STUDIES ON HETEROSIS AND COMBINING ABILITIES WITH RESPECT TO IMPORTANT ECONOMIC TRAITS IN *Capsicum annuum*, L.

By

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THESIS

SUBMITTED IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE DEGREE OF

DOCTOR OF PHILOSOPHY

FACULTY OF AGRICULTURE

KERALA AGRICULTURAL UNIVERSITY

DEPARTMENT OF AGRICULTURAL BOTANY

COLLEGE OF AGRICULTURE

VELLAYANI, TRIVANDRUM

1981

DECLARATION

I hereby declare that this thesis entitled "Studies on heterosis and combining abilities with respect to important economic traits in Capsicum annuum L" is a bonafide record of research work done by me during the course of research and that the thesis has not been 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.

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Certified that this thesis, entitled "Studies on heterosis and combining abilities with respect to important economic traits in *Capsicum annuum* L" is a record of research work done independently by Shri. P. MANIKANTAN NAIR, 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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A C K N O W L E D G E M E N T S

The author owes deep debt of gratitude and sincere thanks to:

Dr. (Mrs.) Mary K. George, Professor and Head, Department of Agricultural Botany, Chairman of the Advisory Committee for the valuable guidance, constant encouragement and critical suggestions during the entire course of investigations and preparation of thesis.

Prof. E.J. Thomas, Head of Department of Agricultural Statistics for providing unstinted co-operation and assistance in laying out the experiment, statistical analysis, going through the manuscript several times and making valuable suggestions.

Dr. V. Gopinathan Nair, Professor and Head, Department of Plant Breeding for constructive and helpful suggestions, going through the manuscript and making valuable suggestions.

Dr. N. Mohanakumaran, Professor of Horticulture, for his kind help and assistance, providing his computer programme for combining ability and gene action analysis, assistance rendered in computer analysis, preparation of graphs, and for going through the manuscript critically.

Shri A.T. Abraham, Associate Professor, Department of Agricultural Botany, Member of the Advisory Committee for his constant encouragement and help throughout the course of investigations.

Smt. P. Saraswathi, Associate Professor, Department of Agricultural Statistics for her kind help in path analysis and interpretation of data.

Dr. C.A. Joseph, Associate Professor, Agricultural Botany for providing his computer programme for D^2 analysis and canonical analysis.

Smt. Alice Abraham, Assistant Professor, Department of Agricultural Chemistry for her help in Vitamin C estimation.

The Director of C.F.C.R.I., Trivandrum and Scientists, especially Dr. S. Narayana Moorthy and Dr. Padmanabhan Potti for their assistance in the estimation of Vitamin A.

Dr. A.C. Mathew, Scientist, Dr. C.S. Narayanan, Scientist and Kumari S. Sankarikutty Amma, Senior Scientific Assistant of the C.S.I.R., Regional Research Laboratory, Pappanamcodu, for their help and assistance in the estimation of Capsaicin and Oleoresin.

Sarvasree A.K. Pujari, Head of the Department, P.M.John, Programmer, A.C. Freddy, Operator, Computer Centre, Kerala University for their help and co-operation in analysing the data.

Dr. N. Sadanandan, Dean, Faculty of Agriculture for providing necessary facilities in conducting the experiment.

The author is grateful to his wife for helping him in all stages of the work.

The author is also indebted to the Kerala Agricultural University for granting him, merit scholarship and study leave.

Vellayani,
31-1-1981.

P. MANIKANTAN NAIR

C O N T E N T S

		Page
INTRODUCTION	...	1
REVIEW OF LITERATURE	...	5
Part A		
1. Genotypic and phenotypic variability, heritability and genetic advance in quantitative traits of Capsicum annuum.	...	5
2. Path coefficient analysis	...	7
3. Genetic divergence	...	9
4. Combining ability	...	10
5. Heterosis	...	11
6. Inheritance of characters	...	15
7. Studies on nutritive and quality attributes in Capsicum annuum.	...	17
(i) Vitamin A	...	17
(ii) Vitamin C	...	17
(iii) Capsaicin	...	19
(iv) Oleoresin	...	21
Part B		
1. Estimation of variability, heritability and correlation	...	23
2. Correlation of variables	...	23
3. Path coefficient analysis	...	25
4. Genetic divergence	...	26

5.	Multivariate analysis	...	26
6.	Heterosis	...	27
7.	Heterosis and Heterobaltiosis	...	28
8.	Types of heterosis	...	28
9.	Diallel analysis	...	31
	(a) Hayman's approach	...	32
	(b) Griffing's approach	...	32
	(i) Graphical approach	...	33
	(ii) Numerical approach	...	35
10.	Combining ability	...	36
MATERIALS AND METHODS		...	39
1.	Observations recorded	...	43
2.	Chemical assay	...	46
3.	Analysis of variance and covariance	...	50
4.	Path coefficient analysis	...	53
5.	Multivariate analysis	...	56
6.	D^2 analysis	...	58
	(i) Formation of clusters	...	60
	(ii) Relative contribution of different characters towards total genetic divergence	...	61
7.	Canonical analysis	...	61
8.	Estimation of heterosis	...	63
9.	Diallel analysis and estimation of combining ability	...	65
10.	Gene action	...	69

RESULTS		...	74
1.	Analysis of variance, covariance and estimation of correlation coefficients and genetic parameters	...	74
2.	Path analysis	...	83
3.	Multivariate analysis	...	85
4.	Genetic divergence among varieties	...	88
	(i) Group constellation and intra and inter-cluster D^2	...	89
	(ii) Relative contribution of different clusters to divergence	...	94
5.	Canonical analysis	...	96
6.	Heterosis	...	100
	(i) Negative heterosis	...	103
	(ii) Studies on nutritive and quality attributes	...	131
7.	Combining ability	...	131
8.	Gene action	...	157
DISCUSSION		...	194
1.	Genetic parameters	...	195
2.	Association of characters and path analysis	...	198
3.	Genetic divergence	...	200
4.	Combining ability and heterosis	...	203
5.	Gene action	...	208
6.	Genetic improvement through heterosis exploitation	...	210
SUMMARY		...	215
REFERENCES		...	i - xix

LIST OF TABLES

No.	Title	Page No.
Table 1	Details of accessions which formed the base material of the study.	47
Table 2	Analysis of variance and covariance table.	51
Table 3	ANOVA table for combining ability analysis.	65
Table 4	Analysis of variance table for the varieties under each character.	76
Table 5	The mean values for 15 characters in 30 varieties.	77
Table 6	Population means and Genetic parameters of different characters.	81
Table 7	Phenotypic, genotypic and environmental correlation between different pairs of characters.	82
Table 8	Phenotypic, genotypic, environmental correlation coefficients between different pairs of characters selected for path analysis.	86
Table 9	Path coefficient analysis showing the direct and indirect effects of first order components on yield.	87
Table 10	Path coefficient analysis showing the direct and indirect effects of the second order components.	87
Table 11	Tocher's computational scheme for finding clusters.	90
Table 12	Varieties included in clusters.	91
Table 13	Average intra and inter-cluster distance ($\sqrt{D^2}$ values).	92

No.	Title	Page No.
Table 14	D^2 and D values among the nine varieties selected for hybridisation.	93
Table 15	Ranking of characters according to D^2 values.	95
Table 16	First four sets of canonical vectors.	97
Table 17	Mean values of the first two canonical variates.	98
Table 18	Canonical roots with their relative contribution.	99
Table 19	Analysis of variance table for the design of experiment.	104
Table 20	The mean values of parents and F_1 hybrids and their positive heterosis in percentage.	105
Table 21	Range and mean values in parents and F_1 hybrids and heterosis.	123
Table 22	The mean values of parents and F_1 hybrids and their negative heterosis in percentage.	128
Table 23	Range and mean values in parents and F_1 hybrids and negative heterosis.	130
Table 24	Analysis of variance table for combining abilities.	132
Table 25	Estimation of g.c.a. effects of parents.	133
Table 26	Estimation of s.c.a. effects of parents and F_1 hybrids.	137

No.	Title	Page No.
Table 27	Estimates of b, sb, (b-0)/sb and (1-0)/sb for the different characters.	158
Table 28	Estimates of components of variation and some statistical parameters.	161

APPENDIX

1	D^2 values among 30 varieties of chillies.	

LIST OF ILLUSTRATIONS

Fig. 1. Correlation diagram of yield and its components in chilli.

Fig. 2. Path diagram of yield and its components in chilli.

Fig. 3. Statistical distance among clusters.

Fig. 4. Scatter diagram showing the position of thirty varieties.

Fig. 5. Vitamin A content in parents and hybrids.

Fig. 6. Vitamin C content in parents and hybrids.

Fig. 7. Capsaicin content in parents and hybrids.

Fig. 8. Oleoresin content in parents and hybrids.

$V_{(i)}$, $W_i(A)$; U_{ii}, W_{ii}^{*} (B) and standardised deviation (C) graphs respectively for the following characters.

Fig. 9. Height.

Fig. 10. Number of primary branches.

Fig. 11. Number of secondary branches.

Fig. 12. Number of leaves.

Fig. 13. Spread.

Fig. 14. Blooming.

Fig. 15. Number of fruits.

Fig. 16. Weight of fruit.

Fig. 17. Length of fruit.

Fig. 18. Girth of fruit.

Fig. 19. Size of fruit.
Fig. 20. Number of seeds/fruit.
Fig. 21. Total yield.
Fig. 22. Life span.
Fig. 23. Vitamin A.
Fig. 24. Vitamin C.
Fig. 25. Capsaicin.
Fig. 26. Oleoresin.

LIST OF PHOTO PLATES

1. The variety Purple round - The best general combiner for height, number of primary branches, spread and life span. Also second best general combiner for total yield, number of fruits and number of leaves.

2. Vella notchi - The best general combiner for total yield and the second best general combiner for weight, girth and size of fruit and Vitamin C content.

3. Purple round x Vella notchi - The most heterotic one for number of fruits, girth and size of fruit, total yield and Oleoresin content.

4. Pant C-1 - Resistant to leaf curl disease. Best general combiner for number of fruits, Capsaicin and Oleoresin content.

5. Purple cluster - The best general combiner for Vitamin A content.

6. Pant C-1 x Purple cluster - The hybrid with erect fruiting habit.

INTRODUCTION

INTRODUCTION

Chilli (Capsicum spp) is originally a native of Tropical America and West Indies, introduced to India by Portuguese in the 17th century (Mathew et al., 1971). In different parts of the world this crop is known by a variety of names, bird, capsicum, cayenne, paprika, red and sweet peppers, depending upon the type. The classification of this genus is still a subject of controversy. Engels (1978), of International germplasm centre, Costa Rica has described five cultivated capsicum species. However, most authorities recognise two major species namely Capsicum annuum and Capsicum frutescens. The cultivated species in India fall under these two species (Purseglove, 1974). Of this Capsicum annuum has a special niche in Indian economy because of it s unique nature, besides being cultivated in larger area than the latter. Capsicum frutescens is perennial, with small fruits, otherwise known as bird chillies having more pungency.

This important spice has a variety of uses. They are used in pickles, pepper sauce such as tabasco made by pickling the pulp in strong vinegar or brine. Extracts of chillies are used in the manufacture of ginger beer and other beverages. Cayenne pepper is incorporated in laying mixtures for poultry. Chilli has unique medicinal properties, used internally as a powerful stimulant and carminative, and externally as a counter-irritant. It is an important and

indispensable ingredient in the common Indian dishes, and consumed in a variety of ways, used either in the green form as a vegetable or dried form as chilli powder.

Chilli fruit contains carbohydrates, proteins, fats, fibre, mineral matter and vitamins especially A and C. In fact, Capsicum is one of the richest sources of Vitamin C (Ascorbic acid). The pungency is due to a crystalline volatile alkaloid known as 'Capsaicin', which is mostly present in the placental tissue. In western countries where blended flavours are being increasingly used in food flavouring, solvent extracted oleoresin is in good demand. It is being used in the pharmaceutical and cosmetic industries. They are required in very small quantities. Oleoresin has an added advantage of not being subject to insect or fungal attack, discolouration and loss of flavour during storage.

In India, chilli occupies an important place among the cultivated crops of Andhra Pradesh, Maharashtra, Karnataka and Tamil Nadu.

Though a self-pollinated crop chilli exhibits considerable outcrossing. Coupled with this phenomenon, it is but natural for a crop plant subjected to such varying conditions of growth and unconscious selection practised by the growers to throw out large genetic variability. The myriads of genetic variations already existing and being multiplied by nature have opened up vast vistas in combining economic attributes.

Eventhough chilli is cultivated in larger areas the production per unit area is less, despite good agronomic practices. One of the reasons is non availability of varieties with high yield potential suited to different agro-climatic conditions. As far as Kerala is concerned this problem assumes much importance. Heterosis breeding is one of the methods to find a solution to this problems.

Positive heterosis for many of the economic characters such as number of fruits, yield as well as nutritive qualities have been reported by many workers (Despande, 1933; Pal, 1949; Greenleaf, 1947; Angeli, 1972; Nair and George, 1973; Alpatev and Khrenova, 1976; Popova and Michajlov, 1976; Novak and Chmela, 1979).

However, except for the release of F_1 hybrids like 'Kalyan' and 'Bharat', conscious efforts to evaluate and exploit the genetic variability present in this crop through heterosis breeding, has been lacking.

The F_1 hybrids are found to possess augmented ability to set more fruits under marginal growing conditions and better tolerance against pests and diseases. The present low yield is made more critical by widespread occurrence of leaf curl complex diseases. Under such circumstances F_1 hybrids are known to serve better.

Breeding for nutritionally rich products is a new development in plant breeding and is assuming unprecedented importance in almost all crops. Among other economically

important traits, four nutritional and quality attributes namely Vitamin A, Vitamin C, Capsaicin and Oleoresin were also examined in the present study.

Yield is a highly complex entity whose inheritence is dependent upon the functioning of an intricately organised polygenic system. Further, the character is influenced by other variables as well. A heterosis breeding programme should be preceeded by detailed investigations on different aspects like the association of yield and it's components, identification and measurement of their magnitude, estimation of genetic divergence between varieties, isolation of parental lines with ability to transfer their desirable features to their progenies, inheritance pattern of economic characters etc. Information regarding these aspects on account of nutritive and quality attributes namely Vitamin A, Vitamin C, Capsaicin and Oleoresin content were hitherto lacking and they are elucidated in the present investigations. With the twin objectives of exploring new avenues in heterosis breeding and explicating the genetic architecture and inheritance pattern of important economic attributes, the present programme of work has been undertaken.

The results of the studies indicate possibilities of popularising two F_1 hybrids (purple round x Vella notchi and Pant C-1 x Purple cluster) with high yield potential and desirable economic attributes including nutritive and quality traits.

REVIEW OF LITERATURE

REVIEW OF LITERATURE

Part A

1. Genotypic and phenotypic variability, heritability and genetic advance in quantitative traits of Capsicum annuum.

A wide range of phenotypic and genotypic variability have been reported in quantitative traits of Capsicum annuum by various workers (Nandpuri et al., 1971; Nair and George, 1973).

In the seven exotic and indigenous varieties of Capsicum annuum studied by Arya and Saini (1977), broad sense heritability, phenotypic and genotypic coefficients of variation, and estimates of genetic gain and genetic advance were reported as high for fruit size, fruit number and green fruit yield per plant. High estimates of genetic advance for height, fruit length and fruit yield was also reported by Awasthi et al. (1976). Soh et al. (1977) recorded high heritability estimates for number of days to flowering, fruit width and fruit weight. High heritability for the number of fruits was noticed by many workers (Singh et al., 1972; Arya and Saini, 1976; Betlach, 1979). Legg and Lippert (1966) and Arya (1979) observed that green fruit yield exhibited highest genetic advance, followed by fruit number, days to ripening and fruit size. The latter has also recorded low genetic advance and low genetic gain value coupled with high

heritability values in characters like days to flower, number of branches and plant height.

Reo et al. (1974) in the analysis of interrelationship and path coefficient of quantitative traits in chillies observed significant differences for all the nine characters studied by them. They also reported that heritability values in the broad sense were also high and ranged from 0.53 for plant height to 0.81 for pod length and concluded that environmental factors had less contribution in the expression of the characters studied. Genetic advance measured as percentage of mean indicated considerable scope for improving the number of fruits per plant, final green fruit and dry fruit yields, fruit shape and fruit setting ability.

Sethupathi Ramalingam and Muruga Rajendran (1977) while studying thirty varieties of Capsicum annuum collected from different agro climatic zones of India had reported that characters like height, number of branches, weight of fruits per plant and length of fruit were found to combine high heritability with high genetic advance. This indicated that high heritability in these attributes might be due to additive gene effects. They had noticed that low heritability was accompanied by low genetic advance in two characters suggesting that these estimates were probably due to non additive gene effects. But Hiremath and Nathapathi (1977) recorded a low genetic advance accompanied by high heritability in characters like length of fruit, number of branches and number of fruits.

They opined that high heritability does not necessarily accompany a high genetic advance. High heritability with low genetic advance indicating non additive gene effects were recorded by Awasthi et al. (1976) for number of branches, fruit diameter and average fruit weight. These inferences suggest that high estimates of heritability is not always an indication of high genetic gain (Johnson et al., 1955; Swarup and Chougale, 1962).

Ramanujam and Thirumalachar (1967) suggested that the heritability values in broad sense will be more reliable if accompanied by the high values of genetic advance.

2. Path coefficient analysis.

A perusal of the results relating to cause and effect relationship indicates that number of fruits is the principal yield attribute because of its very high positive association with yield. Singh et al. (1972) and Mishra et al. (1976) observed that yield, fruit number and primary branches were positively correlated. On the basis of studies of nine quantitative traits in chilli Rao et al. (1974) reported that the association of plant height with other traits was low. They suggested that positive association of days to flower with days to fruit maturing would help in isolating lines with early fruit maturity. Further, the negative association of days to flower with fruit setting ability in summer, number of fruits per plant and green and dry fruit

yield indicated that selection of early flowering genotypes would help in isolating lines with higher number of fruits per plant, and more green and dry fruit yields. They concluded that the principal traits influencing directly or indirectly the green fruit yield, were days to flower, days for fruit maturity and number of fruits per plant. Singh and Singh (1976c) and Chang (1977) recorded similar results.

Correlation studies done by Arya and Saini (1976) indicated that fruit size contributed positively to fruit yield, whilst plant height, leaf length, fruit number and Capsaicin content were negatively correlated with yield. The positive correlation of yield with total number of flowers, fruit length and mean length of secondary branches and were emphasised by Chang (1977) based on varimax analysis. On the basis of correlation, path coefficient and multiple regression analysis, Gill et al. (1977) suggested that selection for high yielding lines should be based on the number of fruits per plant. Identical results were recorded by Lee (1976) and Rocchetta et al. (1976). The latter further opined that in addition to the number, weight of fruits and other characters contributed to yield through the number of fruits. Nandpuri et al. (1970) observed that yield in terms of fruit weight per plant was positively correlated with 100 seed weight, fruit size, fruit number per plant, number of branches per plant and plant height. Furthermore regression analysis showed that three characters namely fruit number

per plant, fruit size and seed weight, account for 92.53 per cent of phenotypic variation in yield and constituted important selection criteria.

3. Genetic divergence.

Selection of genetically diverse varieties has been accepted as an imperative pre-requisite for the exploitation of heterosis and for the development of desirable recombinants.

Singh and Singh (1976b) subjected fortyfive Indian lines of Capsicum annuum to multivariate analysis using Mahalanobis' D^2 statistic. The strains differed significantly for the eight characters considered collectively. Branch number, fruit thickness, number of fruits per plant and yield per plant contributed most towards the total divergence. They have further grouped the varieties into ten clusters depending on the similarities of their D^2 values. Considerable diversity between clusters was also noted. The clustering pattern was found to be depending on their geographical distribution.

Peter and Rai (1976) in a study of genetic divergence of 25 varieties of tomato, observed that the characters viz., days to fruit set, days to fruit maturity, number of primary branches, inflorescence and fruits per plant contributed little towards genetic divergence. More than 75 per cent of the genetic divergence was accounted for by the first two canonical roots. They further concluded that there was no apparent parallelism between genetic and geographic divergence.

The component characters, locules per fruits and plant height were found to be important for the expression of genetic divergence.

4. Combining ability.

The response to selection is expected to be the best in crosses involving parents having high g.c.a. effects (Singh and Singh, 1976a). They observed that both g.c.a. and s.c.a. effects were significant indicating the importance of both additive and non additive variances. General and specific combining ability variances were significant for all the five characters studied by Gill et al. (1973) in a diallel of six varieties. Alloh et al. (1975) in a 4 x 4 diallel cross, both g.c.a. and s.c.a. were estimated for four characters. The inheritance of all four characters involved a relatively high degree of non-additive gene action. This was reflected in the high estimated values of variance of specific combining ability.

Significant g.c.a. and s.c.a. estimates were found in length of pedicel, fruit width, the ratio of length to width and pericarp thickness by Milkova (1978). In a diallel analysis of five varieties Milkova (1977) observed that the highest g.c.a. for tallness was shown by the variety Gold Medal. Bigotti (1973) in a diallel cross of 8 varieties found that 'pole star' was a good general combiner for yield and maturity and 'California wonder' and 'sweet mammoth red' for mean weight of fruit.

Gill et al. (1973) indicated that high yielding parents usually had high general combining ability. In a diallel analysis involving 6 parents studied by them, the variance for g.c.a. and s.c.a. were significant for the characters studied. Singh and Singh (1976a) in an investigation involving 8 Capsicum annuum and three characters found that both general and specific combining effects were significant for the characters studied, the general combining effects being larger. In some cases high specific combining effects were also reported. Singh and Singh (1978) observed higher specific combining ability than general combining ability in days to maturity, height, thickness of fruit and number of fruits.

5. Heterosis.

The phenomenon of heterosis in intervarietal hybrids of Capsicum annuum was reported by many workers.

In India, Deepande (1933) was the first to observe heterosis in Capsicum annuum. The F_1 showed heterosis in general vigour, maturity, plant height, thickness of fruit and productivity measured in terms of total number of fruits produced and total weight of dry fruits. Pal (1945) also observed that the hybrids between two pusa types gave higher yield and matured earlier and had thicker fruits than parents. Greenleaf (1947) discussed the use of heterosis in 'pimento pepper' and suggested that the parental lines should be

selected on the basis of plant vigour, fruit size and high yielding capacity.

Increased number of branches have an indirect effect on total yield in chillies. Nair and George (1973) observed 100 per cent increase in the number of branches in 50 per cent of the crosses studied. In addition to number of branches other economic attributes like number of days to flowering, number of days to maturity, fruit length, fruit thickness, fruit number and yield displayed heterosis (Popova and Funduli, 1973; Bak et al., 1975; Singh and Singh, 1976a). Increase in the number of leaves and leaf area will remarkably enhance photosynthetic efficiency which in turn promote the yield potential. Nair and George (1973) noticed positive heterotic effect in the number of leaves in 50 per cent of the crosses studied by them. Earliness in blooming is also an important economic attribute. Pronounced earliness in 100 per cent of hybrid combinations was not uncommon (Nair and George, 1973 and Soh et al., 1976). Identical results have been recorded by many workers (Alpatev and Khrenova, 1976; Studentsova, 1976).

Gill and Ahmad (1977) observed positive heterosis over mid parental values for plant height and average fruit weight in a 4 x 4 diallel cross of Capsicum annuum varieties. Popova and Mikhailov (1978) noticed the expression of heterosis in plant height, average number of leaves per plant, leaf surface area, length of roots and length of

shoots. They observed that heterosis was apparent immediately after fertilisation. Dominance was largely responsible for the high degree of heterosis observed in plant height, number of branches, number of days to flowering, fruit length, fruit thickness and fruit number (Mishra et al., 1976; Singh and Singh, 1976c; Alpatev and Khrenova, 1976).

As regards size of fruit an intermediate position between parents was recorded by Popova and Vysladky (1965) in his studies on intervarietal hybrids of Capsicum. But no significant increase in fruit weight was noticed by Nair and George (1975) in intervarietal hybrids of Capsicum. Further, they have recorded an intermediate condition in the number of seeds per fruit.

In six hybrid varieties heterosis was detected by Popova and Mikhailov (1976) in whole plant weight, plant height, number of leaves, assimilation area, total root length and embryo length in the F_1 seed. The degree of heterosis in various hybrids for each of these characters was between 5 per cent and 30 per cent. They further suggested that the heterotic effects take inception at the time of fertilisation.

In a 9 x 9 diallel cross, significant heterosis was noticed by Lippert (1975) for dry fruit weight per plant, fruit length and the percentage of mature fruit at harvest. Data collected over many years by Alpatev and Khrenova (1975) showed dominance in earliness, yield, bright fruit colour,

diameter and length of fruit.

Angeli (1972) in studies on intervarietal hybrids observed that all hybrids outyielded their parents while Bak et al. (1975) recorded that yield was higher by 61 per cent on the average in hybrids compared with their parents. Studentsova (1976) observed, high heterosis for yield when parents belonged to different varietal types or when they were similar in biological characteristics but differed in morphological features. The increase in yield was due to increase in number of fruits per plant. Novak and Chmela (1979) in a six variety diallel noticed that heterosis for yield was greatest in the progenies of Yolo wonder, reaching 50 per cent above the yield of better parent in Yolo wonder x Ruby.

It has been widely accepted that genetic diversity of parents is positively correlated with the expression of heterosis in F_1. The degree of expression of heterosis in Capsicum varies with different parental combinations, consequent on the degree of genetic diversity between parents (Nair and George, 1975). Similar results of varying degrees of heterosis in several characters were reported by many workers (Gill et al., 1973; Bak et al., 1975; Allah et al., 1975; Studentsova, 1976; Popova and Mikhailov, 1976; Singh and Singh, 1976c; Alpatev and Khrenova, 1976).

