25.8621	18.9120
Error	58	0.0316	0.1637

Source	df	Map of number of leaves with		
		Weight of hands (4)	Weight of fingers (5)	Number of fingers (6)
Replications	2	-34.0309	-5.1452	-14.1333
Varieties	29	-718.4891	-80.4666	83.8276
Error	58	1.5653	-0.0497	0.6540

Source	df	Map of number of leaves with		
		Length of fingers (7)	Thickness of fingers (8)	Number of buds (9)
Replications	2	-0.4781	-0.7948	-1.4009
Varieties	29	-6.1606	-6.7879	4.7884
Error	58	-0.0501	0.0054	-0.2475

Source	df	Map of number of leaves with	
		Number of fingers per hand (10)	Length of peduncle (11)
Replications	2	-0.5835	-3.5722
Varieties	29	2.1150	2.5900
Error	58	0.4378	-0.0577

Source	df	Map of number of leaves with	
		Number of roots (12)	Yield per plant (13)
Replications	2	-6.6722	-2.3728
Varieties	29	-38.3762	3.4041
Error	58	-0.9133	-0.2050

Map of weight of hands with				
Source	df	Weight of Fingers (5)	Number of Fingers (6)	Length of Fingers (7)
Replications	2	233.8591	498.2655	20.1436
Varieties	29	62853.8486	-47078.2452	2786.1584
Error	58	46.3329	118.5916	4.4664

Map of weight of hands with				
Source	df	Thickness of fingers (8)	Number of hands (9)	Number of fingers per hand (10)
Replications	2	30.8130	41.7432	17.1583
Varieties	29	4842.3941	-2660.8280	-1308.7959
Error	58	7.2883	7.2818	-4.2773

Map of weight of hands with				
Source	df	Length of peduncle (11)	Number of roots (12)	Yield per plant (13)
Replications	2	170.4673	373.3142	95.6382
Varieties	29	-2080.5948	10946.6898	383.6735
Error	58	16.0462	12.6112	23.4236

Map of weight of fingers with				
Source	df	Number of fingers (6)	Length of fingers (7)	Thickness of fingers (8)
Replications	2	81.3005	3.0398	4.8178
Varieties	29	-4791.0684	346.7302	504.7069
Error	58	15.3049	0.6645	0.8331

Map of weight of fingers with				
Source	df	Number of hands (9)	Number of fingers per hand (10)	Length of peduncle (11)
Replications	2	7.6183	3.0563	24.4780
Varieties	29	-238.1951	-177.6480	5.2349
Error	58	0.8839	0.3048	2.8379

Map of weight of fingers with			
Source	df	Number of roots (12)	Yield per plant (13)
Replications	2	50.7168	14.4480
Varieties	29	686.1418	94.3383
Error	58	4.6033	2.9319

Source	df	Map of number of fingers with		
		Length of fingers (7)	Thickness of fingers (8)	Number of hands (9)
Replications	2	8.2940	15.0917	35.6000
Varieties	29	-386.1535	-414.9067	508.3506
Error	58	2.0569	1.4886	10.0655

Source	df	Map of number of fingers with	
		Number of fingers per hand (10)	Length of peduncle (11)
Replications	2	13.5838	52.6733
Varieties	29	275.9578	1701.6351
Error	58	-0.0519	9.8320

Source	df	Map of number of fingers with	
		Number of roots (12)	Yield per plant (13)
Replications	2	71.8833	39.4817
Varieties	29	612.6735	329.1040
Error	58	5.6822	9.0863

Map of length of fingers with				
Source	df	Thickness of fingers (8)	Number of hands (9)	Number of fingers per hand (10)
Replications	2	0.4675	0.8695	0.3412
Varieties	29	26.2609	-17.8331	-10.2828
Error	58	0.0941	0.1094	0.2070

Map of length of fingers with				
Source	df	Length of peduncle (11)	Number of roots (12)	Yield per plant (13)
Replications	2	2.1137	3.9701	1.3597
Varieties	29	-4.9037	-49.8824	-2.3884
Error	58	0.2115	0.6276	0.2559