6. Inheritance of characters.

The predominance of additive variation for number of days to blooming, fruit weight, fruit width, thickness of fruit wall and plant height was recorded by Soh et al. (1976, 1977). Milkova (1977) attributed both additive and non additive gene action to plant height. Based on studies of F_1, F_2 and back cross generations Betlach (1979) concluded that inheritance of number of fruits per plant was due to additive effects predominated with moderate positive dominance. In a diallel cross involving 5 varieties, additive and non additive gene effects were found to control branch number, leaf number and fruit weight (Milkova, 1979). Allah et al. (1975) in a 4 x 4 diallel cross reported that additive gene effects were relatively high for inheritance of fruit weight. For early yield and fruit number per plant additive effects were less important than dominance and epistatic. They were of the opinion that non additive gene action made an important contribution to the genetic variation. The total yield of the fruits was found to be more dependent on over dominant factors (Betlach and Vytopil, 1969).

Singh and Singh (1976c) in a study on component of variances and degree of dominance for yield contributing traits in Chilli observed that additive, dominance and environmental variances were found in varying proportions for the quantitative traits studied by them. While examining

14 characters associated with yield in a diallel analysis of quantitative traits in Capsicum annuum. Silvetti and Giovannelli (1976) found that dominance effects were significant for 13 characters, out of the 14 characters studied. Based on a 9 x 9 diallel cross, Lippert (1975) recorded that additive effects were important than non additive effects in determining variation among hybrids for dry fruit weight per plant, fruit number, length and width and total carotenoid content. He has suggested that reciprocal recurrent selection or reciprocal full sib selection should result in improvement from both additive and non additive gene action and a concomitant improvement in carotenoid content and dry fruit weight per plant.

The role of additive, dominant and epistatic gene effects in various quantitative traits were reported by many workers. Scossiroli et al. (1974) reported the occurrence of epistatic gene action for many of the characters except for fruit ripening. Singh and Singh (1976d) while studying the quantitative characters in Capsicum annuum ascribed additive, dominant and epistatic gene action to plant height, number of branches, days to flowering, fruit length and thickness, fruit number and weight per fruit. They further concluded that among the epistatic effects dominance x dominance effects were the most important, followed by additive x additive. Nandpuri and Kumar (1973) in an investigation of 10 x 10 diallel analysis indicated that complementary epistatics of

additive x additive gene effects and over dominance relationships of alleles for high yield are important in the inheritance of yield.

7. Studies on nutritive and quality attributes in Capsicum annuum.

Capsicum fruit has been considered as a storehouse of many important nutrients including vitamins.

(i) Vitamin A

Beta carotene is the precursor of Vitamin A. Chilli fruit rind is found to be rich in carotene especially when they are ripened. There is a positive correlation of beta carotene in fruits and deep red colour (Ramachandramurthy, 1974). Dry matter, ascorbic acid, crude protein, zinc and copper were high in ripe fruits than the corresponding green fruit contents (Saimbhi et al., 1977). Love (1971) reported more carotene in Capsicum annuum than in other species. Purseglove (1974) recorded that Capsicum annuum contained 100 to 1200 I.U. of Vitamin A. Very little increase of carotene in hybrids was observed by Buczak et al. (1970). Lee et al. (1975), reported that carotenoid concentration was inversely correlated with the concentration of the component of pungency.

(ii) Vitamin C

Capsicum is one of the rich sources of Vitamin C or ascorbic acid ($C_6H_8O_6$). Ascorbic acid was first isolated by

Gyorfli from paprika in Hungary and found to be similar in chemical and antiscorbutic properties with that obtained from adrenal glands. Ascorbic acid was high in Capsicum annuum compared to other species (Cambraia et al., 1973). Purseglove (1974), indicated that Capsicum annuum contained 50-280 mg/100 g and Capsicum frutescens 2-50 mg/100 g. In a chemical assay conducted by Ludilov and Ludilova (1979) the ascorbic acid content ranged between 300 and 370 mg/100 g. Further, ascorbic acid content of fruit increases until full maturity (Butkevic, 1969).

The highest content of ascorbic acid was found at the tip of the fruit and the lowest at the base (Schutt, 1958). Awasthi et al. (1976) have noticed that ascorbic acid content was closely correlated with the age, length and diameter of fruits. Ascorbic acid content was positively correlated with fruit length and negatively correlated with capsaicin content (Nair and George, 1973; Sathe and Phadnavis, 1977). In a chemical assay Kopec and Stevlikova (1980) recorded maximum ascorbic acid content in parents and hybrids as 278 mg/100 g and 315 mg/100 g respectively. They further noticed that this was affected by irrigation, manuring and post-harvest storage.

Gyorffy (1949) reported that the inheritance of ascorbic acid content appeared to be multigenic with the F_1 mean value from crosses of low and high value parents corresponding closely to the geometric parental mean.

Values in the F_2, were distributed between limits of parental lines. Out of the five varieties studied by Thakur and Eren (1975) 2 showed additive gene effects while 2 exhibited complementary epistatic gene effects and the remaining variety had dominance effect. In general, the genes for low ascorbic acid content showed partial dominance. Only one cross namely NP 46 x Long red displayed positive heterosis. They further found that NP 46, Long red and All season were good general combiners. The superiority of hybrids in higher ascorbic acid content was reported by many workers (Nair and George, 1973; Marfutina, 1973; Alyatev and Khremova, 1975; Popova et al., 1979; Kopec and Stevlikova, 1980).

(iii) Capsaicin

The economic importance of Capsicum annuum lies in the pungency and flavour of fruits. Pungency is due to a crystalline volatile alkaloid, which was first isolated by Thresh in 1876 (quoted by Tewari, 1979) who assigned the name Capsaicin, the molecular formula of the compound being $C_{18}H_{27}NO_3$. The ovary walls of the chilli fruit are responsible for the production of Capsaicin. The placental tissue contains most of the alkaloid while the pericarp has a small amount and the seed acquires a certain degree of pungency only through contact with the placenta (Tewari, 1979). The degree of pungency varies from variety to variety, stage of maturity and soil and climatic factor. The degree of pungency varies among varieties probably due to the presence

of genes modifying the factor for pungency and the ratio of placental tissue of seed and pod wall.

Capsaicin content is correlated negatively with fruit yield and rind thickness and positively with fruit number (Mishra, 1969; Arya and Saini, 1977). The smaller the fruit higher will be the content of capsaicin (Kvachadze, 1974). It is considered that pungency is strongly correlated with virus resistance (Awasthi and Singh, 1975).

Nair and George (1973) observed positive heterosis in only one cross out of 4 crosses studied. They have attributed the reduction in capsaicin content to the presence of sucrose content. Webber (1911) quoted by Paul recorded that pungency is a heritable character. They opined that it was a simple monogenic character dominant to non pungency. The proportions of capsaicin secreting tissue and the amount of capsaicin in the tissue were studied in 12 varieties of Capsicum annuum by Ramanujam and Thirumalachar (1966). Variations were large and independent in the two components, postulating that the genetic control of the total content was polygenic. Gill et al. (1973) while studying the hybrids of Hungarian wax x NP 46 recorded that the amount of capsaicin was more in NP 46 than in Hungarian wax and the F_1 plants occupying an intermediate position. The F_2 showed transgressive segregation indicating multifactorial control of capsaicin content. They were of the opinion that capsaicin

content is a complex character under the control of many genes. Quagliotti and Otteviano (1971) by assessing the capsaicin content in F_1, F_2 and back cross progenies confirmed the earlier findings of polygenic control. Kvachadse (1976) observed that the F_1 was intermediate in capsaicin content. He has also reported that in the F_2, F_3 the range of variation which did not extend beyond that of parental forms indicated that the character was controlled by many identical genes. Enhanced capsaicin content in hybrids was reported by Michna (1969). High heritability of this alkaloid in the broad sense was reported by Quagliotti and Otteviano (1971) and Gill et al.(1973).

(iv) Oleoresin

At present chillies are being used in culinary preparations in most of the countries producing it in the form of powder. But in western countries where blended flavours are being increasingly used for flavouring of food solvent extracted chilli oleoresin is in good demand. The pharmaceutical and cosmetic industries use this preparation. Chillies and chilli powder are easily subjected by insect and mould attack, discolouration and loss of flavour during storage. These difficulties are eliminated by conversion to oleoresin. Further, the oleoresin offer convenient way of standardizing the quality and strength of flavour. Oleoresin from chillies consist of fixed oil, capsaicin,

pigments, sugars and resin. Mathew et al. (1971) recorded a range of 8.7 per cent to 16.5 per cent oleoresin content in chillies. But the information regarding the genetic control, heterosis, combining ability and inheritance pattern of oleoresin is meagre.

Part B

1. Estimation of variability, heritability and correlations.

Before proceeding with the detailed statistical analysis of any field data, initially the raw data are processed and analysed for the sources of variation. In most of the plant breeding experiments randomized block design is extensively used. The information regarding the variability existing in the plant population under study, the inter-relationships between different plant characters, and a knowledge regarding heritability and the value of expected genetic advance in the succeeding generation are essential for an effective plant breeding programme.

The correlated components of yield and their relative importance on the basis of the statistically computed parameters heritability, genetic advance and genetic gain at different intensities of selection, were assessed as a prelude to the calculations of path coefficient analysis. Subsequent assessment includes the magnitude of the relative direct and indirect influence of these variables, and also that of the residual factor, on yield of fruits. Here the theory of causation and effect was made applicable and the path coefficient analysis method resorted to.

2. Correlation of variables.

The idea of correlation of variables was first conceived by Galton (1889), for the first time.

Fisher (1918, 1954), developed the method of applying the theory of correlation of variables, in understanding their influence in biological systems.

The expression of inherited characters is often influenced by the genotype, the environment and the genotype environmental interaction.

Burton (1952), introduced a convenient procedure for the calculation of the phenotype and genotype coefficients of correlation.

Genetic parameters like heritability, genetic advance and genetic gain under different probability levels of selection have been of immense use for assessing the relative importance of the inherited and correlated variables.

Hanson et al. (1956) proposed the mathematical relationship of various estimates on computation of heritability. This attribute is generally expressed as the percentage, and in the broad sense it refers to the proportion of variance due to genotype to the variance due to phenotype.

For partitioning the total variance into that due to genotype, phenotype and error, in the analysis of variance, Johnson et al. (1955), introduced a methodology. Error, in this context refers to genotypic environmental interaction.

Lush (1949), and Johnson et al. (1955), devised an accurate and easily manageable procedure for the calculation of the genetic advance under specified intensity of selection.

Johnson et al. (1955), further substantiated the advantage of computing the genetic gain under selection and it's usefulness in relative comparison of variables.

These two parameters, genetic advance and genetic gain, are of prime value to the plant breeder in understanding to what extent they could be possessed, and made use of, in respect of certain desired polygenic characters under specified probability levels of discrimination to particular genotypes during selection.

3. Path coefficient analysis.

Path coefficients are standardised partial regression coefficients. In path coefficient analysis, the correlations among cause and effect are partitioned into direct and indirect effects of causal factors on the effect. This is applied only when we have a linearly related closed system of variables, which could predominantly be assumed to be responsible for the expression of the final end product.

Wright (1921, 1923, 1934), introduced the path coefficient analysis. In this method, the theory of causation and effect is made applicable. The ultimate dependent variable is referred to as the "effect", and the components, which by themselves may or may not be dependent on other variables as the "causes".

Niles (1922, 1923), Tukey (1954), and Dewey and Lu (1959), recommended the application of the path coefficient analysis as a potent method for resolving the dependable

criteria in selection procedures in the breeding of plants and animals.

Durate and Adams (1972), emphasised the identification and the classification of the components (causes) to different orders (First, second, third and etc.) and the vital importance of the formulation of the causal scheme in path analysis studies.

4. Genetic divergence.

Phenotypic divergence in a population has also been often considered as an index and criteria of genetic diversity. Hayes and Olson (1959) and Wellhausen (1965) while summarising the results of F_1 crosses have indicated that Flint x Dent crosses in maize generally have higher performance than Dent x Dent or Flint x Flint crosses. In linseed, ecogeographical aspects has been observed to be more or less correlated or running parallel with genetic diversity (Singh, 1965). However, true under certain conditions, broad generalization in this connection could be rather misleading. Timothy (1965) observed considerable phenotypic divergence between Mexican, Brazelian and Andean maize collections but met with little genetic diversity as expressed in their F_1 crosses.

5. Multivariate analysis.

Multivariate analysis utilizing Mahalanobis' D^2 statistic and canonical variate analysis (Rao, 1952) have been observed to be useful in quantifying the degree of divergence in the

germplasm collection of various crop plants. It has been frequently utilized to assess the relative contributions of different components to the total divergence both at the inter and intra-cluster levels. It has been established that there is a close and intense relationship between the extent of heterosis and the extent of genetic divergence of the parents involved in the F_1 cross. Mahalanobis' D^2 statistic precisely reveals the genetic distance between parents and helps in choosing divergent parents for an effective hybridisation programme.

The details of this technique and its application to evaluate the genetic diversity has been given by Rao (1952) and has successfully been used by Murthy and Pavate (1962), Chandrasekharaiah (1964), Murthy (1965), Murthy et al. (1965) Murthy and Tiwari (1967), and Peter and Rai (1976).

6. Heterosis.

The term heterosis is now widely used, refers to the phenomenon in which the F_1 population obtained by the crossing of the two genetically dissimilar gametes or individuals shows increased or decreased vigour over the better parent or over the mid-parental value (Rai, 1979). Shull referred this phenomenon as the stimulus of heterozygosis and in his words it has been the "interpretation of increased vigour, size, fruitfulness, speed of development, resistance to diseases and to insect pests or to the climatic rigours of

any kind manifested by the out breeding organisms as compared with the corresponding inbreds as the specific results of the unlikeliness in the constitution of the uniting parental gametes". It is now widely recognised that this phenomenon is the result of the action and interaction of the unlike gametes in the heterozygote (Aa) and the heterosis is only the better or worse than expected manifestation of this biological behaviour of the hybrid.

7. Heterosis and heterobeltiosis.

As described earlier, heterosis is the increased or decreased vigour of F_1 over its better parent or the mid parental value. In plant breeding programmes conventionally heterosis is referred to denote the expression of increased vigour of the hybrid over the better parent. But, since heterosis is also expressed over the mid parental value, it needs some distinction. Recently, a new word "heterobeltiosis" has been proposed (Fitzer et al., 1968, Fonseca and Patterson, 1968) to describe the improvement of the heterozygote in relation to the better parent of the cross and now this term is precisely being used to connote the expression of heterosis over the better parent.

8. Types of heterosis.

Depending upon the nature of the origin, adaptability, reproductivity and non-reproductivity, heterosis could be classified in two classes:- (1) Euheterosis (true heterosis)

and (ii) Pseudo heterosis (Luxuriance).

Euheterosis could further be divided into (a) Mutational euheterosis and Balanced euheterosis depending upon the nature and origin of the genes causing heterosis in a biological system (Dobzhansky, 1952).

Development of quantitative genetic theories relating to hybrid vigour has centered around the dominance hypothesis, complementation of the two genotypes was also thought to be a factor contributing to heterosis. Subsequently, Powers (1944), Hull (1945, 1949), Robinson et al. (1949) and Stern (1948) recognised partial dominance, complete dominance and over dominance as different cases of heterosis. The hypothesis of heterozygosity per se was rejected by Mather (1955), Jinks and Mather (1955) and Sentz et al. (1954). They argued that unlike out breeding species where heterosis is a regular property of heterozygosis the same is not always true in inbreeding species. Secondly, the interaction of two allelomorphs at a heterozygous locus giving rise to over dominance was seldom proved in relation to hybrid vigour since it was not easy to distinguish over dominance from nonallelic interaction, in the absence of which the former vanished. Mather concluded that nonallelic interaction was more likely and a more frequent cause of heterosis rather than special relation between the alleles of same locus. similar observations were made by Jinks and Hayman (1953), Robinson et al. (1956) and Allard (1956a).

Wallace (1963) reported that a pair of alleles may show over dominance in one genetic background, but not necessarily in another. It was also pointed out that the apparent over dominance detected under visual observation is not always a case of true over dominance. Fontecorvo (1955) pointed out that in the advanced concept of complex loci, the two terms intraallelic interaction (over dominance) and inter allelic interaction (epistasis) carry no precise meaning as the distinction between the alleles and those of gene complexes often becomes imperceptible.

Other workers who supported the role of epistasis in heterosis were Rasmusson (1934), Comstock and Robinson (1948) and Stringfield (1950) in maize, Singh (1949) in summer squash, Jinks and Jones (1958) in Nicotiana rustica, Swarup et al. (1963) and Swarup and Sharma (1965) in cabbage, Swarup and Pal (1966) and Pal and Swarup (1966) in cauliflower, Povelaitis (1964) and Murthy (1965) in Nicotiana tabacum and Sharma (1965) in bhindi.

Hayman (1957) and Bowman (1959) supported the view that a combination of the three types of gene interaction (dominance, over dominance, and epistasis) might be operative in heterotic crosses. Earlier, Lewis (1955) had recorded that though the over dominance concept was accepted, there was nothing to contradict and much to support complementary action of dominant genes (non-allelic) as the main cause of

heterosis. He quoted Honing (1928), Fisher (1930) and Hersh (1934) to state that the degree of dominance of a gene is conditioned by the environment as well as by the genetic background. Moreover complex characters which manifest heterosis are extremely prone to the environmental influence.

Jinks (1954) analysing the impact of genetic and environmental components affecting quantitative characters in Nicotiana crosses showed that genotype environment interaction could be a major factor in the expression of heterosis. Such observations were made in Lycopersicon by Griffing (1953) and Lewis (1954). There appears to be a relationship between the degree of heterosis in a hybrid and the extent of the difference between parents with respect to the number of alleles, gene actions, genetic background or a combination of all these factors.

9. Diallel analysis

Diallel analysis is a very potent biometrical tool to partition total genetic variance into it's various components. A set of crosses produced by involving 'n' lines in all possible combinations is designated as diallel crosses and the analysis is known as diallel analysis (Singh and Chaudhary, 1979). Such an analysis provides information on (i) the nature and amount of genetic parameters and (ii) general and specific combining ability of parents and their crosses, respectively. The two main approaches being followed for

diallel analysis are:

(i) Hayman's approach

(ii) Griffing's approach

(a) Hayman's approach

The theory of diallel was developed by Jinks and Hayman (1953), Jinks (1954, 1956) and Hayman (1954a,b; 1957 and 1958) using Mather's concept of D and H components of variation.

(b) Griffing's approach

In this approach using a suitable statistical model the component variances due to general and specific combining ability are estimated which in turn may be translated into genetical components such as σ^2_A and σ^2_D under certain assumptions. Griffing (1956) has given 4 methods of diallel depending on the material involved in the analysis.

(i) parents (n), $n(n-1)/2$ F_1's and reciprocals,

(ii) parents and F_1's only,

(iii) F_1's and reciprocals and

(iv) F_1's only

Griffing (1956) has described the methods of analysis for combining ability considering Eisenhart's model i (fixed effect) and model ii (random effect).

Jinks and Hayman's diallel analysis has been widely accepted because of it's versatality. Hayman (1954b) defines a diallel system as "the set of all possible matings between

several genotypes". This gives rise to P^2 combinations including the selfs, crosses and reciprocals among the P parental lines. The diallel analysis provides considerable amount of genetic information (gene action, mean degree of dominance, proportion of genes with positive and negative effects in parents, etc.) which could be of great value in formulating coherent breeding programme.

Jinks and Hayman (1953) and Hayman (1954) have listed the assumptions based on which diallel analysis is done. They are:

(i) diploid segregation,
(ii) no difference between reciprocals,
(iii) independent action of non allelic genes,
(iv) no multiple allelism,
(v) homozygous parents and
(vi) independent distribution of genes between parents.

There are two approaches in the diallel analysis, graphical and numerical to estimate the various genetic parameters. These may be used either singly or in combination.

(i) Graphical approach

Jinks and Hayman (1953) were the first to present the graphical approach, which was based on Mather's (1949) components of variations, D and H and using second degree of statistics such as W_r (Covariance of the r^{th} array and the non-recurring parents), etc. They pointed out the importance

of the slope of regression line (W_r on V_r) and it's position in relation to the limiting parabola ($W_r^2 = V_r \times V_0 L_0$) in indicating the degree of dominance. In the absence of dominance the regression line (W_r, V_r) will be tangential to the limiting parabola, which with complete dominance the regression line will pass through the point of origin. In case of over dominance the regression line will cut the 'y' axis below the point of origin. The distribution of the array points along the regression line and the line of unit slope indicates the dominance relationships among the parental lines, and the types of gene effects, respectively. They also discussed the possibility of prediction of the value of completely dominant and completely recessive parents in case there is a strong correlation between the parental order ($W_r + V_r$) and the parental measurements (Y_r). Jinks (1954) and Hayman (1954) elaborated on the effects of gene interaction on the slope of the regression line (W_r, V_r) and advocated the omission of the interacting members in the arrays before further analysis is done. Otherwise genetic interactions cause apparent over dominance and heterosis in many cases. They also discussed the effect of linkage and different types of epistasis on the W_r, V_r, graph.

Hayman (1954b) introduced a new statistic, W' (the covariance between the array means, and the r^{th} array) for use in the W_r, W' graph. Allard (1956a) realising the importance of W_r, W', graph advocated the use of W_r, V_r and W'

graphs in order to obtain a clear picture of the gene action involved.

Johnson and Aksel (1959) presented a method for standardization of parental measurements (y_p) and the parental order of dominance ($W_p + V_p$). The standardized deviation graph helped to determine whether dominance is due to positive or negative genes.

(ii) Numerical approach

Based on Mather's components of variations D and H, Jinks and Hayman (1953) developed an approach to the analysis of data from diallel crosses of homozygous lines. Determination of the genetic parameters D, H_1, H_2 and F provides the estimate of overall dominance, distribution of dominant and recessive alleles in parents, etc. To test the accuracy after estimates, standard errors were derived from the variance of W_p-V_p. Hayman (1954b) presented in detail the theory and algebraic basis of the analysis of diallel crosses giving new notations and adding two more statistics, h^2 and F_p, in addition to those given by Jinks and Hayman (1953). He further stated that classification of experiment into one of the four categories; exhibiting no dominance, partial dominance, complete dominance, or over dominance is possible by testing the deviation of D-H_1 from zero combined with the test of significance of H_2.

Dickinson and Jinks (1956) extended the method of diallel analysis to crosses using as parents any type of material, homozygous or heterozygous. They listed the different parameters as D_I, D_{II}, H_I, H_{II}, H_{III}, H_{IV}, F_I and F_{II}. The analysis provided estimates of the overall degree of dominance, of the inbreeding coefficient or degree of heterozygosity of loci showing dominance, and of allele frequency at such loci. They could also determine whether dominants and recessives were in excess. Hayman (1957) brought out the realibility of $(H_1/D)^{\frac{1}{2}}$ value as a measure of the degree of dominance. He stated that multiple allelism and non independent distribution of the genes in the parents, though disturbing the (W_r, V_r) graph, do not invalidate $(H_1/D)^{\frac{1}{2}}$ as a measure of the average degree of dominance.

Jinks and Stevens (1959) estimated seven heritable components of variations, namely D, H_1, H_2, I, J, L_1 and L_2. The first three were the same as those defined by Jinks and Hayman (1953). Heterogeneity of I and J indicate correlated gene distribution and linkage of interacting genes, and the significant difference of L_1 and L_2 and showed unequal gene frequencies for the interacting genes. Ducio and Hill (1967) showed that the equation of Mather can be modified to include components which will allow estimation of genotype-environment effects.

10. Combining ability.

In practical plant breeding, it is imperative to know

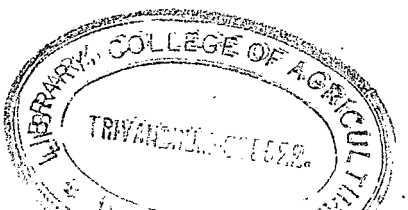
the combining ability effects of different cultivars and the specific combining effects of different combinations. The information on combining ability throws light on the type of gene action governing a particular character. Selection of appropriate breeding method depends on the nature of gene action revealed by such a genetic analysis. The term 'general combining ability' (g.c.a.) was used by Sprague and Tatum (1942) to designate the average performance of a line in a number of hybrid combinations. They used 'specific combining ability' (s.c.a.) to designate those cases in which certain hybrid combination did relatively better or worse than would be expected on the basis of average performance of the lines involved.

Different methods have been used for testing the g.c.a. of inbred lines. Davis (1927) tested the g.c.a. of inbred lines by means of inbred variety cross (top cross). Hayes and Johnson (1939) studied the segregates from the crosses of high and low combining lines and concluded that lines of good combining ability were obtained more frequently from crosses involving good combiners than from crosses of lines having low combining ability. Sprague and Tatum (1942) gave a technique of estimating g.c.a. and s.c.a. variances to detect the amount of additive and dominance variances, respectively in the yield of single crosses of maize.

The method of working out g.c.a. and s.c.a. effects

along with their variances was demonstrated out by Griffing (1956a). The assumption involved in this technique are (i) the parent population must be a random mating population in equilibrium (ii) the experimental set of lines must be a random sample from a population of inbred lines which were derived from parent population by the imposition of an inbreeding system, free from the forces which change gene frequencies, and (iii) ' a modified diallel' crossing system must be used in which the lines themselves are not included in the experimental set. Griffing pointed out that twice the general combining ability variance contains not only the additive genetic variance but also a portion of the epistatic variance (additive x additive) and that specific combining ability include all the dominance and the remaining epistatic variance. When interpreted in terms of the classical method of covariance between relations (Fisher, 1918, 1930) the g.c.a. variances is equal to the covariance between parent and offspring in a random mating population at equilibrium.

MATERIALS AND METHODS



MATERIALS AND METHODS

The present investigation was undertaken at the College of Agriculture, Vellayani during 1976-79. Sixty three varieties of Capsicum annuum, displaying distinct diversity in morphology and performance, and representing ecogeographically different environmental adaptation constituted the base material of the study. Their source, yield potential, adaptation, tolerance to leafcurl complex, which is the dreadful disease as far as chilli is concerned, are presented in table 1. Based on their adaptation, performance and disease tolerance 30 varieties were selected for further studies. These 30 varieties were tried in a Randomised Block Design with 3 replications, the inter and intra row distance being 75 cm and 45 cm respectively. Each treatment consisted of 20 plants of which 10 plants were selected randomly for recording observations.

The following 15 characters were studied.

1. Height
2. Spread
3. Number of primary branches
4. Number of secondary branches
5. Number of days taken for blooming
6. Number of fruits
7. Weight of fruit
8. Life span

9. Number of seeds
10. Length of fruit
11. Girth of fruit
12. Total yield
13. Vitamin A
14. Vitamin C
15. Capsaicin

The cause and effect relationship was estimated by path analysis. Genetic divergence among the varieties was computed by Mahalanobis' D^2 analysis. Based on the information derived from cause and effect relationship and genetic divergence the following 9 varieties were selected as parents for subsequent studies. The parents were selected as per the guidelines provided by Singh and Chaudhary (1979).

1. C.A. 960
2. C.A. 1068
3. G-4
4. Purple round
5. Vella notchi
6. Pant c-1
7. Pusa jwala
8. California wonder
9. Purple cluster

The parents were raised in pot culture I, and selfed by using selfing bags. The inbreds were raised in pot culture

II, crossed in all possible combinations, and a diallel set (without reciprocals) was obtained. The fruit development and subsequent seed formation was poor in one cross (California wonder x Pusa jwala) and as such reciprocals could not be included.

The nine parents and their thirty six F_1 hybrid progenies were put in a final evaluation trial, laid out as a Randomised Block Design with three replications, the inter and intra row distance being 75 cm and 45 cm respectively. Each treatment consisted of 20 plants of which 10 plants were selected randomly for recording observations. The cultural practices recommended by the Kerala Agricultural University were adopted in the experiments. The chronological order of the experiments is detailed below:

(1) 1976 — Observation of the base material and selection based on performance and other attributes.

(2) 1977 (a) Assessment of the relative performance of selected 30 varieties in Randomised Block Design.

(b) Raising selected 9 parents in pot culture I and selfing.

(3) 1978 — Raising inbreds in pot culture II and hybridization in all possible combinations.

(4) 1979 — Raising 9 parents and 36 F_1 hybrids in R.B.D. and evaluation.

Heterosis, combining abilities and gene action were studied with respect to the following 18 characters which included four nutritive and quality attributes namely Vitamin A, Vitamin C, Capsaicin and Oleoresin content.

1. Height
2. Number of primary branches
3. Number of secondary branches
4. Number of leaves
5. Spread
6. Number of days taken for blooming
7. Number of fruits
8. Weight of fruit
9. Length of fruit
10. Girth of fruit
11. Size of fruit
12. Number of seeds/fruit
13. Total yield
14. Life span
15. Vitamin A
16. Vitamin C
17. Capsaicin
18. Oleoresin

From among the parents used in the study, lines that showed good combining abilities (general and specific) were isolated as per Griffing's Method 2 Model 1 (1956).

The inheritence of the above mentioned traits was studied as per the method suggested by Jinks and Hayman (1953).

1. Observations recorded

Observations were recorded on the experimental plants for all the characters mentioned above.

1. Height of plant (cm)

Height of plants were measured from the ground level to the top most bud on the last harvest day, averaged on plot basis and expressed in cm.

2. Number of primary branches

The number of primary branches were counted on the last harvest day and averaged on plot basis.

3. Number of secondary branches

The number of secondary branches were counted on the last harvest day and averaged on plot basis.

4. Number of leaves

The number of leaves were counted on the last harvest day and averaged on plot basis.

5. Spread (cm)

The maximum spread of the plant was taken on the last harvest day, averaged on plot basis and expressed in cm.

6. Number of days taken for blooming

The number of days taken for blooming were reckoned when 50 per cent of the plants on bloom and averaged on plot basis.

7. Number of fruits

The total number of fruits harvested from each of the observational plant was averaged to obtain plot means.

8. Weight of fruit (g)

Ten fruits were collected at random from each of the observational plant and weighed. Plot means were subsequently worked out and expressed in grammes.

9. Length of fruit (cm)

Ten fruits were collected at random from each of the observational plant and measurements taken. Plot means were then worked out and expressed in cm.

10. Girth of fruit (cm)

Ten fruits collected at random for assessing other fruit characters were used for measuring girth. The measurement was taken at base or wherever girth was maximum. Plot means were worked out and expressed in cm.

11. Size of fruit (ml)

The size of fruit was estimated by water displacement method. Ten fruits used for assessing other fruit characters were utilised for measuring size of fruit. The average was computed on plot basis and expressed in millilitres.

12. Number of seeds/fruit

Seeds were extracted from the same ten fruits utilised for studying other fruit characters and plot means worked out.

13. Total yield (g)

Total yield was worked out by taking the weight of all

the fresh fruits harvested from ten randomly selected plants, for studying other attributes, averaged on plot basis and expressed in grammes.

14. Life span

Life span was worked out on seed to seed basis. The number of days taken from sowing to the last harvest was reckoned as life span from 10 randomly selected plants, averaged on plot basis and expressed as number of days.

15. Vitamin A content (I.U.)

Five samples were collected from randomly selected plants and estimated, averaged on plot basis and expressed in international units.

16. Vitamin C content

Five samples were collected from randomly selected plants and estimated, averaged on plot basis and expressed in mg/100 g.

17. Canealcin (percentage)

Five samples were collected from randomly selected plants and estimated, averaged on plot basis and expressed as percentage.

18. Oleoresin (percentage)

Five samples were collected from randomly selected plants and estimated, averaged on plot basis and expressed as percentage.

2. Chemical Assay

(i) Vitamin A

The estimation was carried out as per the colorimetric and spectrophotometric method envisaged by Rao et al. (1966). Well ripe fresh fruits were utilised for estimation.

(ii) Vitamin C

The estimation was done by titration method. Well ripe fresh fruits were utilised for the assay. Phenol Indo 2:6 dichlorophenol dye was used for the titration.

(iii) Capsaicin

Capsaicin was estimated by using thin layer chromatography followed by spectrophotometry method as suggested by Mathew et al. (1971). Acetone was used as solvent for soxhlet-extraction (Sankarikutty et al., 1978). Well ripe and sun dried fruits were utilised for the estimation.

(iv) Oleoresin

Oleoresin was estimated as per the method enumerated by Mathew et al. (1971). Well ripe and sun dried fruits were used for the assay. Cold percolation extraction of powder was carried out using Ethylene dichloride.

Statistical analysis

The data collected in respect of the metric traits, as mentioned above, was tabulated and subjected to statistical analysis.

Table 1. Details of accessions which formed the base material for the study.

Sl. No.	Name of variety	Source	Mean No. of fruits per plant	Adapta-bility	Tolerance to leaf curl complex
1.	Sohmynken rekot	Meghalaya	28.00	N.A.	N.T.
2.	" shena-rit	"	43.00	N.A.	N.T.
3.	" shena-heh	"	32.80	N.A.	N.T.
4.	" Khnai	"	26.70	N.A.	N.T.
5.	" jrong	"	12.70	M.A.	M.T.
6.	" lushai	"	25.47	N.A.	N.T.
7.	" byrwa	"	15.00	M.A.	M.T.
8.	K1	TNAU, Coimbatore	53.50	A	M.T.
9.	K2	"	48.70	M.A.	M.T.
10.	G3	Tea Station, Guntur	33.74	A	M.T.
11.	G4	"	45.12	A	M.T.
12.	G5	"	27.45	A	M.T.
13.	C.A. 960	"	87.23	A	M.T.
14.	C.A. 1068	"	51.90	A	M.T.
15.	LIC 6	"	40.00	M.A.	M.T.
16.	LIC 24	"	41.50	M.A.	M.T.
17.	X-200	"	43.00	M.A.	M.T.
18.	Chinese giant	M/s.Pestonjee F.Pocha Seeds, Poona	9.90	M.A.	N.T.
19.	California wonder	"	4.00	M.A.	N.T.
20.	Long red	"	27.20	N.A.	N.T.
21.	Hungarian wax	"	11.23	N.A.	N.T.
22.	NP-46 A	NSC, New Delhi	76.80	A	M.T.
23.	Pusa jwala	IARI, New Delhi	102.37	A	M.T.

continued...

Table 1 continued

-2-

Sl. No.	Name of variety	Source	Mean No. of fruits per plant	Adaptability	Tolerance to leaf curl complex
24.	Cherry red	Agri-Horti Society, Trivandrum.	29.90	A	M.T.
25.	Black suryamukhi	"	113.28	A	M.T.
26.	Purple cluster	"	8.30	A	M.T.
27.	Indian long red	"	54.20	M.A.	M.T.
28.	Parankimulaku	AHS, Taliparamba.	46.68	M.A.	M.T.
29.	Yolo wonder	Katrain Station, H.P.	3.00	M.A.	N.T.
30.	Bull nose	"	4.00	M.A.	N.T.
31.	Elephant trunk	"	12.50	M.A.	N.T.
32.	Improved Kashmiri long	Modern Seed Farm, Sreenagar.	7.20	N.A.	N.T.
33.	Red long	"	5.50	N.A.	N.T.
34.	Early California wonder	"	2.00	N.A.	N.T.
35.	Oskosh	"	4.00	M.A.	N.T.
36.	Russian Yellow	"	3.00	N.A.	N.T.
37.	Golden California wonder	"	3.50	N.A.	N.T.
38.	World beater	"	4.50	M.A.	N.T.
39.	Red Chilli	Modern Seed Farm, Sreenagar.	21.50	N.A.	N.T.
40.	Byadagi	U.A.S. Hebbal	19.60	M.A.	M.T.
41.	Chikkaballapur	"	21.70	M.A.	M.T.
42.	Samba	Kanyakumari District.	51.80	A	M.T.

continued...

Table 1 continued

-3-

Sl. No.	Name of variety	Source	Mean No.of fruits per plant	Adapta-bility	Tolerance to leaf curl complex
43.	Kar	Kanyakumari District.	39.90	A	M.T.
44.	Kundu vattal	"	43.57	A	M.T.
45.	Vella notchi	"	18.00	A	M.T.
46.	Patcha notchi	"	19.50	A	M.T.
47.	Chemmary Compan (Long)	"	24.13	A	M.T.
48.	Chemmary Compan (Wrinkled)	"	21.37	A	M.T.
49.	Gundumuleku	"	200.80	M.A.	M.T.
50.	Samman	"	46.70	A	M.T.
51.	Pandimuleku	"	49.70	M.A.	M.T.
52.	Pant C-1	Pant Nagar Agrl. Uni-versity.	73.80	A	T
53.	Pant C-2	"	55.60	M.A.	M.T.
54.	Coorg chilli	Coorg	37.70	M.A.	M.T.
55.	Mysore chilli	"	61.50	M.A.	M.T.
56.	Coorg hethur	"	17.00	M.A.	M.T.
57.	Coorg black	"	4.60	M.A.	M.T.
58.	Coorg big	"	3.00	M.A.	M.T.
59.	Pollachi	Palghat District	11.57	N.A.	N.T.
60.	Agali local	"	13.56	N.A.	N.T.
61.	Red Slender	Trivandrum District	281.30	M.A.	N.T.
62.	Purple round	"	35.00	A	T
63.	Mathan Muleku	Nileshwar	31.79	M.A.	M.T.

Note: A - Adaptable
M.A. - Moderately adaptable
N.A. - Not adaptable

T - Tolerant
M.T. - Moderately tolerant
N.T. - Not tolerant

3. Analysis of variance and covariance.

The analysis of variance in the different varieties with respect to each of the characters was done as suggested by Panse and Sukathme (1957). To obtain genotypic variance analysis of variance table was set up as shown in table 2 with the expected mean squares as per Kempthorne (1957).

Analysis of variance provided separate estimates for genotypic (σ^2_g) and environmental (σ^2_e) components of variance.

$$\hat{\sigma}^2_e = M_{13}$$

$$\hat{\sigma}^2_g = (M_{12}-M_{13})/r$$

The phenotypic variance ($\hat{\sigma}^2_p$) was obtained by addition,

$$\hat{\sigma}^2_p = \hat{\sigma}^2_g + \hat{\sigma}^2_e$$ (Singh and Choudhary, 1979).

The genotypic and phenotypic coefficients of variation were computed as $100\,\hat{\sigma}_g/\mu$ and $100\,\hat{\sigma}_p/\mu$ respectively where $\hat{\sigma}_g$ and $\hat{\sigma}_p$ are genotypic and phenotypic standard deviations and μ is the mean of the trait under consideration. Covariance analysis between all the possible pairs of traits and the expectations of the mean sum of products are represented in table 2. Thus the estimates of the genotypic and phenotypic covariance components between two traits were derived by the same method as that of the corresponding variance components.

Table 2. Analysis of variance and covariance table

Source	df	MS_{x_1}	$MSP_{x_1x_2}$	MS_{x_2}	$E(MS_{x_1})$	$E(MSP_{x_1x_2})$
Replication	r-1	M_{11}	P_1	M_{21}		
Varieties	v-1	M_{12}	P_2	M_{22}	$\sigma^2_{e_1} + r\sigma^2_{g_1}$	$\sigma_{e_1e_2} + r\sigma_{g_1g_2}$
Error	(r-1)(v-1)	M_{13}	P_3	M_{23}	$\sigma^2_{e_1}$	$\sigma_{e_1e_2}$

Where $E(MS_{x_1})$ is the expectation of mean squares of character x_1

$E(MSP_{x_1x_2})$ is the expectation of mean sum of products of character x_1 and x_2

r is the number of replications

v is the number of varieties

$\sigma^2_{e_1}$ is the variance due to error in character x_1

$\sigma^2_{g_1}$ is the genotypic variance in character x_1

$\sigma_{e_1e_2}$ is the covariance due to error in characters x_1 and x_2

$\sigma_{g_1g_2}$ is the genotypic covariance in characters x_1 and x_2

These covariance components were substituted in the following formula to calculate the genotypic (r_g) and phenotypic (r_p) correlation coefficients.

Genotypic correlation coefficient $r_{G_1G_2} = \dfrac{\hat{C}_{G_1G_2}}{\hat{C}_{G_1} \cdot \hat{C}_{G_2}}$

where $\hat{C}_{G_1G_2}$ is the genotypic covariance between the two traits,

$\hat{C}_{G_1}$ is the genotypic standard deviation of the first trait and

$\hat{C}_{G_2}$ is the genotypic standard deviation of the second trait

Phenotypic correlation coefficient $r_{P_1P_2} = \dfrac{\hat{C}_{P_1P_2}}{\hat{C}_{P_1} \cdot \hat{C}_{P_2}}$

where $\hat{C}_{P_1P_2}$ is the phenotypic covariance between the two traits,

$\hat{C}_{P_1}$ is the phenotypic standard deviation of the first trait and

$\hat{C}_{P_2}$ is the phenotypic standard deviation of the second trait

Phenotypic coefficient of variation $= \dfrac{\hat{C}_P \times 100}{\text{Mean}}$

Genotypic coefficient of variation $= \dfrac{\hat{C}_G \times 100}{\text{Mean}}$

Heritability in broad sense

$$h^2 = \frac{\hat{V}_G \times 100}{\hat{V}_P}$$

where h^2 = heritability expressed in percentage

$\hat{V}_g$ = estimate of genotypic variance

$\hat{V}_p$ = estimate of phenotypic variance

Expected genetic advance under selection

$$GA = K.h^2 \sqrt{\hat{V}_p}$$

where GA = Genetic advance

h^2 = heritability in broad sense

$\hat{V}_p$ = phenotypic variance

K = selection differential expressed in phenotypic standard deviation

K = 2.06 in the case of 5% of selection in large samples.

4. Path coefficient analysis

The genotypic correlation coefficients of different morphological characters with fruit yield were partitioned into direct and indirect effects.

For determining the cause and effect relationship, important characters were classified as first and second order components. Number of fruits, number of secondary branches, girth of fruit, weight of individual fruit and life span were taken as the first order components of fruit yield. Number of primary branches and spread were taken as the second order components.

For selecting the above first order components of fruit yield it may be pointed out that these may not be the only first order or primary "causes" of yield. Many factors (genetic and non-genetic) might influence yield, but these factors express their influence mainly through effects on number of fruits, number of secondary branches, girth of fruit, weight of individual fruit and life span which are included as first order components.

The estimates of direct and indirect effects were calculated as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). The path coefficients were obtained by the simultaneous solution of the following equations which express the basic relationship between correlations and path coefficients.

$$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + - - - - + r_{1k}P_{ky}$$

$$r_{2y} = r_{21}P_{1y} + P_{2y} + r_{23}P_{3y} + - - - - + r_{2k}P_{ky}$$

$$r_{3y} = r_{31}P_{1y} + r_{32}P_{2y} + P_{3y} + - - - - + r_{3k}P_{ky}$$

$$\vdots$$

$$r_{ky} = r_{k1}P_{1y} + r_{k2}P_{2y} + r_{k3}P_{3y} + - - - + r_{k-1}, {}_kP_{k-1}; y + P_{ky}$$

where

r_{1y} to r_{ky}	denote coefficients of correlation between causal factors 1 to k and the dependent character y.
r_{12} to $r_{k-1,\,k}$	denote coefficients of correlation among all possible combinations of causal factors and
P_{1y} to P_{ky}	denote direct effects of character 1 to k on the character y.

The above equations can be written in the matrix form as shown below:-

$$\begin{Bmatrix} r_{1y} \\ r_{2y} \\ r_{3y} \\ \vdots \\ r_{ky} \end{Bmatrix} = \begin{Bmatrix} 1 & r_{12} & r_{13} & \cdots & r_{1k} \\ & 1 & r_{23} & \cdots & r_{2k} \\ & & 1 & \cdots & r_{3k} \\ & & & \ddots & \vdots \\ & & & & 1 \end{Bmatrix} \begin{Bmatrix} P_{1y} \\ P_{2y} \\ P_{3y} \\ \vdots \\ P_{ky} \end{Bmatrix}$$

i.e. $\underset{\sim}{A} = \underset{\sim}{C}\,\underset{\sim}{B}$

Hence $\underset{\sim}{B} = \underset{\sim}{C}^{-1}\,\underset{\sim}{A}$,

where $\underset{\sim}{C}^{-1}$ = is the inverse of $\underset{\sim}{C}$

$$\text{let } C^{-1} = \begin{Bmatrix} C_{11} & C_{12} & C_{13} \cdots\cdots\cdots C_{1k} \\ & C_{22} & C_{23} \cdots\cdots\cdots C_{2k} \\ & & C_{33} \cdots\cdots\cdots C_{3k} \\ & & \vdots \\ & & C_{kk} \end{Bmatrix}$$

Path coefficients are obtained as

$$\sum P_{1y} = \sum_{i=1}^{k} C_{1i}\ r_{1y}\ !$$

$$P_{2y} = \sum_{i=1} C_{2i}\ P_{1y} \cdots\cdots\text{etc.}$$

The residual factor (x) which measures the contribution of the rest of the characters not considered in the causal scheme was obtained as

$$P_{xy} = \sqrt{1 - R^2}$$

$$\text{Where } R^2 = \sum_{i=1}^{k} P_{iy}^2 + 2 \sum_{i} \sum_{j} P_{iy}\ P_{jy}$$

5. Multivariate analysis

Wilks' Λ criterion (Wilks, 1932) was used to test the significance of the difference between the 30 varieties with regard to the mean values of all the 15 characters simultaneously

as follows:

$$\Lambda = \frac{|E|}{|E + V|}$$

Where E is the matrix of the error sum of squares and E+V sum of products (here the dimension of E is 15 x 15) and E+V is the matrix of the sum of squares and sum of products due to error plus the respective sum of squares and sum of products due to varieties (here also the dimension of E+V is 15 x 15.

or $$\Lambda = \frac{|E|}{|E+V|} = \frac{|\text{Determinant of error matrix}|}{|\text{Determinant of error + Variety matrix}|}$$

From the value of Λ the 'V' statistics was calculated using the relation.

$$V = -m \log_e \Lambda = \frac{-(n-p+q+1)}{2} \log_e \Lambda$$

Where $m = \frac{n-(p+q+1)}{2}$

n = d.f. for error + varieties

= $(N_1+N_2+ \text{-------} N_k)-1$

p = number of characters

q = number of varieties-1 = k-1

N_1, N_2-------N_k are sample size from A_1, A_2-------A_k population (varieties) from which the correlated characters are selected.

This 'V' statistics follows a χ^2 distribution with pq degrees of freedom. Since the degrees of freedom in the

present study exceeds 30, the expression,

$z = \sqrt{2\chi^2} - \sqrt{2n-1}$ was used as a normal deviate (Singh and Chaudhary, 1979). The significance of V statistics shows that the difference between the mean in respect of the effect of 'P' characters between different populations are significant. Hence, further analysis to estimate the D^2 values was made.

6. D^2 analysis

The genetic divergence between the thirty varieties was estimated by using the Mahalanobis' D^2 statistic (Mahalanobis, 1925, 1928, 1936). The D^2 values between two populations on the basis of P characters is given by the relation.

$$D^2_p = (d)\ (\lambda_{ij})^{-1}\ (d)'$$

$$= (d)\ (\lambda^{ij})\ (d)'$$

$$= \sum_{i=1}^{p} \sum_{j=1}^{p} \lambda^{ij}\ d_i d_j$$

where λ^{ij} values are the elements of the reciprocal matrix of the pooled common dispersion matrix having elements of the form λ_{ij}.

d_i = is the difference in the mean values for the i^{th} character between the two populations

(d) is the row matrix of the d_i's

(λ^{ij}) is the square matrix of the λ^{ij}'s

The computation using the above formula is tedious since each D^2 required the sum of P^2 quantities and each quantity itself is the product $\lambda^{ij} \; d_i d_j$ for any i and j. The computation is simplified by working with a set of transformed uncorrelated linear combinations (y's) obtained from the original variables (x's) by pivotal condensation of the common dispersion matrix, (Rao, 1952). Using the relation between y's and x's the mean values of different varieties for the different characters were transformed into the mean values of a set of uncorrelated linear combinations (y's). The D^2 between the i^{th} and j^{th} variety for P characters is calculated separately as

$$D^2_{ij} = \sum_{t=1}^{P} (Y_{it} - Y_{jt})^2$$

where Y_{it} is the mean value of the t^{th} linear combination for the i^{th} variety and Y_{jt} is the mean value of the t^{th} linear combination for the j^{th} variety. Thus D^2_{ij} can be considered as the sum of the P component D^2 values corresponding to $t = 1, 2 \ldots\ldots\ldots P$. The P component D^2 values were calculated separately and added upto get D^2_{ij}. The P component D^2 values for each combination were ranked in the descending order of magnitude, equal values, if they occur, which are very rare, receiving same ranks. The ranks were added up for each component D^2 over all combinations to obtain the rank totals.

The computations were made using the computer programme of Murthy and Arunachalam (1967) with suitable modifications. The significance of the total D^2 between any two varieties was tested using the method suggested by Nair and Mukherji (1950). They suggested that for testing the significance of the mean values of p characters for any two populations out of k from which the common dispersion matrix was computed, the expression,

$$\frac{n_1 n_2 (n_1+n_2+\cdots\cdots+n_k-k-p+1)}{p(n_1+n_2)\,(n_1+n_2+\cdots\cdots+n_k-k)} \; D^2_{1,2}$$

may be used as a variance ratio (F) with degrees of freedom

$$(p,\ \sum_{i=1}^{k} n_i-k-p+1)$$

In the above expression n_1, n_2 $\cdots\cdots$ n_k are sample sizes of the two populations under consideration.

(1) Formation of clusters

Clusters were formed by adopting Tocher's method (Rao, 1952) such that the intra-cluster average D^2 is small while the inter-cluster average D^2 is large. The first step is to start with two closely associated groups and find a third group which has the smallest average D^2 from the first two; similarly, the fourth is chosen to have the smallest D^2 from the first three and so on. If at any stage the average D^2 of a group from those already listed appears to be high, and finds not fitting in with the former groups the same is taken outside the former cluster. The groups of the first

cluster are then omitted and the rest are treated similarly. The change in average D^2 with a cluster due to the inclusion of an additional group is also calculated. If the change is appreciable, then the newly added group has to be considered as outside the cluster. The intracluster average D^2 was computed by adding up the D^2 values for all possible comparisons among the varieties included in that cluster taken two at a time and dividing the total D^2 so obtained by the number of D^2's. Similarly, the intercluster average D^2 was obtained by summing up the D^2 values in all possible combinations between each variety of one cluster and those of the other and dividing the total D^2 by the number of D^2's. Having formed the clusters, D, the square root of a intercluster D^2 was used to represent the comparative location of the clusters diagramatically.

(ii) Relative contribution of the different characters towards total genetic divergence

The character with the minimum rank total was considered to have contributed the maximum towards the divergence, while the one with the maximum rank total was considered to have contributed the least.

7. Canonical analysis.

Canonical analysis helps in confirming the group of constellations arrived at by the D^2 statistic. It also facilitates in many cases the representation of the population in a two dimensional chart. The magnitude of the coefficients

in the successive canonical vectors indicate the relative importance of the characters in the major and secondary axes of differentiation.

The first four canonical roots and the first four canonical vectors were computed by the iteration method described by Rao (1952). The computation method consisted of the following steps.

1. Starting from the matrix of Y-values i.e., the mean values of the uncorrelated linear combinations for all the characters and for all the varieties (used in the computation of D^2 values), the between sum of products matrix for the character was computed (Matrix A).