Map of thickness of fingers with				
Source	df	Number of hands (9)	Number of fingers per hand (10)	Length of peduncle (11)
Replications	2	1.7175	0.6633	3.2439
Varieties	29	-21.3970	-16.4533	-22.3665
Error	58	0.1293	0.1101	0.3380

Source	df	Map of thickness of fingers with	
		Number of roots (12)	Yield per plant (13)
Replications	2	3.3492	2.2238
Varieties	29	24.7751	0.4079
Error	56	0.6651	0.3568

Source	df	Map of number of hands with	
		Number of fingers per hand (10)	Length of peduncle (11)
Replications	2	1.8179	4.4646
Varieties	29	11.2721	99.2774
Error	56	-1.0987	0.6725

Source	df	Map of number of hands with	
		Number of roots (12)	Yield per plant (13)
Replications	2	2.5444	4.1456
Varieties	29	28.1709	16.4577
Error	56	1.2745	0.8065

Source	df	Map of number of fingers per hand with		
		Length of peduncle (11)	Number of roots (12)	Yield per plant (13)
Replications	2	1.8305	1.3697	1.6280
Varieties	29	24.2988	-38.4772	6.8733
Error	58	-0.3814	-1.1390	-0.3736

Source	df	Map of Length of peduncle with	
		Number of roots (12)	Yield per plant (13)
Replications	2	39.0028	10.0397
Varieties	29	-365.8339	118.9717
Error	58	1.2385	1.1384

Source	df	Map of number of roots with
		Yield per plant (13)
Replications	2	18.8172
Varieties	29	74.0459
Error	58	2.3414

**A COMPARATIVE STUDY OF THE
CONTRIBUTION OF BIOMETRIC CHARACTERS
ON YIELD IN
DESSERT AND CULINARY
VARIETIES OF BANANA**

**BY
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ABSTRACT OF A THESIS

Submitted in partial fulfilment of the
requirements for the degree of

Master of Science (Agricultural Statistics)

Faculty of Agriculture

Kerala Agricultural University

Department of Statistics

COLLEGE OF VETERINARY & ANIMAL SCIENCES

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ABSTRACT

Investigations on the different morphological characters were undertaken from the crop raised at the University Banana Research Farm, Kanara. The plants were grown in randomized blocks of 3 replications. There were 50 varieties in dessert type and 50 in culinary varieties of bananas.

The important morphological characters studied were height, girth, number of leaves, weight of hands, weight of fingers, number of fingers, length of fingers, thickness of fingers, number of hands, number of fingers per hand, length of peduncle and the yield.

In both of the groups all of these characters were shown high significant difference among varieties. In many characters and in yield the 'average values' were slightly greater in culinary varieties.

The correlation studies revealed that the phenotypic and genotypic correlations of all these characters with yield is positive. The path coefficient analysis on dessert varieties has shown that the character having maximum contribution to yield is weight of hands. The weight of fingers and number of fingers also influences the yield indirectly.

In the case of culinary varieties of bananas the number of fingers had the maximum direct contribution to yield. In this group the conclusion made was that when the number of hands increases, the number of fingers per hand decreases which will bring down the yield.

Studies on the discriminant function were also carried out in both the varieties. The genetic advance through discriminant function didn't reveal any worth significance as the genetic advances through these functions were less than that calculated by straight selection (in both groups). Thus straight selection is enough for such purposes in these banana varieties.

By fixing index values for all the varieties in the two groups selection was made easy. The best varieties obtained by this method were Chakradali and Red Banana in dessert group and Puykunnan and Walha in the culinary varieties.

The results from the path analysis has revealed that there is no need of putting any restriction on the dessert varieties. In the other group after putting restriction on 'girth' the genetic advance were calculated individually for the significant (the ones taken in this analysis) morphological characters.

It has been seen that 'number of fingers' had the maximum genetic advance.

Finally by combining all the varieties in the dessert and culinary groups a combined selection index was also fitted. The genetic advance of this index was found to be nearer to that obtained from the analysis of culinary varieties.

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