2. The fourth power of Matrix A was computed to quicken the iteration process.

3. Assuming a trial vector, (1,1,----------1) as many iterations as needed were made until the difference between each element in any two successive vectors did not exceed 0.0009. The vector was standardised and designated as canonical vector 1 and the first canonical root was extracted.

4. The residual matrix after eliminating vector 1 was found out and the process repeated to get the next vector and so on until the first four vectors and roots were obtained.

5. The mean values of the first two vectors designated as Z_1 and Z_2 were computed for each variety.

6. Sum of all canonical roots and the percentage contribution of the first 4 roots to the total variation were also computed.

The canonical analysis of 30 varieties of C. annuum scored for fifteen characters was done as above, using the computer programme of Arumachalam (1967) with suitable modifications.

8. Estimation of heterosis

In a specific cross, heterosis is usually measured in terms of two parameters namely (i) Heterosis over the mid-parental value and (ii) Heterosis over the better parent. Recently a new term heterobeltiosis has been proposed (Bitzer et al., 1968; Fonseca and Patterson, 1968 and quoted by Rai, 1979). In plant breeding programmes, however it is also estimated in terms of heterosis over the check variety. For commercial exploitations this value is perhaps the most important one.

In each combination a parent having increased height, more number of leaves, higher yield as the case may be considered to be a better parent, than the other. The heterosis was expressed as the percentage of increase of the mean value of the F_1 over those of the mid-parent and better parent using the relation

$$H = \left(\frac{\bar{X}_{F_1} - \bar{X}_P}{\bar{X}_P} \right) \times 100$$

Where $\bar{X}_{F1}$ = Mean value of F_1

and $\bar{X}_p$ = Mean value of mid parent or better parent as the case may be

Negative heterosis, expressed as the percentage of decrease of the mean value of the F_1 over those of mid parent and better parent were worked out with respect to two characteristics namely number of days taken for blooming and number of seeds per fruit.

For testing the significance of the difference between the mean value of the F_1 and those of the mid-parent, better parent, the critical difference values were calculated as follows:

(a) for testing the significance over mid parent (CD_1)

$$CD_1(.05) = t_e^{(0.05)} \sqrt{\frac{3\ MS_e}{2\ r}}$$

$$C.D.1\ (.01) = t_e^{(.01)} \sqrt{\frac{3\ MS_e}{2\ r}}$$

(b) for testing the significance over better parent (CD_2)

$$CD_2(.05) = t_e^{(.05)} \sqrt{\frac{2\ MS_e}{r}}$$

$$CD_2(.01) = t_e^{(.01)} \sqrt{\frac{2\ MS_e}{r}}$$

$t_e^{(.05)}$ and $t_e^{(.01)}$ = The critical value of t corresponding to error d.f. at 0.05 level and 0.01 level respectively.

MS_e = mean square for error and,

r = number of replications.

9. Diallel analysis and estimation of combining ability

The combining ability analysis was based on plot means. The estimation of general and specific combining ability was done as per Method 2 and Model I of Griffing (1956).

Table 3. R.B.D. ANOVA Table (Based on plot mean)

Source	df	SS	MS	Expectations of MS
Varieties	(a-1)	S_v	M_v	$\sigma^2_e + b\,\phi(v)$
Blocks	(b-1)	S_b	M_b	$\sigma^2_e + a\,\phi(b)$
Error (VxB)	(a-1)(b-1)	S_e	M_e	σ^2_e

Where a = Number of genotypes = $p(p+1)/2$

b = Number of blocks

p = Number of parents

σ^2_e = Variance due to error

$\phi(v)$ = $\frac{1}{(a-1)} \leqslant V_i^2$

$\phi(b)$ = $\frac{1}{(b-1)} \leqslant_k b_k^2$

V_i = Effect for the i^{th} genotype

b_k = k^{th} block effect

The test for the differences among genotypes was made by using the following F test.

$$F\left[(a-1),\ m\right] = \frac{M_V}{M_e}$$

Where a-1 and m are the degrees of freedom associated with the numerator and denominator of the F ratio, and M_V and M_e are the variety and error mean squares respectively in the randomised block analysis.

The ANOVA table for g.c.a. and s.c.a. giving expectations of mean squares was as follows:-

Source	df	SS	MS	Expectations of MS
General combining ability	p-1	S_g	M_g	$\sigma^2 + (p+2)\left(\frac{1}{p-1}\right) \leq \sigma_i^2$
Specific combining ability	p(p-1)/2	S_s	M_s	$\sigma^2 + \frac{2}{p(p-1)} \leq_i \leq_j \sigma_{ij}^2$
Error	m	S_e	M_e	σ^2

Where $S_g = \frac{1}{p+2}\left\{\leq_i (X_{i.} + x_{ii})^2 - \frac{4}{p} X_{..}^2\right\}$

$S_s = \leq_i \leq_j x_{ij}^2 + \frac{1}{p+2} \leq_i (X_{i.} + x_{ii})^2 + \frac{2}{(p+1)(p+2)} X_{..}^2$

m = Degrees of freedom for error from the RBD ANOVA

$M_e' = \frac{M_e}{b.c}$, where M_e is the error mean square from the RBD ANOVA

c = Number of plants per plot

$X_{i.} = \sum x_{ij} = x_{i1} + x_{i2} + \text{-------} + x_{ij}$, where

$X_{..} = \sum_i \sum_j x_{ij} = x_{11} + x_{12} + \text{----------} x_{p-1, p}$

$x_{ij} = \mu + g_i + g_j + s_{ij} + \frac{1}{b.c} \sum_k \sum_l e_{ijkl}$ $\begin{cases} i,j = 1,2,\ldots,p \\ k = 1,2,\ldots,b \\ l = 1,2,\ldots,c \end{cases}$

where μ = Population mean

g_i = The g.c.a. effect of the i^{th} parent

s_{ij} = The s.c.a. effect of the i^{th} and j^{th} parent

e_{ijkl} = The random component associated with the observation

The restriction $\sum_i g_i = 0$ and

$\sum_j s_{ij} + s_{ii} = 0$ (for each i) were imposed

The following F ratios were used to test the g.c.a. and s.c.a. effects.

For differences among g.c.a. effect

$$F\ ((p-1), m) = \frac{M_g}{M_e};$$

For differences among s.c.a. effects

$$F\left[\left(\frac{p(p-1)}{2}, m\right)\right] = \frac{M_s}{M_e},$$

The effects were estimated as follows:-

$$\hat{\mu} = \frac{2}{p(p+1)} X_{..}$$

$$\hat{g}_i = \frac{1}{p+2}\left(X_{i.} + X_{ii} - \frac{2}{p} X_{..}\right)$$

$$\hat{s}_{ij} = x_{ij} - \frac{1}{p+2}\left(X_{i.} + x_{ii} + X_{j.} + x_{jj}\right) + \frac{2}{(p+1)(p+2)} X_{..}$$

The variance of any parent or F_1 mean value is

$\text{var}(x_{ij}) = \hat{\sigma}^2 = M_e$ and

the variance of the difference between any two mean values is

$\text{var}(x_{ij} - x_{kl})$

Variances of effects and difference between effects was estimated as follows:-

$$\text{Var}(\hat{\mu}) = \frac{2}{p(p+1)} \hat{\sigma}^2$$

$$\text{Var}(\hat{g}_i) = \frac{p-1}{p(p+2)} \hat{\sigma}^2$$

$$\text{Var}(\hat{s}_{ii}) = \frac{p(p-1)}{(p+1)(p+2)} \hat{\sigma}^2$$

$$\text{Var}(\hat{s}_{ij}) = \frac{p^2+p+2}{(p+1)(p+2)} \hat{\sigma}^2 \quad (i \neq j)$$

$$\text{Var}(\hat{g}_i - \hat{g}_j) = \frac{2}{p+2} \hat{\sigma}^2 \quad (i \neq j)$$

$$\text{Var}(\hat{s}_{ii} - \hat{s}_{jj}) = \frac{2(p-2)}{(p+2)} \hat{\sigma}^2 \quad (i \neq j)$$

$$\text{Var}(\hat{s}_{ij} - \hat{s}_{ik}) = \frac{2(p+1)}{p+2} \hat{\sigma}^2 \quad (i \neq j,\ k;\ j \neq k)$$

$$\text{Var}(\hat{s}_{ij} - \hat{s}_{ki}) = \frac{2p}{p+2} \hat{\sigma}^2 \quad (i \neq j,\ k,\ l,\ k,l;\ k \neq l)$$

10. Gene action

Gene action was studied by conducting the diallel analysis (Hayman, 1954).

Assuming that the parental varieties and their progeny do not differ in response to environmental changes, a common environmental component of variation, E, as measured by block x treatment interaction was calculated by the ordinary method of analysis from the ANOVA done under combining ability analysis.

But the total sum of squares was divided into two portions only, that is, between and within treatment SS with (a-1) and a(b-1) degrees of freedom, respectively, the block SS being included within treatment SS. Thus the environmental component of variation became,

$$E = \frac{1}{b}\left[(S_b + S_e)/a(b-1)\right]$$

Before calculating other statistics a diallel table was formed in which the respective values for the three blocks were totalled. This table provided basis for calculating the variance of the parents ($V_0 L_0$), variance of the arrays (V_r), the covariance between the individual arrays and the non-recurring parents (W_r), etc.

The uniformity of W_r-V_r was then tested. The 't' for testing this was given by the following formula of Hayman (1954).

$$t^2 = \frac{n-2}{4} \frac{(\text{Var } V_r - \text{Var } W_r)^2}{\text{Var } V_r \cdot \text{Var } W_r - \text{Co } v^2(V_r, W_r)}$$

with p-2 degrees of freedom

The significance of 't' was taken to indicate failure of hypothesis.

The regression coefficient, b, of W_r on V_r was calculated as:

$$b = \frac{\text{Cov}\ (V_r,\ W_r)}{\text{Var}\ V_r}$$

The standard error of b, S_b, was calculated as per the formula given by Smith (1954):

$$S_b = \left\{\left[(y-\bar{y})^2 - b \Sigma (x-\bar{x})\ (y-\bar{y})\right] / (p-2) \Sigma (x-\bar{x})^2\right\}^{\frac{1}{2}}$$

where $x = V_r$; $y = W_r$. The 't' values of $(b-0)/S_b$ and $(1-b)/S_b$ with p-2 degrees of freedom were used as measures for testing significant deviations of b values from zero and unity, respectively.

In cases where the uniformity of W_r-V_r was observed and the $(b-0)/S_b$ was significant further diallel analysis was continued.

Where the 't' testing the homogeneity of W_r-V_r showed significance and where the b value was not significantly different from zero, sub-diallel tables were constructed by omitting each array in turn and then testing for the homogeneity of W_r-V_r and the significance of b from zero in each of the resulting (n-1) x (n-1) diallel tables where n is the number of parents used as suggested by Hayman (1954). When these tests were satisfied the sub-diallel was assumed to satisfy

the hypotheses.

In some cases where none of the (n-1) x (n-1) sub-diallel sets satisfied the hypotheses, the line whose omission minimised the heterogeneity together with each of the remaining lines was omitted and the tests conducted. The sub-diallel which was near the satisfactory proposition was selected for further studies.

The following were then computed.

E	:	The expected environmental component of variation
V_0L_0	:	Variance of the parents
V_r	:	Variance of the r^{th} array
V_1L_1	:	Mean variance of the arrays
M_r	:	The covariance between non-recurring parents and the offspring of the r^{th} array
M_0L_{01}	:	The mean covariance between the parents and the arrays
M'	:	The covariance between the array means and the offspring of the r^{th} array
V_0L_1	:	The variance of the means of the arrays and
$M_{L1}-M_{L0}$	:	The difference between the mean of the parents and the mean of their progeny.

Using the above values, the various genetic components were calculated based on the formula of Hayman (1954) as

demonstrated by Aksel and Johnson (1963).

$\hat{D} = V_0L_0 - \hat{E}$,

$\hat{F} = 2V_0L_0 - 4W_0L_{01} - 2(n-2)\ \hat{E}/n$,

$\hat{H}_1 = V_0L_0 - 4W_0L_{01} + 4V_1L_1 - (3n-2)\ \hat{E}/n$,

$\hat{H}_2 = 4V_1L_1 - 4V_0L_1 - 2\hat{E}$,

$\hat{h}^2 = 4(M_{L1} - M_{L0})^2 - 4(n-1)\ \hat{E}/n^2$

The standard errors for the estimates of these components were calculated using the equation $\frac{1}{r}\ \mathrm{Var}\ (W_r - V_r) = S^2$ as the common multiplier and the terms of the main diagonal of the covariance matrix given by Hayman (1954) as corresponding multipliers. Thus the standard error of $\hat{D}$, $S_{\hat{D}} = \sqrt{S^2 \times C\hat{D}}$, the standard error $\hat{F}$, $S_{\hat{F}} = \sqrt{S^2 \times C\hat{F}}$, etc. The significance of each component was tested using the respective standard errors.

Then the following were also calculated:

(i) mean degree of dominance $(\hat{H}_1/\hat{D})^{\frac{1}{2}}$

(ii) the proportion of genes with positive and negative effects in parents $(\hat{H}_2/4\hat{H}_1)$

(iii) the proportion of dominant and recessive genes in the parents $\dfrac{(4\,\hat{D}\,\hat{H}_1)^{\frac{1}{2}} + \hat{F}}{(4\,\hat{D}\,\hat{H}_1)^{\frac{1}{2}} - \hat{F}}$

(iv) the number of groups of genes which control the character and exhibit dominance $(\hat{h}^2/\hat{H}_2)$ and

(v) the coefficient of correlation, r, between the parental measurements (V_p) and the parental order of dominance (W_p+V_p).

In cases where r^2 was close to unity prediction of measurements of the completely dominant and recessive parents was done as demonstrated by Aksel and Johnson (1963).

The V_p, W_p graph, taking V_p on the x-axis and W_p on the y-axis was drawn as suggested by Jinks and Hayman (1953). The observed regression line (W_p, V_p) was fitted using the formula $W_p = a+b\ V_p$, where a = the intercept value and b = the regression coefficient of W_p on V_p. The expected regression line of unit slope was also drawn.

The W_p, W' graph was constructed by taking W_p values on the x-axis and W' values on the y-axis, together with the theoretical regression line of $\frac{1}{4}$ slope as suggested by Allard (1956a).

The standard deviation of Y_p, the parental measurements and (W_p+V_p), the order of dominance of the parents were computed by the formula $(x_i-\bar{x})/s$ where x_i is the value of the individual parent, $\bar{x}$, the mean of the parents and s, the standard deviation (Johnson and Aksel, 1959). The standardized deviation graph was drawn by taking the standardized values of Y_p on the x-axis and those of (W_p+V_p) on the y-axis.

The analysis of the data was carried out at the Computing Centre of the University of Kerala, using the I.B.M. 316 Model Computer.

RESULTS

RESULTS

1. Analysis of variance, covariance and estimation of correlation coefficients and genetic parameters.

Analysis of variance of plot means displayed highly significant differences among the varieties except for the character capsaicin content (Table 4). The mean values for the fifteen characters in thirty varieties are presented in table 5. The different varieties displayed considerable variation with respect to the characters studied.

The general mean of fifteen characters along with phenotypic, genotypic and environmental coefficient of variability, heritability in the broad sense, genetic advance due to selection are presented in table 6.

The environmental coefficient of variability was comparatively less for all the characters. The phenotypic as well as genotypic coefficient of variability was maximum for number of fruits, while life span possessed minimum. Heritability in the broad sense varied from 70.915 (number of primary branches) to 99.924 (girth of fruit). The genetic advance due to selection was higher for important economic attributes like total yield, number of fruits and weight of fruit. The corresponding figures for nutritive and quality characters were also high.

The phenotypic, genotypic and environmental correlation coefficients were estimated and are presented in table 7.

The different character pairs showed different degrees of correlations. Among the 105 character pair combinations 12 were significant at 5 per cent level and 26 at 1 per cent in the phenotypic correlation coefficients, while the corresponding numbers were 9 and 30 respectively in the genotypic correlation coefficients.

The genotypic correlation coefficients were of higher magnitude than the phenotypic correlation coefficients in general. Wherever both phenotypic and genotypic correlations were significant they were both of the same sign (either positive or negative). At the genotypic level fruit yield exhibited significant positive correlation with number of fruits at 1 per cent level. The number of fruits exhibited significant positive correlation with primary branches, secondary branches and total yield at 1 per cent level. At the same time it showed significant negative correlation with number of seeds at 1 per cent level and with weight and girth of fruit at 5 per cent level. Vitamin C content displayed significant positive correlation with weight of fruit, number of seeds, length of fruit, and girth of fruit at 1 per cent level, while it showed significant negative correlation with number of days taken for blooming and life span. The capsaicin content exhibited significant negative correlation with number of seeds at 1 per cent level while it showed significant negative correlation with weight of fruit and Vitamin C-content at 5 per cent level.

Table 4. Analysis of variance table for the varieties under each character.

Source	df	Blooming	Height	Spread	Number of primary branches	Number of secondary branches	Number of fruits	Weight of fruit
Replication	2	4.015	0.211	6.398	0.677	4.900	7.507	0.157
Varieties	29	482.269**	515.235**	204.312**	5.387**	410.256**	10979.485**	98.535**
Error	58	2.482	7.820	4.561	0.648	7.325	15.614	0.313

Life span	Number of seeds	Length of fruit	Girth of fruit	Total yield	Vitamin A	Vitamin C	Capsaicin
73.750	31.343	0.244	0.047	42.125	40959.992	7.00	0.0001
707.146**	4242.343**	12.473**	42.002**	92094.016**	25123086.00**	4951.132**	0.103
6.101	22.586	0.414	0.010	455.081	18974.894	4.474	0.0001

**Significant at 1 per cent level

Table 5. Mean values of the thirty varieties of chillies, with respect to 15 characters studied for the estimation of genetic divergence.

Varieties	Characters							
	Blooming	Height	Spread	Number of primary branches	Number of secondary branches	Number of fruits	Weight of fruits	Life span
1. Jrong	76.00	58.33	39.00	5.00	8.40	10.34	10.20	142.34
2. Red slender	77.33	69.67	55.00	7.40	51.34	278.33	1.36	150.33
3. Purple cluster	64.66	40.00	21.00	2.66	12.66	7.40	2.03	165.67
4. Gundu mulaku	63.33	43.67	33.00	4.67	16.67	202.67	4.70	143.34
5. CA 1068	69.00	64.67	45.00	5.70	48.70	49.40	2.90	141.66
6. Chemmary compan (Long)	62.00	76.34	56.33	4.66	11.00	23.00	8.53	122.00
7. Coorg big	85.00	66.00	43.00	3.70	10.00	2.33	14.00	147.67
8. CA 960	84.66	59.66	37.00	4.67	20.00	85.00	4.00	143.66
9. Pant C-1	72.00	33.67	38.34	4.33	14.00	71.34	1.16	133.70
10. Chemmary compan (Wrinkled)	80.00	33.66	45.00	4.40	28.34	19.00	8.30	137.67
11. Pusa jwala	73.00	40.67	45.33	5.00	42.40	98.40	2.86	138.00
12. Black Suryamukhi	80.33	39.00	38.00	5.67	21.67	115.66	2.56	150.34
13. G3	90.00	48.00	39.00	5.40	27.40	32.67	1.73	157.40
14. G4	89.66	43.66	27.34	4.67	26.00	42.00	1.83	151.00
15. G5	83.33	42.67	24.40	7.33	14.34	25.40	1.63	145.67

continued...

Table 5 continued

Varieties	Characters							
	Blooming	Height	Spread	Number of primary branches	Number of secondary branches	Number of fruits	Weight of fruits	Life span
16. California wonder	42.66	44.66	31.00	2.40	7.40	3.66	22.66	104.33
17. Chinese giant	42.00	45.00	31.00	2.66	5.70	5.00	24.66	107.70
18. Hungarian wax	50.00	53.67	38.00	4.34	10.00	10.34	6.76	116.66
19. Coorg black	70.00	55.33	48.70	3.00	16.67	4.40	6.77	132.34
20. Coorg hethur	84.66	31.00	39.34	4.33	14.70	15.67	3.16	150.33
21. Mysore chilli	82.00	76.66	54.33	5.00	27.00	58.00	2.96	148.67
22. Purple round	93.00	64.00	39.40	7.00	14.33	31.70	4.33	171.00
23. NP-46A	70.66	42.34	44.00	7.67	33.40	78.33	2.86	147.00
24. Byrwa	69.66	60.70	35.34	3.34	19.00	13.00	3.46	155.33
25. Vella notchi	62.66	33.67	44.00	4.40	26.00	15.34	7.10	124.34
26. Patcha notchi	64.33	34.00	43.00	4.33	22.00	18.00	7.20	126.67
27. K1	71.00	40.34	46.33	5.67	36.34	54.40	2.90	138.40
28. LIC 24	76.33	42.33	40.00	4.34	26.00	42.00	2.86	149.67
29. LIC 6	68.33	42.00	43.00	5.00	24.70	42.00	2.46	150.00
30. X-200	68.00	43.33	42.00	5.00	27.34	41.00	2.53	152.00

continued...

Table 5 continued

Varieties	Number of seeds	Length of fruit	Girth of fruit	Total yield	Vitamin A	Vitamin C	Capsaicin
1. Jrong	132.00	8.44	5.43	106.00	6592.00	128.41	0.056
2. Red slender	25.34	4.40	2.50	380.34	2373.67	70.45	0.316
3. Purple cluster	28.40	3.10	3.93	14.67	8851.66	61.48	0.213
4. Gundu mulaku	28.00	2.73	4.44	947.99	11036.34	94.34	0.153
5. CA 1068	57.33	8.14	3.24	143.66	3111.00	86.48	0.160
6. Chemmary compan (Long)	98.40	8.20	6.93	196.00	5559.00	167.20	0.066
7. Coorg big	85.00	5.43	8.53	32.66	4555.00	60.28	0.113
8. CA 960	88.67	9.67	3.46	342.34	9028.67	68.52	0.143
9. Pant C-1	44.70	5.56	2.63	82.67	10925.34	119.56	0.519
10. Chemmary compan (Wrinkled)	105.00	7.46	7.06	156.67	6037.00	165.52	0.048
11. Pusa jwala	49.33	10.10	2.86	281.34	3851.66	143.94	0.220
12. Black Suryamukhi	33.67	4.46	2.53	296.66	9009.00	136.11	0.208
13. G3	47.66	7.27	2.70	56.00	2333.00	90.37	0.128
14. G4	44.70	5.56	2.96	76.70	8259.34	65.84	0.233
15. G5	70.33	4.47	5.10	41.00	10555.34	77.44	0.160

Continued...

Table 5 continued

Varieties	Number of seeds	Length of fruit	Girth of fruit	Total yield	Vitamin A	Vitamin C	Capsaicin
16. California wonder	171.66	7.10	18.06	83.67	3555.00	159.83	0.023
17. Chinese giant	144.00	6.40	16.30	123.33	3447.67	177.63	0.016
18. Hungarian wax	74.67	7.13	7.26	69.67	3718.00	180.64	0.023
19. Coorg black	76.33	4.60	4.03	29.00	2536.67	88.11	0.143
20. Coorg hethur	47.34	5.40	4.96	49.66	3536.67	76.85	0.160
21. Mysore chilli	64.67	3.30	3.93	171.67	3470.00	73.07	0.186
22. Purple round	24.66	2.93	7.60	137.40	5503.67	108.09	0.150
23. NP-46A	52.70	9.70	2.80	226.00	3311.00	147.99	0.213
24. Byrwa	19.67	4.26	8.53	45.00	4481.34	68.16	1.010
25. Vella notchi	114.00	7.43	7.00	108.67	6111.00	166.52	0.051
26. Patcha notchi	103.33	7.53	7.03	129.33	6037.00	159.50	0.061
27. K1	94.00	7.40	3.13	157.34	3856.00	94.08	0.240
28. LIC 24	87.66	6.83	3.03	121.00	2518.34	70.18	0.186
29. LIC 6	79.67	6.70	2.96	103.00	2373.67	78.94	0.193
30. K-200	36.00	5.63	3.06	104.00	2488.34	91.99	0.166

Table 6. Population means and Genetic Parameters of different characters.

Characters	General mean	Coefficient of variability			Heritability (in broad sense) %	Genetic advance due to selection	
		Phenotype	Genotype	Environmental		5% level	10% level
1. Blooming	72.1889	17.6538	17.5184	0.1354	98.4716	35.8110	30.4219
2. Height	48.9556	27.1728	26.5656	0.6072	95.5807	53.5021	45.4509
3. Spread	40.2000	20.9820	20.2982	0.6838	93.5889	40.4518	34.3644
4. Primary branches	4.7778	31.2386	26.3063	4.9323	70.9150	45.6348	38.7674
5. Secondary branches	22.1000	53.8510	52.4400	1.4111	94.8281	105.1957	89.3653
6. Number of fruits	49.8444	121.5431	121.2843	0.2588	99.5745	249.3135	211.7955
7. Weight of fruit	5.6856	101.1313	100.6502	0.4811	99.0507	206.3529	175.2998
8. Life span	141.4889	10.9443	10.8041	0.1402	97.4555	21.9715	18.6651
9. Number of seeds	76.6222	52.0593	51.6463	0.4130	98.4198	105.5474	89.6641
10. Length of fruit	6.2444	33.7211	32.1065	1.6146	90.6534	62.9727	53.4953
11. Girth of fruit	5.4689	68.4362	68.4102	0.0260	99.9240	140.8713	119.6723
12. Total yield	160.4444	109.7402	108.9318	0.8084	98.5321	222.7463	189.2262
13. Vitamin A content	300.7321	52.4182	52.3538	0.0644	99.7542	107.7161	91.5064
14. Vitamin C content	109.2528	37.2178	37.1674	0.0504	99.7294	76.4612	64.9549
15. Capsaicin content	0.1856	100.0052	99.9192	0.0930	99.9122	205.6274	174.6835

Table 7. Phenotypic, Genotypic and Environmental correlation between different pairs of characters in Cowpea genus

		Blooming	Height	Spread	Primary branches	Secondary branches	No.of fruits	Weight of fruit	Life span	No.of seeds	Length of fruit	Girth of fruit	Total yield	Vitamin A	Vitamin C
Height	P	0.1571													
	G	0.1572													
	E	0.1532													
Spread	P	0.0985	0.4225*												
	G	0.1033	0.4539*												
	E	-.0276	-.1258												
Primary branches	P	0.4508*	0.1345	0.2457											
	G	0.5340**	0.1558	0.2919											
	E	0.2188	0.0551	0.0575											
Secondary branches	P	0.2571	0.0460	0.4641**	0.4932**										
	G	0.2637	0.0400	0.4827**	0.5483**										
	E	0.0126	0.1653	0.1657	0.3554										
Number of fruits	P	0.1496	0.1275	0.2459	0.4455*	0.5502**									
	G	0.1503	0.1535	0.2553	0.5197**	0.5455**									
	E	0.0941	-.1975	0.3043	0.2492	0.0079									
Weight of fruit	P	-.6030**	0.0548	-.1281	-.4991**	-.5159**	-.3645*								
	G	-.6081**	0.0598	-.1324	-.5946**	-.5295**	-.3673*								
	E	-.2076	-.1657	-.0270	-.0158	-.0332	0.0409								
Life span	P	0.7547**	0.1081	-.0078	0.3924*	0.2628	0.2127	-.6972**							
	G	0.7794**	0.1147	-.0920	0.4590*	0.2765	0.2158	-.7098**							
	E	0.0615	-.0768	0.0002	0.1259	-.0028	0.0082	0.0151							
Number of seeds	P	-.5166**	-.0968	0.0579	-.3545	-.3246	-.4661**	0.7600**	-.7271**						
	G	-.5251**	-.0978	0.0564	-.4309*	-.3404	-.4707**	0.7691**	-.7456**						
	E	0.0245	-.0719	0.0951	0.1032	0.1481	-.0095	0.0496	0.1566						
Length of fruit	P	-.1659	-.1155	0.2586	0.0500	0.2993	-.1617	0.1495	-.4001	0.4657*					
	G	-.1760	-.1512	0.2650	0.0604	0.2512	-.1756	0.1580	-.4258	0.4857**					
	E	0.0096	0.1024	-.0559	-.0291	0.0917	0.1609	-.0093	0.0028	0.1300					
Girth of fruit	P	-.5994**	0.0378	-.2472	-.4775**	-.5482**	-.4147*	0.9146**	-.6241**	0.6299**	0.0046				
	G	-.6043**	0.0402	-.2558	-.5068**	-.5693**	-.4157*	0.9184**	-.6385**	0.6349**	0.0057				
	E	0.0162	-.2559	0.0249	-.0158	0.0257	0.0155	-.0256	0.0106	0.0948	0.1334				
Total yield	P	-.0457	0.0457	0.1024	0.2147	0.2057	0.7736**	-.1180	0.0256	-.2479	-.0997	-.1852			
	G	-.0454	0.0558	0.0994	0.2545	0.2131	0.7763**	-.1191	0.0246	-.2519	-.1090	-.1841			
	E	-.0659	-.3325	0.2254	0.0304	-.0116	0.5857	0.4[illegible]**	-.0251	0.0[illegible]0	0.0873	-.1526			
Vitamin A	P	0.1579	-.2416	-.5084**	0.0248	-.3560	0.1458	-.1667	0.0909	-.2064	-.2413	-.1247	0.3280		
	G	0.1599	-.2458	-.5203**	0.0263	-.3450	0.1472	-.1701	0.0921	-.2095	-.2582	-.1250	0.3304		
	E	0.0068	-.1485	0.1620	0.0893	-.0419	0.0422	0.0788	0.0118	-.1255	0.2829	0.0995	0.0742		
Vitamin C	P	-.5857**	-.2345	0.1315	-.1051	-.1996	-.1944	0.5094**	-.7223**	0.5130**	0.4411*	0.4815**	0.0159	-.0295	
	G	-.5890**	-.2400	0.1539	-.1207	-.2054	-.1992	0.5157**	-.7330**	0.5171**	0.4645**	0.4825**	0.0163	-.0297	
	E	-.3146	-.0160	0.1472	0.0336	0.0152	0.0350	-.2197	0.1382	0.1075	-.0368	-.0796	-.0.416	0.1041	
Capsicain	P	0.1659	0.0825	-.0652	0.0067	0.1589	0.1657	-.4004*	0.3746*	-.5504**	-.2729	-.2054	-.0517	0.0864	-.4074*
	G	0.1671	0.0820	-.0667	0.0069	0.1618	0.1667	-.4022*	0.3794*	-.5561**	-.2072	-.2058	-.0514	0.0867	-.4088*
	E	0.0309	0.2306	-.0630	0.0356	0.1540	-.1807	-.1146	0.0568	0.1386	0.0215	0.1093	-.1378	-.0746	0.1743

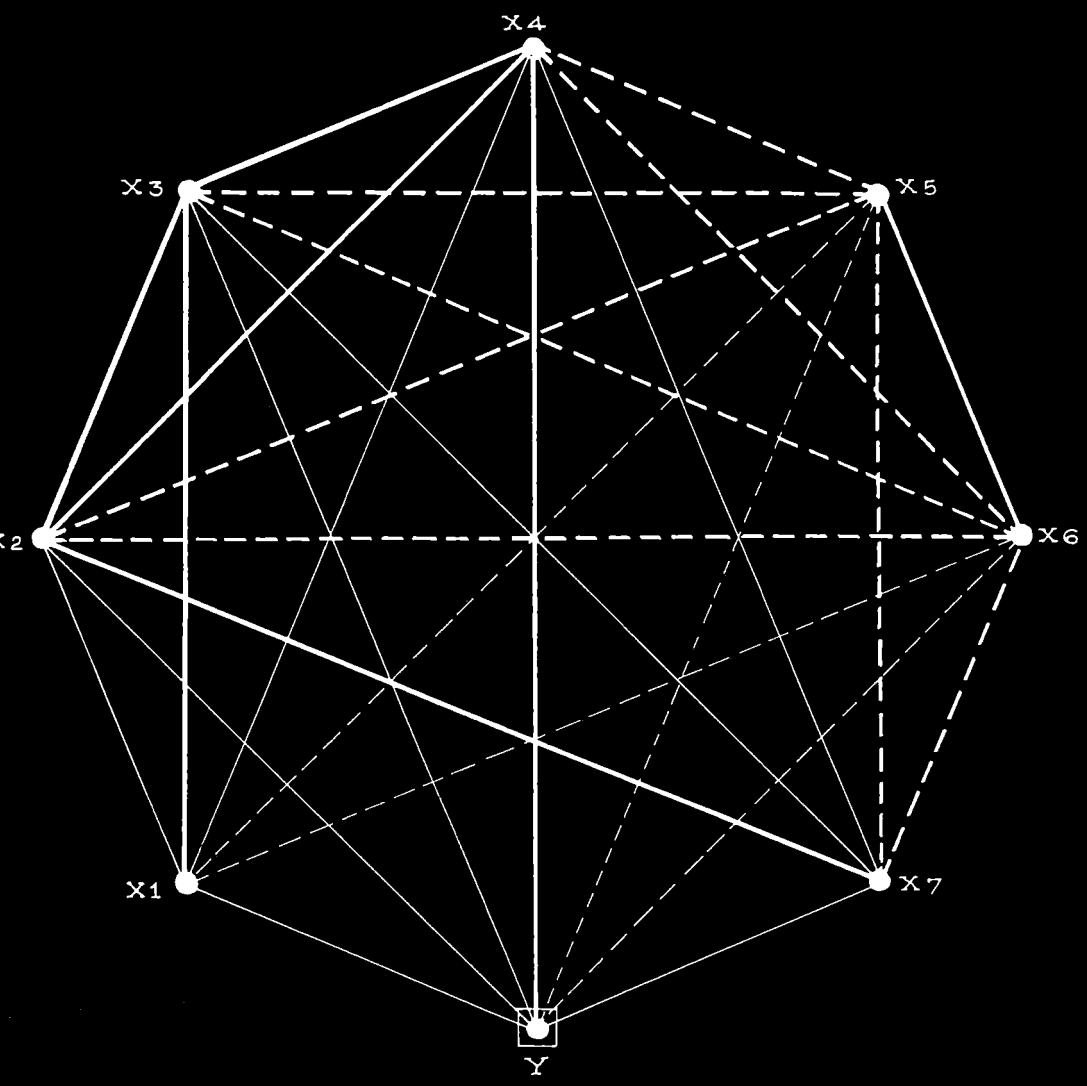
*Significant at 5 per cent level
**Significant at 1 per cent level

Figure 1

Y	=	Total yield/plant
X_1	=	Spread
X_2	=	Number of primary branches
X_3	=	Number of secondary branches
X_4	=	Number of fruits
X_5	=	Weight of individual fruit
X_6	=	Girth of fruit
X_7	=	Life span

FIG. 1

CORRELATION DIAGRAM OF YIELD AND IT'S COMPONENTS IN *Capsicum annuum*.



SIGNIFICANT POSITIVE

NON SIGNIFICANT POSITIVE

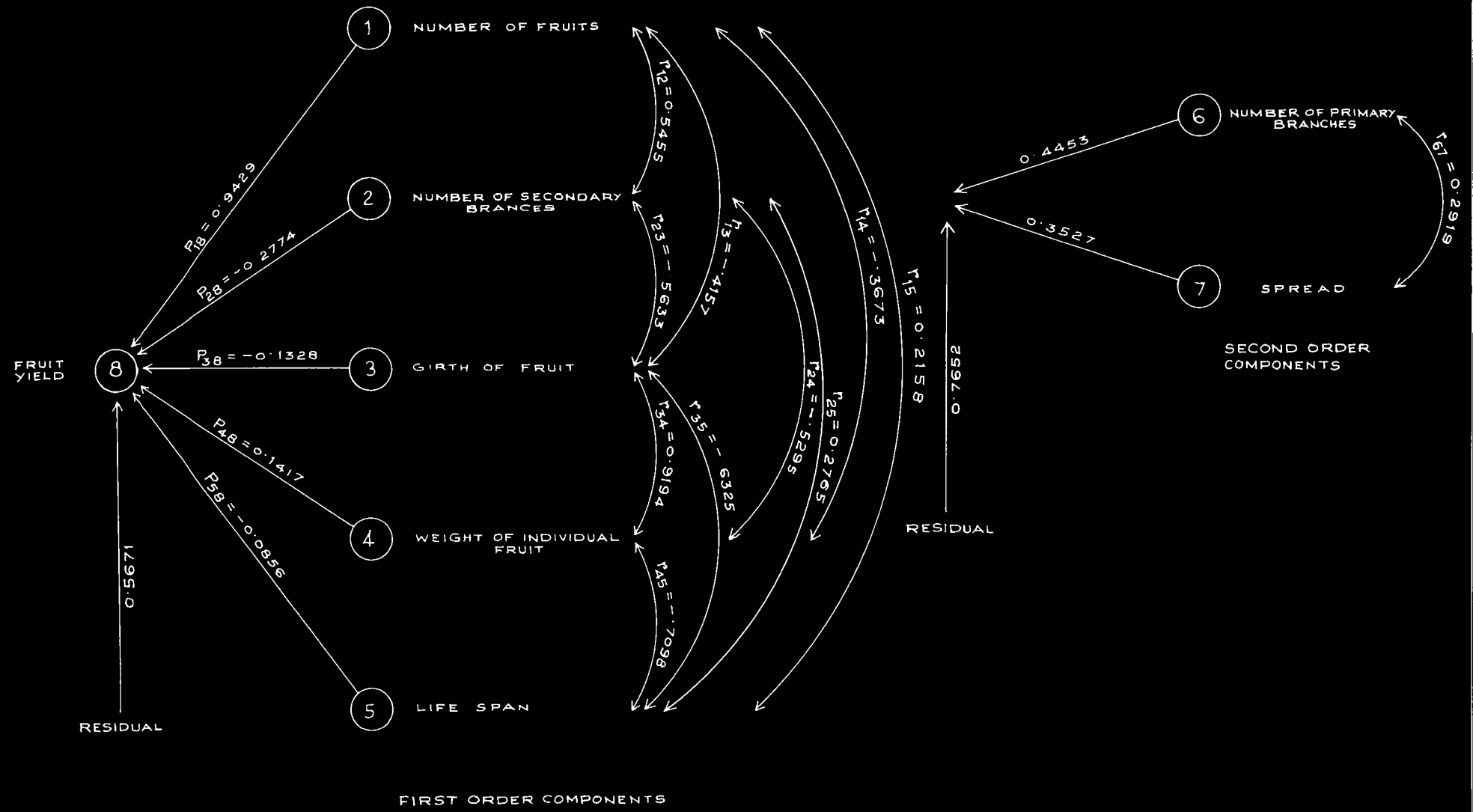
SIGNIFICANT NEGATIVE

NON SIGNIFICANT NEGATIVE

2. Path analysis

With a view to elucidate the cause and effect relationship of various plant characters and yield, a path coefficient analysis was undertaken. The phenotypic, genotypic and environmental correlation coefficients between different pairs of characters selected for path analysis are presented in table 8. The genotypic correlation of yield and it's components are diagramatically represented in Figure 1. Among 28 correlation coefficients studied, 7 were positive and significant and 8 positive but non significant. The number of significant negative and non significant negative coefficients were 8 and 5 respectively. In determining the cause and effect relationships the important plant characters were divided into first order and second order components, depending on their influence on yield.

Yield in chilli can be considered as the effect of five first order components namely, number of fruits, number of secondary branches, girth of fruit, weight of individual fruit and life span. The variation in the number of secondary branches was attributed to second order components namely primary branches and spread. The observed genotypic correlation coefficients between the characters were partitioned into direct and indirect effects. The direct and indirect effects of the first and second order components are presented in table 9 and table 10. The cause and effect relationship


1
NUMBER OF FRUITS
2
NUMBER OF SECONDARY BRANCES
3
GIRTH OF FRUIT
4
WEIGHT OF INDIVIDUAL FRUIT
5
LIFE SPAN
8
FRUIT YIELD
RESIDUAL
0.5671
P18 = 0.9429
P28 = -0.2774
P38 = -0.1328
P48 = 0.1417
P58 = -0.0856
r12 = 0.5455
r13 = -.4157
r14 = -.3673
r15 = 0.2158
r23 = -.5633
r24 = -.5285
r25 = 0.2795
r34 = 0.9194
r35 = -.6325
r45 = -.7068
FIRST ORDER COMPONENTS
6
NUMBER OF PRIMARY BRANCHES
7
SPREAD
0.4453
0.3527
r67 = 0.2918
2597.0
RESIDUAL
SECOND ORDER COMPONENTS

brought out by the path coefficient analysis is represented diagramatically in Fig. 2.

Sixty eight per cent of the variability in yield was attributed to the factors, namely number of fruits, number of secondary branches, girth of fruits, weight of individual fruit and life span of the crop. The maximum direct effect (0.9429) was contributed by the number of fruits. The positive direct effect of the number of fruits, though it was somewhat diminished by the factors number of secondary branches (-.1513) weight of individual fruit (-.052) and life span (-.0165), thereby accounting a highly significant correlation of 0.7763. Though the direct effect of the secondary branches is negative (-.2774) the high indirect effects of number of fruits (0.5144), girth of fruit (0.0748) and weight of individual fruit (0.0750) gave a significant correlation of 0.2131.

There was no significant association between girth of fruit, weight of individual fruit and life span with yield. The direct effect of the girth of fruit was negative (-.1328) and the effect through number of fruits was also negative (-.392). When the girth increased the number of fruits decreased.

Though the direct effect of the weight of individual fruit was positive (0.1417) and increased by lifespan (0.0608) and number of secondary branches (0.1469) it was highly reduced by the indirect effect of the number of fruits (-.3463), thereby accounting a nonsignificant correlation of

0.1191. The contribution of the residual factors worked out to 0.5671.

The second order components were number of primary branches and spread influencing yield through the number of secondary branches. The number of secondary branches was highly correlated with the number of primary branches and spread. The direct effect of the primary branches was positive (0.4453), and increased through spread (0.103), thereby accounting a correlation of 0.5483. The direct effect of spread was also positive (0.3527) and along with the indirect effect (0.130) via primary branches gave a significent correlation of 0.4827. The residual factors worked out to 0.7652. The number of primary branches and spread accounted for 42 per cent of the variability in the number of secondary branches.

3. Multivariate analysis

The test of significance of the difference among the thirty varieties, when all the fifteen characters were considered simultaneously, was carried out using Wilk's Λ criterion which was estimated as

$$\frac{|E|}{|E+V|} = 0.313886 \times 10^{-30}$$

The significance of Λ was tested using the relation

$$V = -m \log_e \Lambda$$

$$= 4670.7125\ (0.313886 \times 10^{-30})$$

$$= 83.346$$

Table 8. Phenotypic, genotypic and environmental correlation coefficients between different pairs of characters selected for path analysis.

Characters		Spread	No. of primary branches	No. of secondary branches	No. of fruits	Weight of individual fruit	Girth of fruit	Life span	Total yield
Number of primary branches	P	0.2457							
	G	0.2919							
	E	0.0575							
Number of secondary branches	P	0.4641	0.4932						
	G	0.4827**	0.5483**						
	E	0.1637	0.3554						
Number of fruits	P	0.2495	0.4455	0.5302					
	G	0.2533	0.5197**	0.5455*					
	E	0.3043	0.2492	0.0079					
Weight of individual fruit	P	-.1281	-.4991	-.5139	-.5645				
	G	-.1324	-.5946**	-.5295**	-.3673*				
	E	-.0270	-.0158	-.0332	-.0409				
Girth of fruit	P	-.2472	-.4773	-.5482	-.4147	0.9146			
	G	-.2558	-.5668**	-.5633**	-.4157*	0.9194**			
	E	0.0249	-.0138	0.0257	0.0135	-.0256			
Life span	P	-.0878	0.3924	0.2628	0.2127	-.6972	-.6241		
	G	-.0920	0.4590*	0.2765	0.2158	-.7098**	-.6325**		
	E	.0002	0.1259	-.0828	0.0082	0.0131	0.0106		
Total yield	P	0.1024	0.2147	0.2057	0.7736	-.1120	-.1832	0.0236	
	G	0.0994	0.2545	0.2131	0.7763**	-.1191	-.1841	0.0246	
	E	0.2254	0.0304	-.0116	0.5837	0.4828	-.1526	-.0251	

*Significant at 5 per cent level
**Significant at 1 per cent level

Table 9. Path coefficient analysis showing the direct and indirect effects of first order components on yield.

Variables	Direct effect on fruit yield	Indirect effects on fruit yield via					Genotypic correlation with total yield
		Number of fruits	No. of secondary branches	Girth of fruit	Weight of individual fruit	Life span	
1. Number of fruits	0.9429	-	-.1513	0.0552	-.0520	-.0185	0.7763
2. Number of secondary branches	-.2774	0.5144	-	0.0748	0.0750	-.0237	0.2131
3. Girth of fruit	-.1328	-.3920	0.1563	-	0.1303	0.0541	-.1841
4. Weight of individual fruit	0.1417	-.3463	0.1469	-.1221	-	0.0608	-.1191
5. Life span	-.0856	0.2035	-.0767	0.0840	-.1006	-	0.0246

Residual factor = 0.5671

Table 10. Path coefficient analysis showing the direct and indirect effects of second order components

Variables	Direct effect	Indirect effects via		Genotypic correlation with secondary branches
		No. of primary branches	Spread	
No. of primary branches	0.4453	-	0.1030	0.5483
Spread	0.3527	0.1300	-	0.4827

Residual factor = 0.7652

Since the statistic V follows a chi-square distribution and the degree of freedom in the present case exceeded 30, $\sqrt{2\chi^2} - \sqrt{2n-1} = 67.1892$ was used as a standard normal variate. The observed value was highly significant at 1 per cent level indicating that when the pooled effect of the 15 variables considered, the differences among the 30 varieties of chillies studied were highly significant.

4. Genetic divergence (D^2) among the varieties

The means of thirty varieties for the correlated characters were transformed into standardised uncorrelated means using the relationships obtained as a result of pivotal condensation of the error variance-covariance matrix. Using the values of the uncorrelated linear combinations for the fifteen characters of the thirty varieties, the statistical distance (D^2 of Mahalanobis') between pairs of varieties were obtained by summing the squares of the differences between the transformed variables relating to the pairs of varieties. The 435 values obtained by taking thirty varieties, two at a time are presented in Appendix I.

The D^2 values ranged from 25.48 to 47713.04. Out of 435 comparisons only one value (D^2 between variety 25 and 26) was significant at 5% level while all the remaining values were significant at 1% level. These results clearly indicate the presence of appreciable amount of genetic divergence between the varieties studied.

(1) Group constellations: Intra- and inter-cluster D^2

The clustering of the varieties was done by Tocher's method (Table 11) in such a way that the intra-cluster distance was small and the inter-cluster distance large. Accordingly 30 varieties were grouped into 16 clusters including four single variety clusters (Table 12). Average intra and inter-cluster distance (D values) are presented in table 13.

The larger number of constellations indicated the high magnitude of genetic diversity available in the species. The significance of all the D^2 values also confirmed the inference. The intra-cluster D values ranged from 0.0 (in the case of single variety clusters) to 43.495, while the inter-cluster D values ranged from 17.238 to 215.172. The intra-cluster distance for groups 13, 14, 15 and 16 was 0.0 because they constituted only one variety each. The average intra-cluster distance (D) was the least in the remaining clusters which indicated that the variability within clusters was the least and between clusters more. In otherwords they are sets or groups of varieties which are genetically homogenous within, but heterogenous between different clusters. Hence it can be assumed that the grouping gives rise to reasonably homogenous sets. The maximum inter-cluster distance was displayed between groups V and XV. Among the sixteen clusters, clusters I and II included three varieties each while clusters XIII, XIV, XV and XVI had one variety each. The remaining clusters

Table 11. Tocher's computational scheme for finding clusters in 30 varieties of *Capsicum annuum*.

Cluster No.	Variety added	Total D^2	Number of terms of $D^2(n)$	Increase in D^2 / Increase in n	Average D^2 ($\leq D^2/n$)
I	25,26	25.48	1		
	10	474.26	3	224.39	158.087
II	28,29	54.76	1		
	30	277.11	3	111.175	92.37
III	11,23	138.86	1	-	138.86
IV	5,27	352.67	1	-	352.67
V	16,17	498.10	1	-	498.10
VI	19,20	498.72	1	-	498.72
VII	6,18	657.96	1	-	657.96
VIII	3,14	699.89	1	-	699.89
IX	8,15	836.57	1	-	836.57
X	13,21	1236.17	1	-	1236.17
XI	7,22	1381.87	1	-	1381.87
XII	9,12	1891.67	1	-	1891.67
XIII	1	-	-	-	-
XIV	4	-	-	-	-
XV	2	-	-	-	-
XVI	24	-	-	-	-

Table 12. Varieties included in clusters

Cluster	Varieties
I	25, 26, 10
II	28, 29, 30
III	11, 23
IV	5, 27
V	16, 17
VI	19, 20
VII	6, 18
VIII	3, 14
IX	8, 15
X	13, 21
XI	7, 22
XII	9, 12
XIII	1
XIV	4
XV	2
XVI	24

Table 13. Average intra and inter cluster distance ($\sqrt{D^2}$ values)

	I	II	III	IVI	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I	12.573	77.711	63.837	71.534	122.947	62.843	28.685	60.336	60.047	72.307	53.008	91.132	31.151	104.331	126.269	123.751
II		9.611	41.559	17.238	180.792	26.592	84.534	56.909	68.039	25.117	71.494	76.195	62.328	102.245	81.719	103.285
III			11.784	36.007	174.697	45.521	71.645	69.372	76.714	42.696	77.005	67.757	58.217	101.577	85.278	111.895
IV				18.779	177.215	28.457	79.400	52.771	61.667	25.628	68.137	68.678	56.670	94.577	79.251	101.498
V					22.318	162.046	115.896	191.991	180.799	175.337	126.761	198.888	140.817	188.176	213.172	180.306
VI						22.232	69.139	60.597	67.618	28.162	54.458	80.752	49.778	104.330	95.547	100.093
VII							25.651	102.160	94.702	79.239	57.887	105.851	44.905	115.004	132.668	127.218
VIII								26.455	32.230	57.694	77.721	50.957	68.262	71.563	91.916	102.347
IX									20.924	65.597	72.729	55.249	59.402	58.520	90.743	110.526
X										35.159	63.628	75.917	57.274	99.049	84.225	104.369
XI											37.174	96.482	47.857	98.777	116.510	100.534
XII												43.494	76.854	73.031	88.505	110.695
XIII													0	92.787	114.473	118.441
XIV														0	100.959	125.285
XV															0	121.157
XVI																0

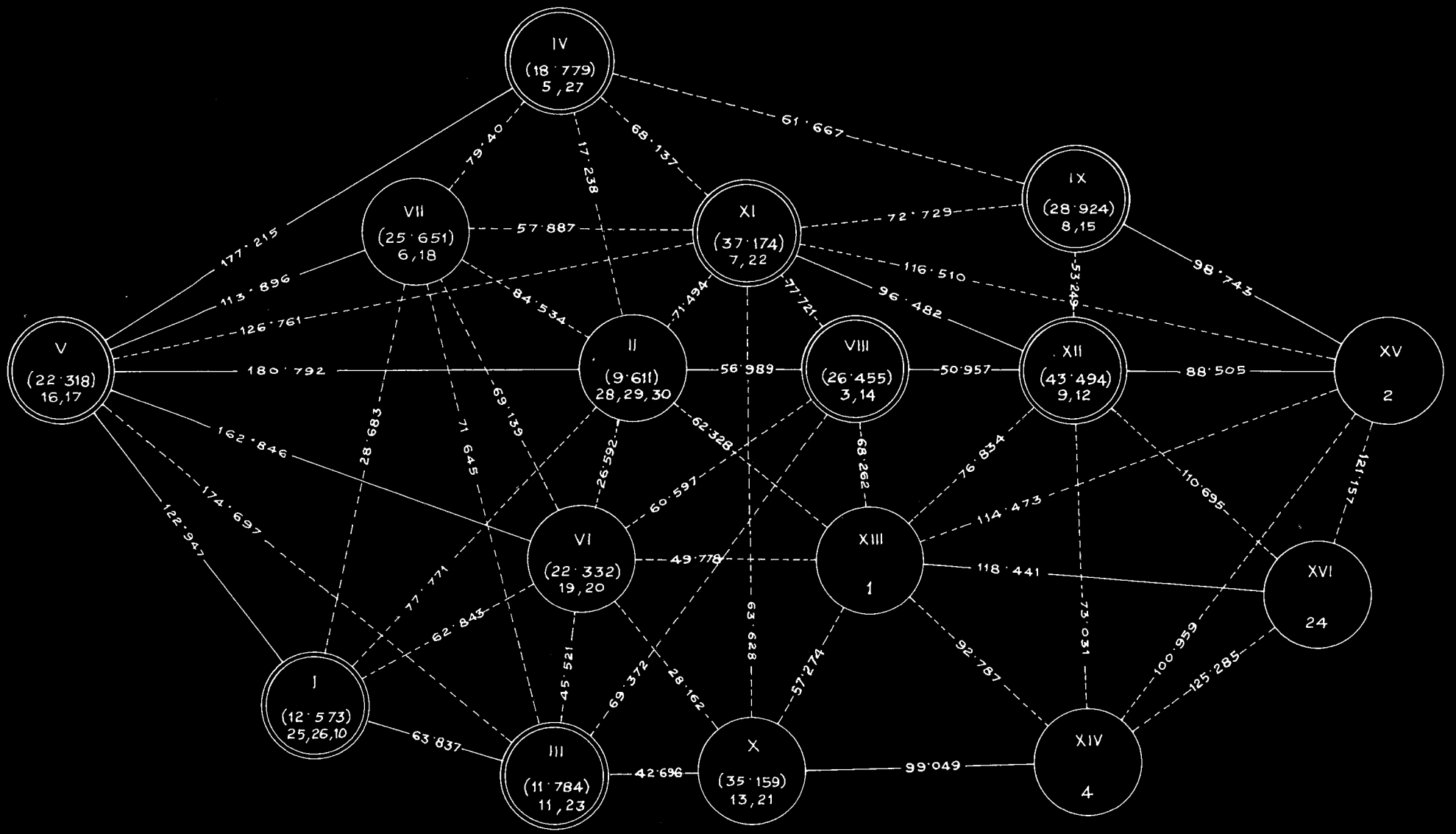
Table 14. D^2 and D values among the 9 varieties of Capsicum annuum selected for hybridisation.

Varieties	5	8	9	11	14	16	22	25
3	3376.64 (58.111)	1192.10 (34.53)	3378.45 (58.13)	5726.43 (75.67)	699.89 (26.45)	37452.12 (193.53)	5332.81 (73.03)	7880.28 (88.77)
5		3321.85 (57.64)	6819.52 (82.58)	1436.68 (37.90)	2742.75 (52.37)	32692.01 (180.81)	4040.15 (63.56)	4998.29 (70.69)
8			3326.23 (57.67)	4813.16 (69.37)	765.15 (27.67)	36170.58 (190.18)	5161.87 (71.58)	6774.48 (82.31)
9				5795.06 (76.13)	2198.43 (46.89)	45707.20 (213.79)	10038.03 (100.19)	10533.23 (102.63)
11					3966.13 (62.98)	33432.08 (182.85)	4969.94 (70.49)	4166.38 (64.55)
14						40096.75 (200.24)	5726.59 (75.67)	7653.77 (87.48)
16							18361.87 (135.51)	16846.54 (129.79)
22								2372.74 (48.71)

D values in parenthesis

All D^2 values are significant at 1 per cent level

FIG. 3 GROUP CONSTELLATION AND STATISTICAL DISTANCE AMONG 30 VARIETIES OF *Capsicum annuum*.



INTRA-CLUSTER D VALUES GIVEN IN PARENTHESIS.

INTER-CLUSTER D VALUES GIVEN ALONG THE LINES.

VARIETY NUMBERS OF EACH CLUSTER GIVEN INSIDE THE CIRCLE.

◎ CLUSTERS USED FOR HYBRIDIZATION.

represented two varieties each. The average D^2 values between clusters selected for hybridization are presented in table 14. All the D^2 values were significant at 1 per cent level which indicated appreciable amount of genetic divergence between the selected clusters. The inter-cluster relationships are represented diagrametically in Figure 3 where the clusters have been represented as being distributed in a multidimensional space, the square root of average D^2 between the clusters being used to represent the relative disposition of the clusters. Since the clusters occupy a multidimensional space, the relative distance between all the clusters in all the cases could not be shown accurately in the two dimensional diagram wherein the lines connecting two clusters could not be drawn to scale has been indicated by using broken lines.

(ii) Relative contribution of different characters to divergence

The relative contribution of different characters to divergence was assessed by ranking them according to D^2 values. The highest D^2 value was ranked first while the lowest was given rank fifteen. The rank totals for various characters were as follows:

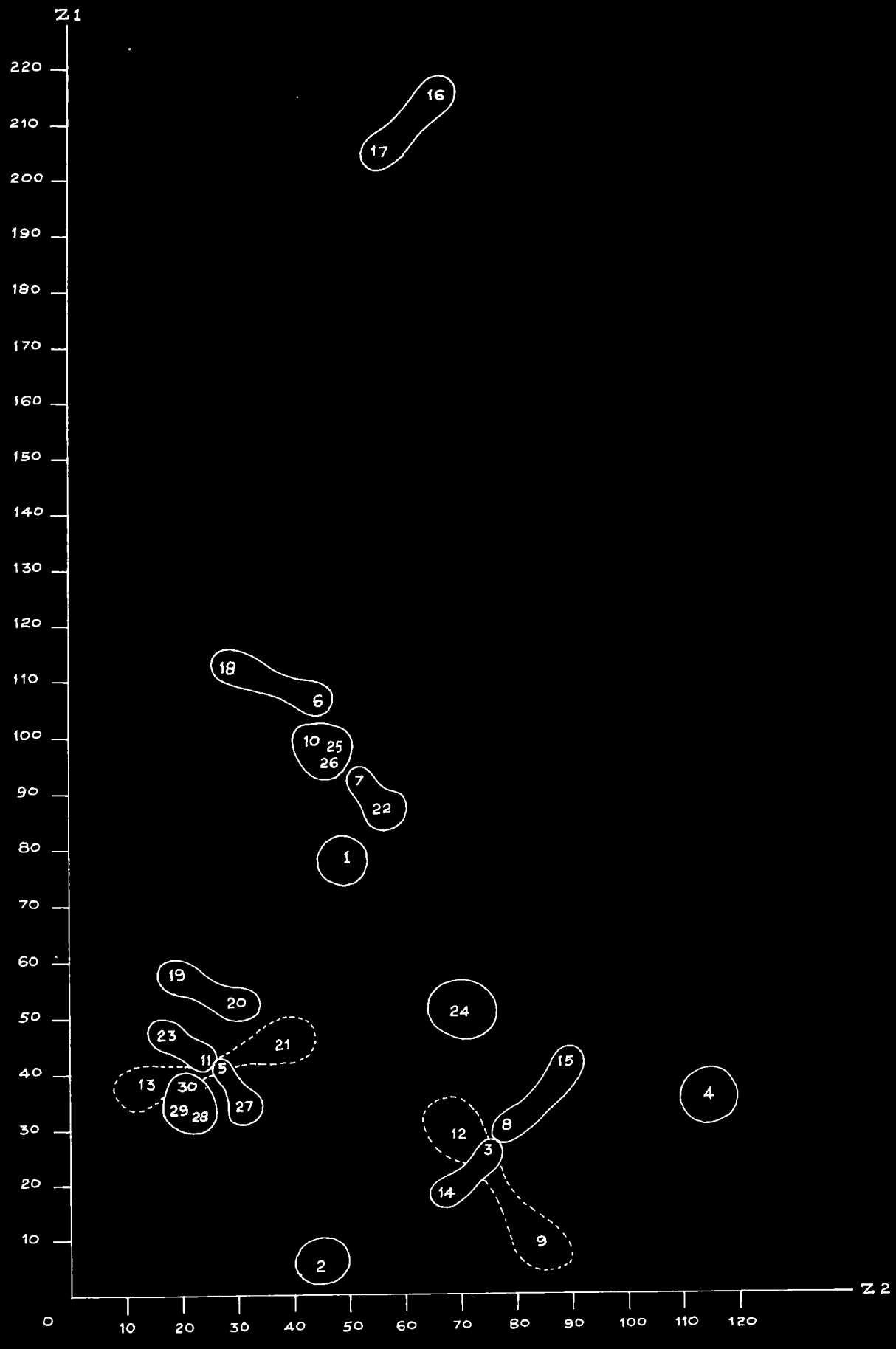
Table 15. Ranking of characters according to D^2 values.

Character	Ranks assigned	Rank total
1. Number of days taken for blooming	8	3638
2. Height	5	4345
3. Spread	2	4592
4. Number of primary branches	1	5581
5. Number of secondary branches	4	4373
6. Number of fruits per plant	10	3197
7. Weight of fruit	7	3935
8. Life span	3	4504
9. Number of seeds	15	1784
10. Length of fruit	6	3966
11. Girth of fruit	13	2112
12. Total yield	14	1792
13. Vitamin A	12	2201
14. Vitamin C	9	3386
15. Capsaicin	11	2796

It was evident that the number of seeds and number of primary branches had contributed to maximum and minimum divergence respectively.

FIG. 4

SCATTER DIAGRAM SHOWING THE POSITION OF THIRTY VARIETIES.



5. Canonical analysis

Canonical analysis was done by using the matrix of Y values i.e. the mean values of the uncorrelated linear combinations for 15 characters in 30 varieties. The first 4 sets of canonical vectors computed are given in table 16. The mean values of the first two canonical variates and the canonical roots with their relative contribution are presented in tables 17 and 18 respectively.

It was found that the first two canonical roots together contributed 73.7 per cent of the total variation. Hence it can be concluded that vectors corresponding to the first canonical roots will give the best sets of linear functions (canonical variates), which explains the maximum variation in the population.

As these two sets of canonical variates are obtained from the first two canonical roots and since two roots together cover 73.7 per cent of the total variation, a scatter diagram of $Z_{(1)}$ and $Z_{(2)}$ as shown in the Fig.No.4 will explain the proximity and divergence of all the thirty varieties with respect to the fifteen characters. From the Figure 4 it was evident that the grouping was the same as obtained by Tocher's method.

Table 16. The first 4 sets of canonical vectors.

Characters	Canonical vectors 1	2	3	4
1. Number of days taken for blooming	-.1034	-.0076	-.0129	-.1374
2. Height	0.0175	-.0105	0.0726	0.0493
3. Spread	-.0089	-.0919	-.0011	0.0964
4. Number of primary branches	0.0070	-.0004	-.0181	0.0555
5. Number of secondary branches	-.0523	-.0593	-.0013	0.0928
6. Number of fruits	-.1524	0.1816	-.0059	0.8347
7. Weight of fruit	0.1838	0.0234	0.0598	-.0304
8. Life span	0.0550	-.1003	-.0620	-.1949
9. Number of seeds	0.7398	0.3427	0.4648	0.0609
10. Length of fruit	0.0663	-.0183	-.0858	0.0206
11. Girth of fruit	-.1564	0.8550	-.4137	-.1140
12. Total yield	0.3947	-.1503	-.4004	0.3653
13. Vitamin A	-.3363	0.1691	0.6439	0.1133
14. Vitamin C	-.1605	0.0371	0.1390	-.0801
15. Capsaicin	0.2037	0.1889	-.0019	-.2284

Table 17. Mean values of the first two canonical variates.

Variety	z_1	z_2
1	78.44	50.55
2	5.60	45.81
3	26.66	75.78
4	36.19	114.79
5	41.04	27.12
6	106.17	45.06
7	93.54	52.05
8	29.95	78.42
9	9.65	85.20
10	99.82	45.46
11	43.40	26.23
12	28.15	70.47
13	38.56	14.68
14	18.84	67.74
15	42.40	89.53
16	215.77	66.57
17	203.54	56.87
18	112.84	29.07
19	56.02	20.63
20	53.58	30.96
21	45.07	39.08
22	67.08	57.88
23	46.67	19.72
24	51.78	71.52
25	98.26	46.34
26	96.78	46.81
27	35.12	32.05
28	33.40	23.80
29	34.35	20.92
30	39.51	21.86

Table 18. Canonical roots with their relative contribution.

Canonical roots	λ_1	λ_2	λ_3	λ_4	Sum of other canonical roots	Total
Value	71688.09	17802.09	13262.63	7477.40	11183.46	121413.69
% Contribution	59.00	14.70	10.90	6.20	9.20	100.00

6. Heterosis

The analysis of variance for the design of experiment is presented in table 19. The mean values of the parents and the F_1s along with the percentage of positive heterosis are computed over mid-parental value and better parent resulting from the diallel cross for all the 18 characters studied and presented in table 20.

Pusa jwala (7) was found to be the best performing parent for six of the characters studied, namely, number of leaves, spread of plant, number of fruits, length of fruit, capsaicin and oleoresin contents. As regards weight, girth and size of fruit, number of seeds per fruit, California Wonder (8) topped the list. Purple round (4) was the best performing parent for primary branches and life span. CA-1068 (2) performed best in plant height and number of secondary branches. CA-960 (1) surpassed all parents for total yield. Pant C-1 (6) was the top parent as far as Vitamin A is concerned while Vella notchi (5) possessed maximum quantity of Vitamin C.

All the characters under investigation manifested heterosis over the mid parental values, though there was wide variation for different traits in different cross combinations. Maximum heterosis was noticed in number of primary branches and Vitamin C content. As regards the five fruit characters namely weight, length, girth and size of fruits and number of seeds per fruit, there was very little

positive heterosis. Only four crosses displayed positive heterosis for weight of fruit when heterosis was computed over mid parental value and no heterosis over better parent. As regards length of fruit, only 4 hybrids namely Vella notchi x Pant C-1, Vella notchi x Purple cluster, Pant C-1 x California wonder and California wonder x Purple cluster exhibited positive heterosis over mid parental value while none of the crosses showed heterosis over better parent. Out of 36 crosses only 5 crosses displayed heterosis over mid parental value as regards the girth of fruit, while only 2 crosses manifested heterosis over better parent and number of seeds. Only five hybrids manifested heterosis over mid parental value for size of fruit while 4 hybrids showed heterosis over mid parental value.

A comparison of the average heterosis $\frac{(\bar{F}_1 - \bar{P} \times 100)}{\bar{P}}$

for the various characters revealed that number of secondary branches topped the list followed by Vitamin C content, capsaicin content and number of primary branches. When heterosis was computed over mid parental value, 100 per cent significant heterotic crosses were obtained in two traits namely number of primary branches and Vitamin C content. The corresponding figures for secondary branches, oleoresin content, life span and capsaicin content were 97.3, 97.3, 94.5 and 91.7 respectively. Length of fruit and weight of fruit showed the lowest percentage (11.2 each).

Purple round in combination with Vella notchi (4 x 5) produced the best performing F_1 with respect to three important economic traits namely number of fruits, total yield and life span. But, purple round x Pant C-1 (4 x 6) displayed maximum height, primary branches and spread. As far as secondary branches are concerned CA-1068 x Vella notchi (2 x 5) performed better, while CA-1068 x Purple round (2 x 4) produced maximum number of leaves and was late in flowering. As regards Vitamin C content Vella notchi x California wonder (5 x 8) surpassed the other hybrids. The cross between Pant C-1 x Pusa jwala (6 x 7) excelled in capsaicin content, while hybrid of CA-960 x Pusa jwala (1 x 7) performed well in oleoresin content.

Table 21 represents the range of values for the parents and F_1s, overall mean values for parents and F_1s, range of heterosis and average heterosis. Percentage of significantly heterotic crosses, the best performing F_1, and the most heterotic F_1 are also identified in the table with respect to the different characters under study. Purple round x Vella notchi (4 x 5) was the most heterotic one for five important attributes namely number of fruits, girth of fruit, size of fruit, total yield and oleoresin content. Purple round x Pant C-1 (4 x 6) manifested maximum heterosis for height of plant. CA-960 x CA-1068 (1 x 2) produced the most heterotic F_1 for primary branches while the same female parent with purple cluster (1 x 9) gave the most heterotic F_1 for

Vitamin C content. CA-1068 x Purple round (2 x 4), CA-1068 x Pusa jwala (2 x 7), and CA-1068 x California wonder (2 x 8) produced the most heterotic F_1s for number of leaves, Vitamin A content and life span respectively. Vella nstchi in combination with California wonder (5 x 8) produced the most heterotic one for weight of fruit while Vella natchi in combination with purple cluster (5 x 9) displayed maximum heterosis for length of fruit. The most heterotic F_1 for number of seeds was produced by 64 x Purple cluster (3 x 9).

(1) Negative heterosis

Negative heterosis was manifested in two important economic attributes namely number of days taken for blooming and number of seeds/fruit. The percentage of negative heterosis computed over mid parental value and better parent are presented in table 22 along with the mean values of parents and F_1s. Table 23 represents the average heterosis, top parent, best performing F_1, percentage of significantly heterotic crosses, range of heterosis and most heterotic F_1. Among the parents, California wonder (8) availed minimum number of days for blooming and Purple round (4) possessed minimum number of seeds per fruit. California wonder x Purple cluster (8 x 9) displayed maximum negative heterosis for number of days taken for blooming, besides being the most heterotic F_1 for the character concerned as well as the number of seeds per fruit when computed over mid parental value. The hybrid Purple round x Purple cluster (4 x 9) manifested

Table 19. Analysis of variance table for the design of experiment.

Characters	Source of variation: Blocks DF	Blocks M.S.S.	Treatments DF	Treatments M.S.S.	Error DF	Error M.S.S.
Height	2	18.063	44	857.158**	88	3.141
Primary branches	2	0.293	44	43.212**	88	0.311
Secondary branches	2	57.575	44	2723.693**	88	5.956
Number of leaves	2	54143.950	44	28644180.000**	88	383527.680
Spread	2	6.250	44	1203.209**	88	3.363
No. of days taken for blooming	2	47.875	44	271.100**	88	0.927
Number of fruits	2	19.750	44	10110.149**	88	42.733
Weight of fruit	2	0.353	44	60.598**	88	0.059
Length of fruit	2	0.156	44	10.663**	88	0.018
Girth of fruit	2	0.069	44	22.855**	88	0.021
Size of fruit	2	0.689	44	57.786**	88	0.764
No.of seeds/fruit	2	8.129	44	3062.736**	88	2.321
Total yield	2	1363.498	44	139987.940**	88	1547.920
Life span	2	15.000	44	2247.179**	88	2.318
Vitamin A	2	3327.998	44	14447727.000**	88	6952.723
Vitamin C	2	338.499	44	24464.126**	88	25.477
Capsaicin	2	0.029	44	0.458**	88	0.001
Oleoresin	2	3.271	44	42.522**	88	0.811

**Significant at 1 per cent level

Table 20. The mean values of parents and F_1 hybrids and their positive heterosis in percentage.

Parents and hybrids	Height			Number of primary branches		
	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent
1	59.3	-	-	5.7	-	-
2	66.1	-	-	5.8	-	-
3	47.5	-	-	5.5	-	-
4	66.0	-	-	7.6	-	-
5	35.7	-	-	5.4	-	-
6	35.8	-	-	4.6	-	-
7	42.3	-	-	5.3	-	-
8	41.4	-	-	3.0	-	-
9	24.3	-	-	4.4	-	-
1 x 2	30.5	-	-	18.5	221.739**	218.965**
1 x 3	45.3	-	-	10.4	85.714**	82.456**
1 x 4	51.2	-	-	10.9	93.909**	43.421**
1 x 5	40.6	-	-	10.2	83.783**	78.947**
1 x 6	51.4	8.096**	-	9.5	68.141**	66.670**
1 x 7	50.6	-	-	11.2	103.636**	96.491**
1 x 8	44.3	-	-	6.1	40.229**	7.017**
1 x 9	42.4	1.435	-	11.5	127.722**	101.754**
2 x 3	53.1	-	-	8.1	43.362**	39.655**
2 x 4	83.1	25.813**	25.718**	16.9	152.238**	122.368**
2 x 5	39.8	-	-	9.9	76.785**	70.689**
2 x 6	56.2	10.300**	-	8.3	45.614**	43.103**
2 x 7	46.7	-	-	9.5	71.171**	63.793**
2 x 8	44.5	-	-	5.6	27.272**	-
2 x 9	44.6	-	-	10.0	96.078**	72.413**

continued..

Table 20 continued

Parents and hybrids	Height			Number of primary branches		
	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent
3 x 4	70.7	24.560**	7.12**	14.4	119.047**	89.473**
3 x 5	32.9	-	-	5.8	6.422**	3.454**
3 x 6	54.5	30.85**	14.73**	10.5	89.189**	87.500**
3 x 7	46.8	4.23**	-	10.7	98.148**	94.545**
3 x 8	46.4	4.38**	-	7.3	71.764**	32.727**
3 x 9	31.7	-	-	7.6	53.535**	38.181**
4 x 5	84.7	66.57**	28.34**	11.0	69.230**	44.736**
4 x 6	109.0	114.145**	65.15**	19.0	187.878**	150.000**
4 x 7	32.2	-	-	9.3	44.186**	22.368**
4 x 8	46.7	-	-	9.7	83.018**	27.631**
4 x 9	76.1	68.93**	15.30**	18.2	203.34**	139.473**
5 x 6	37.7	5.45**	5.31**	7.3	32.727**	30.357**
5 x 7	34.5	-	-	6.3	17.757**	16.67**
5 x 8	45.1	16.99**	8.93**	7.2	71.428**	33.34**
5 x 9	38.0	26.67**	6.44**	6.3	28.571**	16.67**
6 x 7	41.5	6.27**	-	10.0	83.486**	78.571**
6 x 8	42.6	10.36**	2.89*	6.2	44.186**	10.714**
6 x 9	41.3	37.43**	15.363**	13.3	166.000**	137.500**
7 x 8	44.6	6.571**	5.437**	8.2	97.590**	54.716**
7 x 9	27.7	-	-	6.4	31.958**	20.734**
8 x 9	42.0	27.85**	1.449	5.1	37.837**	15.909**
C.D.5%		2.494	2.879		0.783	0.904
C.D.1%		3.304	3.815		1.037	1.198

continued..

Table 20 continued

Parents and hybrids	Number of secondary branches			Number of leaves		
	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent
1	21.9	-	-	1531.5	-	-
2	47.8	-	-	1556.9	-	-
3	27.1	-	-	6915.2	-	-
4	14.6	-	-	3355.9	-	-
5	29.8	-	-	322.1	-	-
6	15.0	-	-	1177.2	-	-
7	45.7	-	-	11006.6	-	-
8	9.0	-	-	268.8	-	-
9	19.8	-	-	422.1	-	-
1 x 2	55.9	60.401**	16.945**	5656.1	266.28	263.29
1 x 3	93.1	288.163**	250.922**	2372.7	-	-
1 x 4	37.5	105.479**	71.232**	2014.5	-	-
1 x 5	103.4	300.00**	246.979**	2020.3	117.98	31.916
1 x 6	42.7	131.45**	94.977**	1565.7	15.605	2.233
1 x 7	110.2	226.03**	141.137**	6139.0	-	-
1 x 8	36.3	134.451**	65.753**	1139.4	26.57	-
1 x 9	102.6	392.086**	368.493**	1483.5	51.67	-
2 x 3	48.9	30.574**	2.301	2374.6	-	-
2 x 4	69.0	121.153**	44.351**	39030.6	1488.935**	1063.04**
2 x 5	116.0	198.969**	142.677**	1914.0	103.725	22.936
2 x 6	41.7	32.002**	-	1504.7	10.069	-
2 x 7	110.2	155.721**	130.545**	22023.4	250.593	100.092
2 x 8	32.3	13.732**	-	1006.1	10.215	-
2 x 9	88.7	162.426**	85.564**	1377.6	39.221	-

continued...

Table 20 continued

Parents and hybrids	Number of secondary branches			Number of leaves		
	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent
3 x 4	53.8	156.033**	98.523**	3027.7	-	-
3 x 5	56.7	99.297**	90.268**	2047.2	-	-
3 x 6	45.2	114.726**	66.789**	5958.5	-	-
3 x 7	106.8	193.406**	135.698**	2452.3	-	-
3 x 8	30.4	68.421**	12.177**	3105.6	-	-
3 x 9	87.7	273.987**	233.616**	2776.1	-	-
4 x 5	66.0	197.297**	121.476**	4032.6	119.282	20.164
4 x 6	91.2	516.216**	508.000**	5598.2	146.948	66.786
4 x 7	65.0	108.955**	37.855**	5328.7	-	-
4 x 8	29.6	150.581**	102.739**	1928.8	6.425	-
4 x 9	94.7	450.591**	378.282**	10220.3	441.04	204.547
5 x 6	40.4	60.357**	35.570**	1048.1	39.811	-
5 x 7	70.1	85.695**	53.391**	1917.3	-	-
5 x 8	39.5	105.608**	32.550**	373.2	26.315	15.864
5 x 9	40.1	61.693**	34.563**	357.0	-	-
6 x 7	62.2	104.942**	36.105**	7069.8	16.052	-
6 x 8	21.7	80.84**	44.67**	886.4	22.600	-
6 x 9	67.3	286.781**	239.898**	2973.7	271.875	152.607
7 x 8	43.3	58.318**	-	3109.1	-	-
7 x 9	28.1	-	-	2070.7	-	-
8 x 9	31.0	115.280**	56.565**	378.0	9.422	-
C.D. 5%		3.450	3.984		869.937	1004.517
C.D.1%		4.571	5.278		1152.470	1330.758

Table 20 continued

Parents and hybrids	Spread			No.of days taken for bloomi		
	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent
1	39.4	-	-	87.6	-	-
2	44.1	-	-	74.3	-	-
3	29.9	-	-	87.1	-	-
4	39.5	-	-	97.1	-	-
5	46.0	-	-	74.4	-	-
6	41.1	-	-	78.3	-	-
7	47.9	-	-	83.4	-	-
8	35.1	-	-	58.4	-	-
9	22.8	-	-	75.4	-	-
1 x 2	32.7	-	-	83.4	3.027**	-
1 x 3	54.2	56.421**	37.563**	88.0	0.744	0.457
1 x 4	51.6	30.798**	30.633**	92.3	-	-
1 x 5	56.0	31.147**	21.739**	74.2	-	-
1 x 6	37.4	-	-	79.5	-	-
1 x 7	55.3	26.689**	15.448**	83.7	-	-
1 x 8	45.6	25.793**	15.736**	83.8	14.795**	-
1 x 9	48.6	56.270**	23.350**	79.0	-	-
2 x 3	42.2	14.054**	-	80.6	-	-
2 x 4	66.6	59.330**	51.020**	100.1	16.805**	3.089**
2 x 5	54.8	21.642**	19.130**	80.7	8.541**	8.467**
2 x 6	37.2	-	-	92.3	20.969**	17.879**
2 x 7	54.5	18.476**	13.778**	92.0	16.677**	10.312**
2 x 8	42.4	9.844**	-	86.7	30.671**	16.689**
2 x 9	50.5	50.971**	14.512**	75.5	0.868	0.133

continued...

Table 20 continued

Parents and hybrids	Spread			No.of days taken for blooming		
	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent
3 x 4	69.4	100.00**	75.695**	88.1	-	-
3 x 5	39.2	3.293*	-	81.4	0.805	-
3 x 6	90.6	155.211**	120.436**	79.9	-	-
3 x 7	54.6	40.359**	13.987**	75.4	-	-
3 x 8	44.5	41.269**	34.441**	68.7	-	-
3 x 9	38.3	45.351**	28.094**	85.1	2.277**	-
4 x 5	97.2	127.368**	111.304**	76.9	-	-
4 x 6	155.1	230.273**	223.844**	75.3	-	-
4 x 7	39.1	-	-	86.6	-	-
4 x 8	43.0	18.457**	8.861**	69.1	-	-
4 x 9	69.6	123.434**	76.203**	88.8	2.957**	-
5 x 6	54.0	23.995**	17.331**	79.3	3.864**	1.277
5 x 7	57.2	-	-	77.3	-	-
5 x 8	55.8	41.087**	21.304**	66.0	-	-
5 x 9	51.4	49.419**	11.739**	83.1	10.948**	10.212**
6 x 7	54.3	22.022**	13.361**	76.7	-	-
6 x 8	45.1	16.173**	4.856**	69.8	2.121**	-
6 x 9	37.9	18.623**	-	75.6	-	-
7 x 8	54.9	33.556**	14.614**	62.4	-	-
7 x 9	22.4	-	-	91.3	14.987**	9.472**
8 x 9	40.5	44.901**	22.356**	54.6	-	-
C.D. 5%		2.586	2.966		1.541	1.549
C.D. 1%		3.428	3.959		1.771	2.052

continued...

Table 20 continued

Parents and hybrids	No.of fruits per plant			Weight of fruit		
	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent
1	68.2	-	-	4.2	-	-
2	50.0	-	-	2.9	-	-
3	43.7	-	-	2.0	-	-
4	32.7	-	-	4.6	-	-
5	19.7	-	-	8.1	-	-
6	74.9	-	-	1.2	-	-
7	99.7	-	-	3.0	-	-
8	3.6	-	-	24.4	-	-
9	25.6	-	-	2.0	-	-
1 x 2	40.0	-	-	1.7	-	-
1 x 3	97.9	48.445**	10.998*	1.5	-	-
1 x 4	11.7	-	-	3.1	-	-
1 x 5	102.1	89.249**	15.759**	4.0	-	-
1 x 6	131.0	60.638**	48.526**	2.9	7.407**	-
1 x 7	154.9	64.675**	55.366**	3.2	-	-
1 x 8	57.5	25.272**	-	6.5	-	-
1 x 9	62.0	8.963	-	1.3	-	-
2 x 3	32.2	-	-	1.3	-	-
2 x 4	91.6	121.524**	83.200**	1.8	-	-
2 x 5	79.1	126.973**	58.200**	3.1	-	-
2 x 6	118.7	90.072**	58.478**	1.4	-	-
2 x 7	115.3	54.041**	15.647**	1.9	-	-
2 x 8	65.4	144.029**	30.8**	5.5	-	-
2 x 9	53.3	41.003**	6.6	1.8	-	-

continued...

Table 20 continued

Parents and hybrids	No.of fruits per plant			Weight of fruit		
	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent
3 x 4	150.2	295.194**	243.707**	1.8	-	-
3 x 5	76.0	139.747	73.913**	3.0	-	-
3 x 6	99.9	68.465**	33.378**	2.0	25.0**	-
3 x 7	100.5	40.167**	0.802	1.6	-	-
3 x 8	62.5	164.271**	43.021**	4.8	-	-
3 x 9	112.3	224.098**	156.979**	1.6	-	-
4 x 5	954.0	1174.809**	921.407**	6.3	-	-
4 x 6	181.9	238.104**	142.857**	2.3	-	-
4 x 7	61.0	-	-	1.9	-	-
4 x 8	46.5	167.218**	48.318**	8.3	-	-
4 x 9	20.2	-	-	1.1	-	-
5 x 6	99.8	110.993**	35.244**	3.7	-	-
5 x 7	44.5	-	-	3.3	-	-
5 x 8	29.2	150.649**	48.223**	21.2	30.462**	-
5 x 9	33.3	47.019**	30.076**	3.2	-	-
6 x 7	127.9	46.506**	28.285**	2.3	9.524**	-
6 x 8	59.5	0.637	-	2.3	-	-
6 x 9	142.8	184.179**	90.654**	1.4	-	-
7 x 8	39.7	-	-	4.2	-	-
7 x 9	31.2	-	-	1.2	-	-
8 x 9	19.6	34.247**	-	5.7	-	-
C.D. 5%		9.189	10.611		0.339	0.392
C.D. 1%		12.173	14.056		0.450	0.520

Table 20 continued

Parents and hybrids	Length of fruit			Girth of fruit		
	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent
1	10.2	-	-	3.4	-	-
2	8.4	-	-	3.3	-	-
3	7.6	-	-	3.0	-	-
4	3.0	-	-	7.5	-	-
5	7.5	-	-	7.1	-	-
6	5.6	-	-	2.7	-	-
7	10.2	-	-	3.0	-	-
8	7.1	-	-	10.1	-	-
9	3.0	-	-	3.9	-	-
1 x 2	5.2	-	-	3.1	-	-
1 x 3	6.2	-	-	2.9	-	-
1 x 4	3.9	-	-	4.2	-	-
1 x 5	6.7	-	-	4.2	-	-
1 x 6	4.3	-	-	3.1	-	-
1 x 7	6.6	-	-	3.1	-	-
1 x 8	8.2	-	-	8.1	-	-
1 x 9	4.0	-	-	2.8	-	-
2 x 3	4.2	-	-	2.3	-	-
2 x 4	4.0	-	-	4.2	-	-
2 x 5	6.2	-	-	4.4	-	-
2 x 6	4.3	-	-	3.0	-	-
2 x 7	6.2	-	-	5.2	1.567**	-
2 x 8	7.7	-	-	7.0	-	-
2 x 9	4.3	-	-	3.0	-	-

continued..

Table 20 continued

Parents and hybrids	Length of fruit			Girth of fruit		
	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent
3 x 4	3.5	-	-	4.5	-	-
3 x 5	5.4	-	-	4.5	-	-
3 x 6	5.5	-	-	3.0	5.263**	-
3 x 7	5.4	-	-	3.0	-	-
3 x 8	6.5	-	-	6.9	-	-
3 x 9	4.1	-	-	3.2	-	-
4 x 5	3.3	-	-	9.2	28.027**	22.667**
4 x 6	3.8	-	-	5.1	-	-
4 x 7	3.6	-	-	4.9	-	-
4 x 8	5.0	-	-	7.4	-	-
4 x 9	2.4	-	-	4.7	-	-
5 x 6	7.0	6.870**	-	4.7	-	-
5 x 7	6.8	-	-	5.0	-	-
5 x 8	6.9	-	-	9.9	-	-
5 x 9	6.9	31.429**		4.0	-	-
6 x 7	7.8	-	-	3.1	8.772**	3.4**
6 x 8	6.8	7.087**	-	6.4	-	-
6 x 9	3.6	-	-	3.5	6.061**	-
7 x 8	7.3	-	-	6.0	-	-
7 x 9	3.8	-	-	2.9	-	-
8 x 9	5.7	12.671**	-	6.1	-	-
C.D. 5%		0.190	0.219		0.205	0.237
C.D. 1%		0.252	0.291		0.272	0.314

continued..

Table 20 continued

Parents and hybrids	Size of fruit			No.of seeds/fruit		
	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent
1	3.9	-	-	92.2	-	-
2	3.9	-	-	57.2	-	-
3	3.0	-	-	46.0	-	-
4	3.0	-	-	23.2	-	-
5	8.9	-	-	100.1	-	-
6	2.6	-	-	45.2	-	-
7	3.3	-	-	51.1	-	-
8	24.3	-	-	157.9	-	-
9	2.6	-	-	27.8	-	-
1 x 2	3.1	-	-	50.4	-	-
1 x 3	2.8	-	-	50.1	-	-
1 x 4	2.5	-	-	20.9	-	-
1 x 5	5.0	-	-	130.7	59.955**	30.569**
1 x 6	2.3	-	-	60.3	-	-
1 x 7	2.5	-	-	50.1	-	-
1 x 8	6.1	-	-	101.2	-	-
1 x 9	2.1	-	-	38.6	-	-
2 x 3	2.1	-	-	24.4	-	-
2 x 4	2.5	-	-	14.6	-	-
2 x 5	5.1	-	-	91.1	15.829**	-
2 x 6	2.1	-	-	47.0	-	-
2 x 7	2.6	-	-	38.1	-	-
2 x 8	9.7	-	-	67.6	-	-
2 x 9	2.2	-	-	30.3	-	-

continued..

Table 20 continued

Parents and hybrids	Size of fruit			No. of seeds/fruit		
	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent
3 x 4	3.2	6.667**	6.667**	12.1	-	-
3 x 5	5.1	-	-	64.8	-	-
3 x 6	2.4	-	-	31.9	-	-
3 x 7	2.9	-	-	44.9	-	-
3 x 8	5.4	-	-	52.2	-	-
3 x 9	2.5	-	-	53.6	45.157**	16.522**
4 x 5	12.7	115.445**	42.697**	26.7	-	-
4 x 6	4.2	50.000**	40.000**	17.0	-	-
4 x 7	3.1	-	-	17.1	-	-
4 x 8	8.8	-	-	31.4	-	-
4 x 9	2.2	-	-	10.4	-	-
5 x 6	4.7	-	-	36.4	-	-
5 x 7	5.6	-	-	66.4	14.286**	-
5 x 8	21.6	31.307**	-	99.5	-	-
5 x 9	4.7	-	-	30.2	-	-
6 x 7	3.7	25.424**	12.121**	32.6	-	-
6 x 8	3.1	-	-	45.4	-	-
6 x 9	2.4	-	-	44.2	21.096**	-
7 x 8	4.6	-	-	50.8	-	-
7 x 9	2.1	-	-	37.4	-	-
8 x 9	4.0	-	-	28.6	-	-
C.D. 5%		0.284	0.328		2.139	2.470
C.D. 1%		0.377	0.435		2.833	3.272

Table 20 continued

Parents and hybrids	Total yield/plant			Life span		
	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent
1	291.2	-	-	144.1	-	-
2	138.2	-	-	140.8	-	-
3	89.6	-	-	149.9	-	-
4	107.2	-	-	168.3	-	-
5	89.7	-	-	139.8	-	-
6	80.3	-	-	135.8	-	-
7	94.9	-	-	135.4	-	-
8	88.2	-	-	105.4	-	-
9	17.9	-	-	167.3	-	-
1 x 2	59.3	-	-	190.3	32.591**	32.061**
1 x 3	134.7	-	-	199.5	35.714**	33.089**
1 x 4	31.7	-	-	191.9	22.855**	14.023**
1 x 5	292.0	53.321	0.275	137.6	-	-
1 x 6	241.4	27.220	-	191.8	38.035**	33.102**
1 x 7	371.2	92.282**	27.475	194.1	38.891**	34.698**
1 x 8	300.7	58.513*	3.262	172.4	38.196**	19.639**
1 x 9	70.3	-	-	187.8	20.617**	12.253**
2 x 3	35.8	-	-	195.0	34.158**	30.087**
2 x 4	144.5	17.767	4.559	195.6	26.561**	16.221**
2 x 5	251.4	103.071**	67.458*	137.6	-	-
22 x 6	142.4	25.739	3.039	196.6	43.190**	39.630**
2 x 7	190.0	63.020*	37.482	196.8	42.505**	39.772**
2 x 8	270.8	139.223**	95.948*	199.0	61.657**	41.335**
2 x 9	81.1	3.908	-	181.6	17.884**	8.548**

continued..

Table 20 continued

Parents and hybrids	Total yield/plant			Life span		
	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent
3 x 4	216.8	120.325**	102.239**	216.0	35.764**	28.342**
3 x 5	205.6	129.336**	129.208**	209.3	44.494**	39.626**
3 x 6	105.2	18.269	17.411	163.1	29.080**	22.148**
3 x 7	143.0	55.014	50.685	207.0	45.110**	38.092**
3 x 8	215.5	142.407**	140.513**	171.2	34.117**	14.209**
3 x 9	146.1	171.814**	65.058	196.6	25.959**	17.513**
4 x 5	1443.8	1366.531**	1246.828**	230.2	49.432**	36.779**
4 x 6	364.7	273.095**	240.205**	220.5	45.978**	31.016**
4 x 7	96.7	-	-	219.9	44.814**	30.659**
4 x 8	172.3	76.356**	60.728	183.3	33.942**	8.913**
4 x 9	24.9	-	-	209.7	24.970**	24.599**
5 x 6	242.0	171.910**	169.788**	181.7	32.822**	29.971**
5 x 7	109.2	18.309	15.068	193.0	30.262**	38.054**
5 x 8	436.8	391.062**	386.957**	164.4	34.095**	17.596**
5 x 9	85.0	34.275	-	195.3	27.189**	16.736**
6 x 7	172.2	67.991**	81.454	180.5	34.101**	33.309**
6 x 8	83.7	-	-	161.3	34.866**	20.553**
6 x 9	162.3	205.649**	85.805	194.3	29.060**	16.139**
7 x 8	137.6	50.300	44.995	166.3	38.123**	22.821**
7 x 9	30.4	-	-	195.6	29.237**	16.916**
8 x 9	63.2	19.133	-	179.7	31.793**	7.412**
C.D. 5%		55.249	63.796		2.133	2.463
C.D. 1%		73.192	84.515		2.825	3.263

continued...

Table 20 continued

Parents and hybrids	Vitamin A			Vitamin C		
	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent
1	9028.7	-	-	68.5	-	-
2	3111.0	-	-	86.5	-	-
3	8259.3	-	-	65.8	-	-
4	5503.7	-	-	108.1	-	-
5	6036.0	-	-	165.5	-	-
6	10925.3	-	-	119.6	-	-
7	3851.7	-	-	143.9	-	-
8	3555.0	-	-	159.8	-	-
9	8851.7	-	-	61.5	-	-
1 x 2	2989.3	-	-	183.1	136.258**	111.676**
1 x 3	7090.3	-	-	127.3	89.875**	86.131**
1 x 4	4545.3	-	-	195.0	120.838**	80.309**
1 x 5	4595.1	-	-	179.2	53.162**	8.278*
1 x 6	1450.9	-	-	212.0	125.541**	77.258**
1 x 7	6703.1	4.082	-	250.5	117.043**	60.161**
1 x 8	4553.3	-	-	315.6	176.478**	97.497**
1 x 9	8244.6	-	-	388.8	498.154**	467.591**
2 x 3	6650.0	16.971	-	178.6	134.537**	106.474**
2 x 4	2314.1	-	-	224.4	130.627**	107.586**
2 x 5	4538.1	-	-	182.6	44.921**	10.352*
2 x 6	1339.8	-	-	222.0	115.429**	89.619**
2 x 7	6746.2	93.781	75.149	161.3	40.017**	12.092**
2 x 8	1202.0	-	-	325.4	164.230**	103.629**
2 x 9	8273.6	38.323	-	281.1	279.666**	224.971**

continued..

Table 20 continued

Parents and hybrids	Vitamin A			Vitamin C		
	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent
3 x 4	6476.7	-	-	195.8	125.187**	81.129**
3 x 5	5240.1	-	-	301.2	160.441**	81.994**
3 x 6	4610.7	-	-	210.3	126.861**	75.836**
3 x 7	5309.4	-	-	220.5	110.30**	53.231**
3 x 8	4208.8	-	-	301.5	167.287**	88.673**
3 x 9	5934.5	-	-	152.0	138.806**	131.003**
4 x 5	6761.5	17.177	12.001	307.6	124.854**	85.861**
4 x 6	4199.4	-	-	173.9	52.745**	45.401**
4 x 7	3271.9	-	-	241.1	91.349**	67.547**
4 x 8	1305.0	-	-	450.4	205.636**	156.195**
4 x 9	4309.0	-	-	240.7	183.844**	122.664**
5 x 6	5794.3	-	-	353.0	147.632**	113.293**
5 x 7	3685.9	-	-	286.0	84.874**	72.809**
5 x 8	5604.1	16.849	-	415.5	155.457**	151.057**
5 x 9	6680.8	-	-	253.7	123.524**	53.293**
6 x 7	6379.0	-	-	263.1	114.877**	96.734**
6 x 8	5514.9	-	-	333.6	140.229**	110.013**
6 x 9	8162.9	-	-	139.7	54.279**	16.606**
7 x 8	3835.5	4.999	0.955	313.2	106.256**	93.995**
7 x 9	6229.8	-	-	227.9	121.908**	58.374**
8 x 9	5476.1	-	-	281.8	154.677**	76.345**
C.D. 5%		117.852	136.824		7.072	8.166
C.D. 1%		156.128	180.281		9.363	10.818

continued..

Table 20 continued

Parents and hybrids	Capsaicin			Oleoresin		
	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent
1	0.143	-	-	8.9	-	-
2	0.155	-	-	8.9	-	-
3	0.240	-	-	8.5	-	-
4	0.150	-	-	6.0	-	-
5	0.048	-	-	4.5	-	-
6	0.519	-	-	8.9	-	-
7	0.590	-	-	9.0	-	-
8	0.024	-	-	3.5	-	-
9	0.214	-	-	7.3	-	-
1 x 2	0.474	220.270**	209.000**	15.4	73.034**	73.034**
1 x 3	0.574	200.524**	139.167**	8.9	2.298**	-
1 x 4	0.364	149.315**	142.667**	11.9	99.732**	33.708**
1 x 5	0.169	76.963**	18.182**	7.1	5.970**	-
1 x 6	0.891	169.063**	71.599**	15.6	75.281**	75.281**
1 x 7	0.760	85.366**	10.145**	16.1	79.889**	78.889**
1 x 8	0.097	16.867**	304.167**	6.9	11.290**	-
1 x 9	0.570	220.224**	166.355**	14.8	77.246**	66.292**
2 x 3	0.590	195.918**	141.667**	16.0	83.908**	79.775**
2 x 4	0.401	164.422**	161.830**	13.1	75.839**	47.191**
2 x 5	0.132	32.000**	-	7.9	17.910**	-
2 x 6	0.485	43.750**	-	15.9	78.652**	78.652**
2 x 7	0.3[illegible]	-	-	10.2	13.966**	13.333**
2 x 8	0.100	12.994**	-	6.9	11.290**	-
2 x 9	0.477	159.945**	122.697**	15.0	79.641**	68.539**

continued...

Table 20 continued

Parents and hybrids	Capsaicin			Oleoresin		
	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent
3 x 4	1.167	498.462**	386.25**	5.6	-	-
3 x 5	0.17	18.056**	-	9.1	40.0**	7.059**
3 x 6	1.267	234.300**	144.123**	15.7	80.459**	76.404**
3 x 7	0.690	48.452**	-	15.7	79.428**	74.444**
3 x 8	0.139	5.032**	-	7.7	28.353**	-
3 x 9	0.784	248.444**	226.667**	8.4	3.067**	-
4 x 5	0.897	806.061**	498.0**	11.9	126.667**	98.4**
4 x 6	1.324	295.22**	155.106**	10.9	46.309**	22.472**
4 x 7	1.234	193.809**	78.841**	7.9	5.333**	-
4 x 8	0.94	980.459**	526.667**	5.9	24.211**	-
4 x 9	0.617	239.011**	188.318**	12.8	85.507**	64.103**
5 x 6	0.315	10.915**	-	7.8	16.418**	-
5 x 7	0.087	-	-	7.9	17.037**	-
5 x 8	0.055	52.778**	14.595**	4.5	12.50**	-
5 x 9	0.176	34.351**	-	7.3	18.699**	-
6 x 7	1.404	132.067**	103.478**	15.7	75.419**	74.444**
6 x 8	0.298	9.559**	-	7.1	14.516**	-
6 x 9	0.426	16.076**	-	14.9	78.443**	67.416**
7 x 8	0.354	-	-	6.8	8.80**	-
7 x 9	1.114	146.460**	61.449**	14.9	8.40**	65.556**
8 x 9	0.127	6.723**	-	6.1	7.965**	-
C.D. 5%		0.050	0.058		0.229	0.265
C.D. 1%		0.067	0.077		0.304	0.351

Table 21. Range and mean values in parents and F_1 hybrids and heterosis.

	Height of plant	Primary branches	Secondary branches	Number of leaves
Range				
a. Parents	24.3-66.1	3-7.6	9-47.8	268.8-11006.6
b. F_1's	27.7-109.0	5.1-19	21.7-116	357-39030.6
Mean values				
a. Parents	46.489	5.366	25.64	3172.93
b. F_1's	48.627	9.9	62.758	4341.094
Average heterosis (%)	4.598	84.494	144.765	36.816
Top parent	2	4	2	7
Best performing F_1	4 x 6	4 x 6	2 x 5	2 x 4
*Percentage of significantly heterotic crosses				
a. Over midparental value	30.0	100.00	97.3	2.8
b. Over better parent	30.6	97.3	86.2	2.8
Range of heterosis				
a. Over midparental values	1.43-114.14	6.422-221.74	13.73-516.22	6.42-1488.93
b. Over better parent	1.45-65.15	5.45-218.96	2.30-508.0	2.22-1063.04
*Most heterotic F_1	4 x 6	1 x 2	4 x 6	2 x 4

*Computed over mid parental value

Table 21 continued

	Spread of plant	Number of days taken for blooming	Number of fruits	Weight of fruit
Range				
a. Parents	22.6-47.9	58.4-97.1	3.6-99.7	1.2-24.4
b. F_1's	22.4-133.1	54.6-100.1	11.7-334	1.1-21.2
Mean values				
a. Parents	33.2	79.56	48.68	5.83
b. F_1's	52.769	79.928	65.2	2.983
Average heterosis (%)	58.198	0.462	75.020	-
Top parent	7	4	7	6
Best performing F_1	4 x 6	2 x 4	4 x 5	-
Percentage of significantly heterotic crosses				
a. Over midparental value	80.6	36.2	72.3	11.2
b. Over better parent	72.3	19.5	58.4	-
Range of heterosis				
a. Over midparental value	3.29-230.27	0.75-30.67	0.637-1174.81	7.40-30.46
b. Over better parent	4.87-223.65	0.14-17.87	0.802-243.70	-
Most heterotic F_1	4 x 6	2 x 8	4 x 5	5 x 8

continued...

Table 21 continued

	Length of fruit	Girth of fruit	Size of fruit	Number of seeds/fruit
Range				
a. Parents	3-10.2	2.7-18.1	2.6-24.3	23.2-157.9
b. F_1's	2.4-8.2	2.5-9.9	2.1-21.6	10.4-130.7
Mean values				
a. Parents	6.96	5.8	6.17	66.75
b. F_1's	5.363	4.628	4.380	46.94
Average heterosis (%)				
Top parent	7	8	8	8
Best performing F_1	-	-	-	-
Percentage of significantly heterotic crosses				
a. Over midparental value	11.2	13.9	13.9	13.9
b. Over better parent	-	5.6	11.2	5.6
Range of heterosis				
a. Over midparental value	6.87-31.43	1.567-26.02	6.66-113.44	14.28-45.25
b. Over better parent	-	3.4-22.66	6.66-42.69	16.52-30.56
Most heterotic F_1	5 x 9	4 x 5	4 x 5	3 x 9

continued

Table 21 continued

	Total yield	Life span	Vitamin A	Vitamin C
Range				
a. Parents	17.9-291.2	105.4-168.3	3111-10925.3	61.5-165.5
b. F_1's	24.9-1443.8	137.6-250.2	1202-8273.6	139.7-415.5
Mean values				
a. Parents	111.669	142.76	6568.27	108.8
b. F_1's	201.452	189.625	5018.9138	251.406
Average heterosis (%)	80.368	32.827	-	131.072
Top parent	1	4	6	5
Best performing F_1	4 x 5	4 x 5	-	5 x 8
Percentage of significantly heterotic crosses				
a. Over midparental value	38.9	94.5	-	100.00
b. Over better parent	19.5	94.5	-	94.5
Range of heterosis				
a. Over midparental value	3.90-1366.55	17.88-61.65	4.08-93.78	40.01-490.15
b. Over better parent	0.27-1246.82	7.41-41.33	0.95-75.14	8.27-467.59
Most heterotic F_1	4 x 5	2 x 8	2 x 7	1 x 9

continued..

Table 21 continued

	Sepsalcin	Oleoresin
Range		
a. Parents	0.024-0.69	3.5-9.0
b. F_1's	0.055-1.404	4.5-16.1
Mean values		
a. Parents	0.242	7.4
b. F_1's	0.556	10.73
Average heterosis (%)	129.752	45.0
Top parent	7	7
Best performing F_1	6 x 7	1 x 7
Percentage of significantly heterotic crosses		
a. Over midparental value	91.7	97.3
b. Over better parent	61.2	52.8
Range of heterosis		
a. Over mid parental value	5.05-980.45	2.29-126.66
b. Over better parent	10.14-526.66	7.059-98.4
Most heterotic F_1	4 x 8	4 x 5

Table 22. The mean values of parents and F_1 hybrids and their negative heterosis in percentage.

Parents and hybrids	Number of days taken for blooming			Number of seeds/fruit		
	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent	Mean	Heterosis per cent over mid-parental value	Heterosis per cent over better parent
1	87.6	-	-	92.2	-	-
2	74.3	-	-	57.2	-	-
3	87.1	-	-	46.0	-	-
4	97.1	-	-	23.2	-	-
5	74.4	-	-	100.1	-	-
6	78.3	-	-	45.2	-	-
7	83.4	-	-	51.1	-	-
8	58.4	-	-	157.9	-	-
9	75.4	-	-	27.8	-	-
1x2	83.3	-	4.794**	50.4	32.530**	45.336**
1x3	88.0	-	-	50.1	27.496**	45.661**
1x4	92.3	-	4.943**	20.9	63.778**	77.352**
1x5	74.2	8.399**	15.296**	130.7	-	-
1x6	75.5	8.981**	13.812**	60.3	12.227**	34.598**
1x7	83.7	2.105**	4.452**	50.1	30.076**	45.662**
1x8	83.8	-	4.337**	101.2	19.072**	35.908**
1x9	79.0	3.067**	9.817**	38.6	35.700**	58.134**
2x3	80.6	0.123	7.462**	24.4	52.713**	57.342**
2x4	100.1	-	-	14.6	63.681**	74.475**
2x5	80.7	-	-	91.1	-	8.991**
2x6	92.3	-	-	47.0	8.203**	17.832**
2x7	92.0	-	-	38.1	29.639**	33.391**
2x8	86.7	-	-	87.6	18.549**	44.522**
2x9	75.5	-	-	30.3	29.206**	47.027**

continued..

Table 22 continued

Parents and hybrids	Number of days taken for blooming: Mean	Heterosis per cent over mid parental value	Heterosis per cent over better parent	Number of seeds/fruit: Mean	Heterosis per cent over mid parental value	Heterosis per cent over better parent
3x4	88.1	4.343**	9.268**	12.1	65.028**	73.695**
3x5	81.4	-	6.544**	64.8	11.293**	35.265**
3x6	79.9	3.385**	8.266**	31.9	30.043**	30.652**
3x7	75.4	11.554**	13.432**	44.9	7.518**	12.133**
3x8	68.7	5.567**	21.125**	52.2	48.798**	66.941**
3x9	83.1	-	4.592**	53.6	-	-
4x5	76.9	10.320**	20.803**	26.7	56.690**	73.326**
4x6	75.3	14.139**	22.451**	17.0	48.538**	61.061**
4x7	86.6	4.044**	10.813**	17.1	53.970**	66.536**
4x8	69.1	11.125**	28.836**	31.4	65.323**	80.114**
4x9	88.8	-	8.547**	10.4	59.215**	62.589**
5x6	79.3	-	-	36.4	49.896**	63.636**
5x7	77.5	1.774**	7.074**	86.4	-	13.686**
5x8	66.0	0.602	11.290**	99.5	22.868**	36.965**
5x9	83.1	-	-	30.2	52.775**	69.830**
6x7	76.7	5.132**	8.033**	32.6	32.294**	36.203**
6x8	69.8	-	10.855**	45.4	55.292**	71.248**
6x9	75.6	1.626*	3.448**	44.2	-	2.212
7x8	62.4	11.988**	25.179**	50.8	51.367**	67.827**
7x9	91.3	-	-	37.4	5.196**	26.810**
8x9	94.6	18.355**	27.586**	28.6	69.197**	81.867**
C.D. 5%		1.341	1.549		2.139	2.470
C.D. 1%		1.771	2.052		2.833	3.272

Table 23. Range and mean values in parents and F_1 hybrids and negative heterosis.

	Number of days taken for blooming	Number of seeds/fruit
Range		
a. Parents	58.4-97.1	23.2-157.9
b. F_1's	54.6-100.1	10.4-130.7
Mean values		
a. Parents	79.56	66.75
b. F_1's	79.928	46.94
Average heterosis (%) (Negative)	-	29.68
Top parent	8	4
Best performing F_1	8x9	4x9
Percentage of significantly heterotic (negative) crosses		
a. Over midparental value	44.45	86.12
b. Over better parent	72.23	91.67
Range of negative heterosis		
a. Over midparental value	0.123-18.385	5.196-69.197
b. Over better parent	3.448-28.836	2.212-81.887
*Most heterotic (negative) F_1	8 x 9	8 x 9

*Computed over midparental value

FIG. 5

VITAMIN A CONTENT IN PARENTS AND HYBRIDS

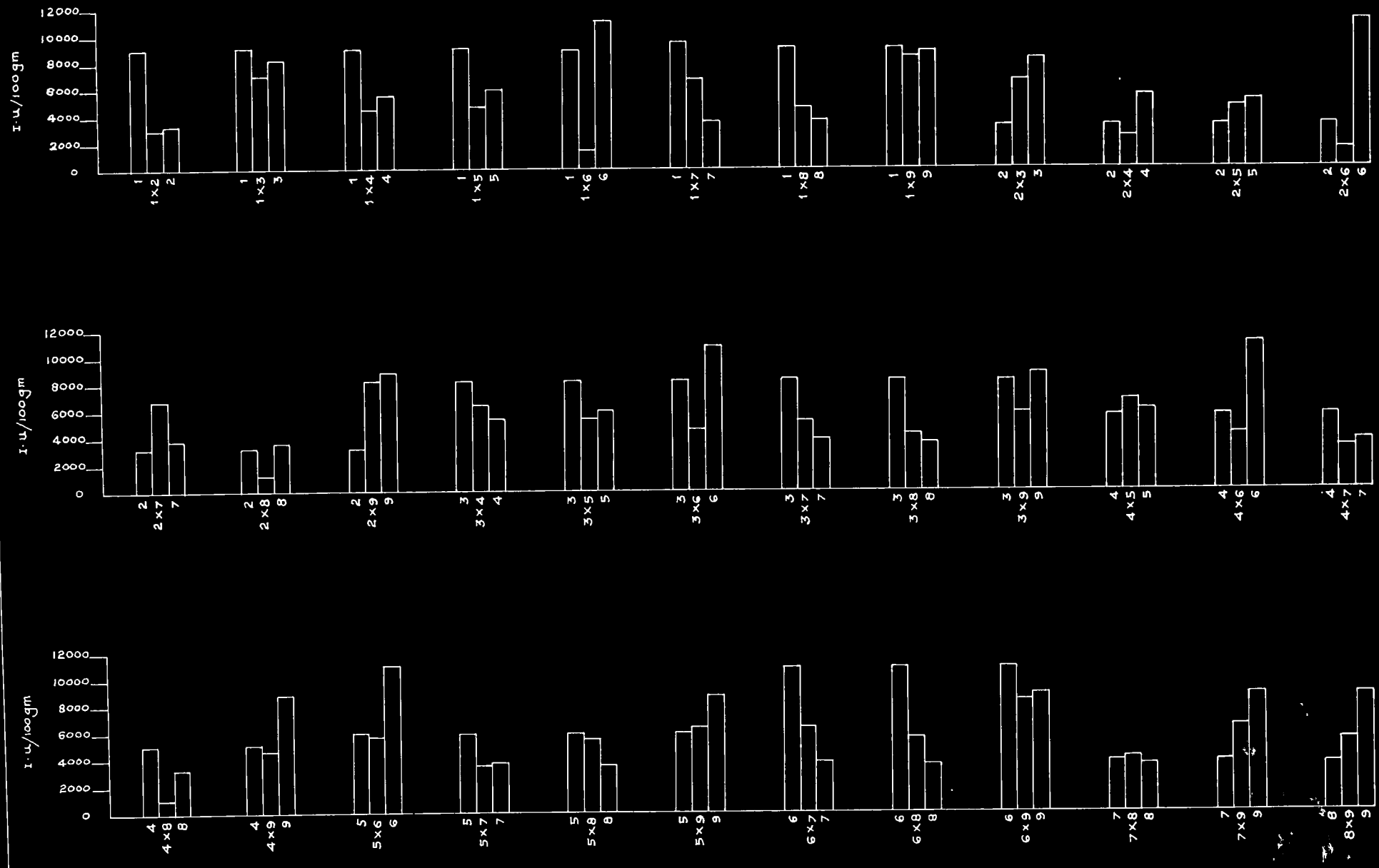


FIG.6 VITAMIN C CONTENT IN PARENTS AND HYBRIDS.

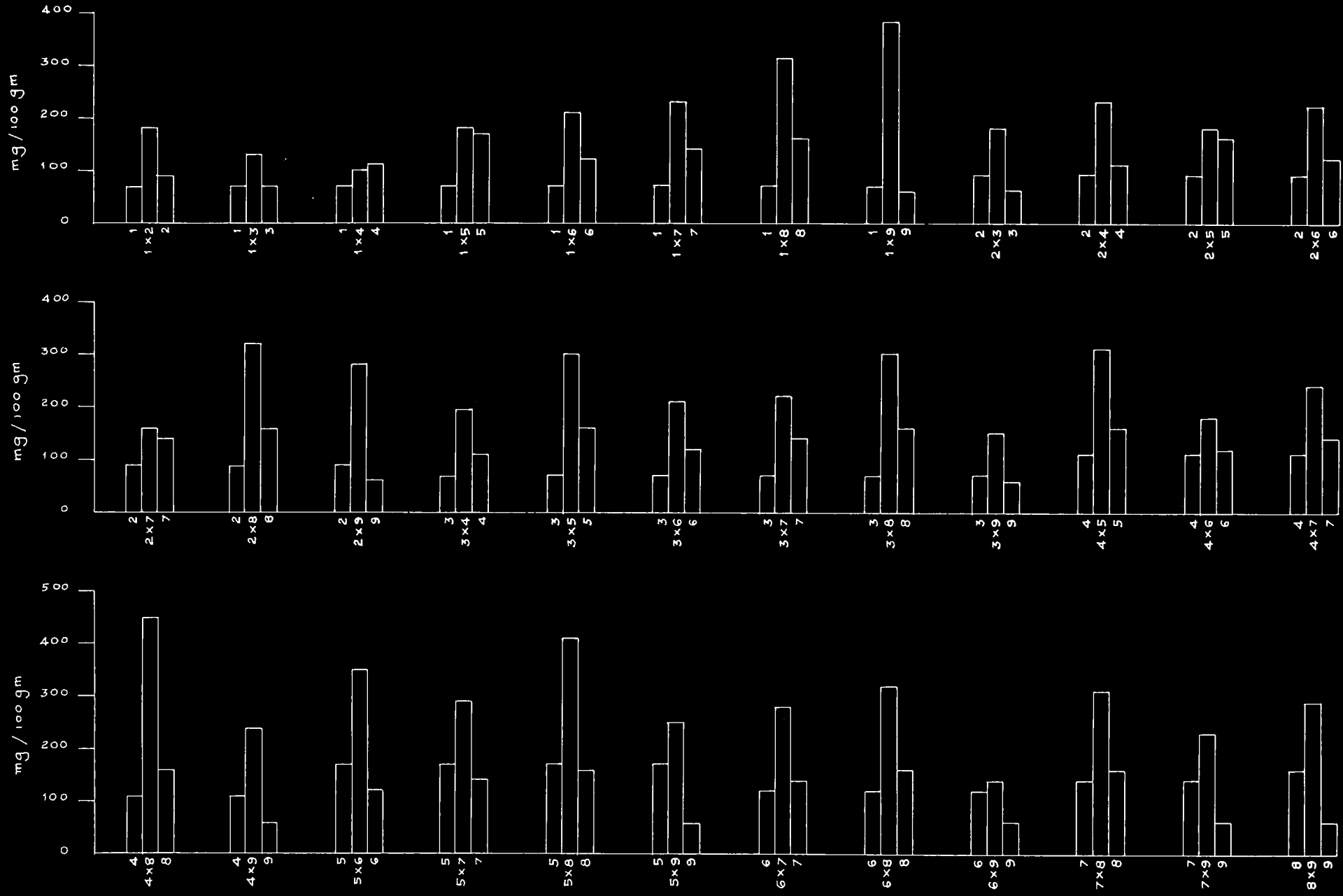


FIG. 7 CAPSAICIN CONTENT IN PARENTS AND HYBRIDS.

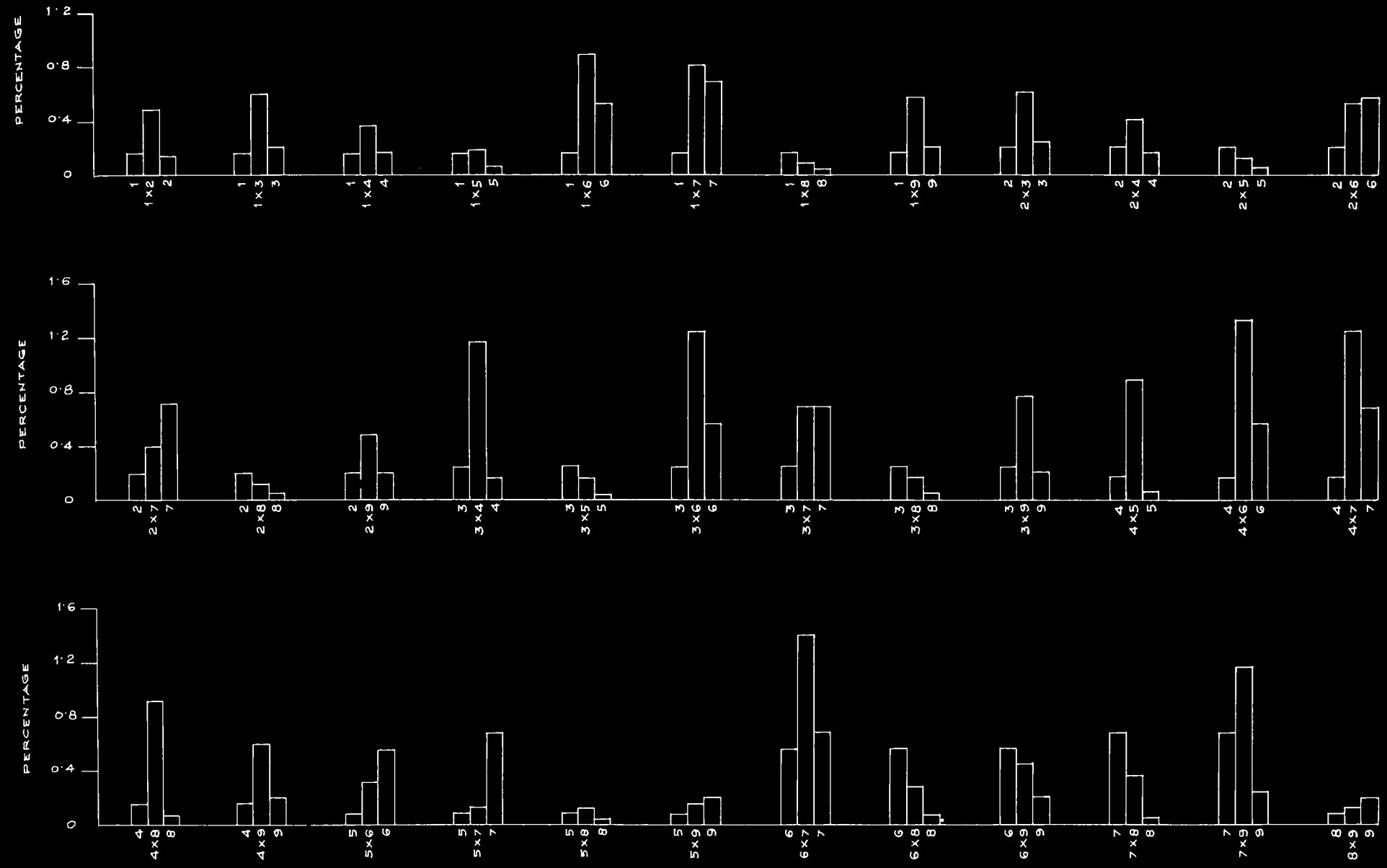
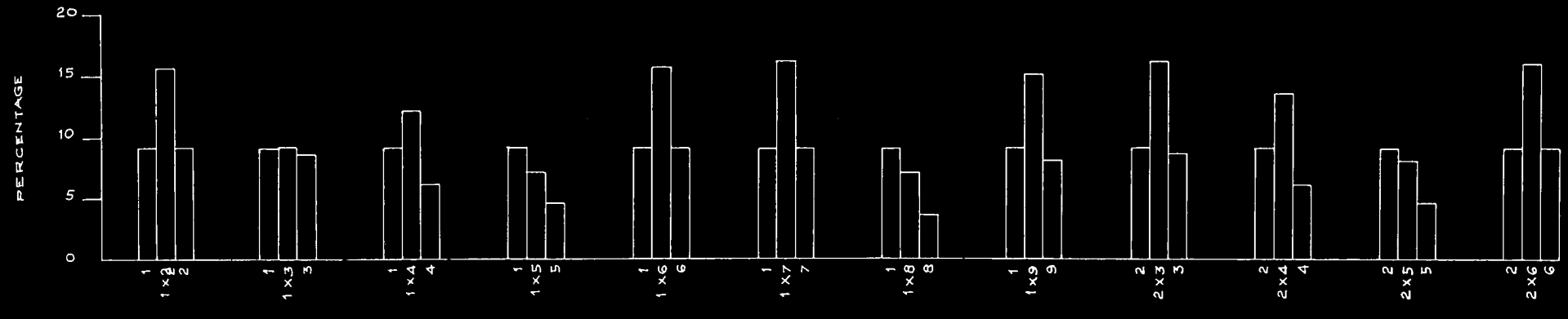
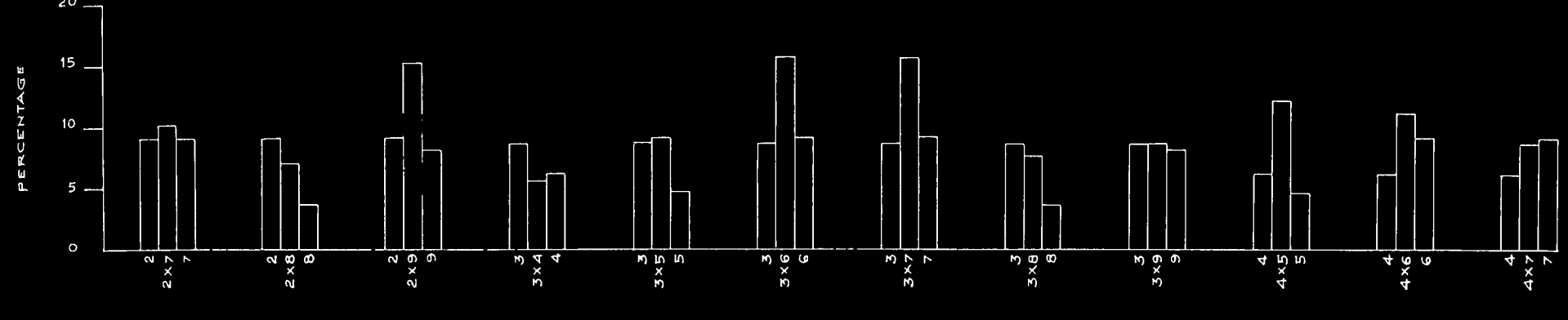
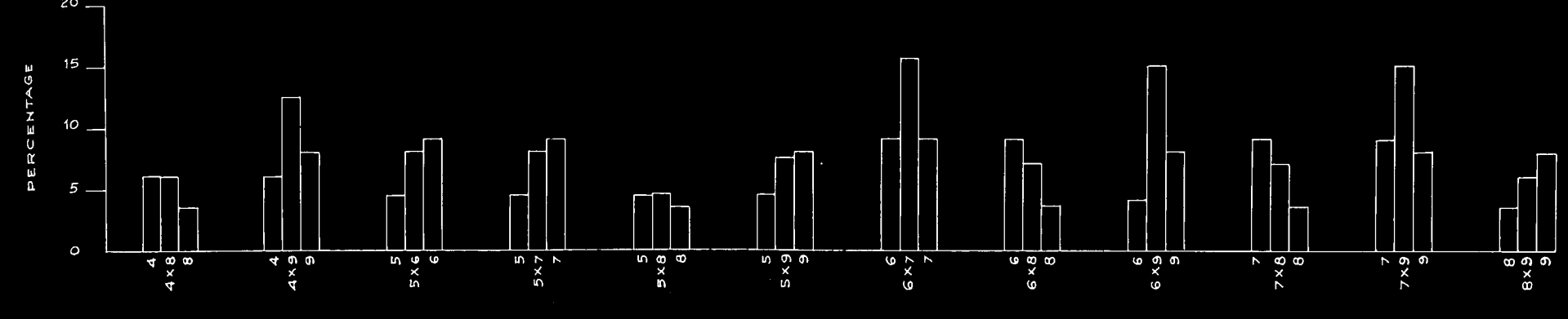


FIG.8

OLEORESIN CONTENT IN PARENTS AND HYBRIDS.







maximum negative heterosis for the number of seeds per fruit.

(ii) Studies on nutritive and quality attributes

Four important nutritive and quality attributes namely Vitamin A, Vitamin C, Capsaicin and Oleoresin content of nine parents and thirty six hybrids have been studied. They are graphically represented in Figs. 5, 6, 7 and 8 respectively. In general, very little expression of hybrid vigour in Vitamin A content was displayed. Only 2 hybrids (2 x 7 and 4 x 5) have exceeded their better parents, as far as this trait is concerned. But, there was considerable manifestation of hybrid vigour in Vitamin C and Oleoresin content. Out of 36 hybrid combinations, all hybrids transgressed their better parents except one (1 x 4). Nineteen hybrids have manifested hybrid vigour in Oleoresin content.

7. Combining ability

The results of analysis of variance for general and specific combining abilities are summarised in table 24. For all the eighteen characters the variance due to both general combining ability and specific combining ability were highly significant. The mean squares for g.c.a. were larger than those for s.c.a. in all the characters. The estimated effects of general and specific combining abilities of parents ($\hat{g}_i$ and $\hat{s}_{ii}$) as well as the estimates of specific combining ability effects of F_1 hybrids ($\hat{s}_{ij}$) for each of the eighteen characters are presented in tables 25 and 26.

Table 24. Analysis of variance table for combining abilities.

Characters	Source of variation					
	g.c.a.		s.c.a.		Error	
	df	M.S.S.	df	M.S.S.	df	M.S.S.
Height	8	909.511**	36	146.998**	88	1.047
Primary brenches	8	28.777**	36	11.209**	88	0.103
Secondary branches	8	1395.545**	36	799.434**	88	1.985
Number of leaves	8	68250272.000**	36	37244048.000**	88	127775.950
Spread	8	692.091**	36	336.305**	88	1.127
Number of days taken for blooming	8	285.227**	36	46.869**	88	0.309
Number of fruits	8	4410.632**	36	3138.659**	88	14.244
Weight of fruit	8	73.730**	36	8.303**	88	0.019
Length of fruit	8	12.619**	36	1.539**	88	0.006
Girth of fruit	8	35.004**	36	1.532**	88	0.007
Size of fruit	8	70.455**	36	7.885**	88	0.261
Number of seeds/fruit	8	3858.714**	36	390.212**	88	0.774
Total yield	8	52210.864**	36	45429.608**	88	515.974
Life span	8	1127.091**	36	664.999**	88	0.772
Vitamin A	8	10565061.000**	36	3538334.400**	88	2317.574
Vitamin C	8	12722.53**	36	7139.579**	88	8.492
Capsaicin	8	0.425**	36	0.091**	88	0.0004
Oleoresin	8	40.857**	36	8.243**	88	0.270

*Significant at 5 per cent level
**Significant at 1 per cent level

Table 25. Estimates of g.c.a. effects of parents.

Parents	Height	Primary branches	Secondary branches	Number of leaves	Spread
1. CA 960	-1.67**	0.68**	6.76**	-1420.05**	-4.50**
2. CA 1068	3.41**	0.77**	9.56**	3356.91**	-3.70**
3. G4	-1.55**	-.39**	2.33**	-102.59	-1.52**
4. Purple round	22.06**	3.16**	-1.73**	3347.05**	17.16**
5. Vella motchi	-6.25**	-1.37**	3.43**	-2429.16**	2.54**
6. Pant C-1	1.17**	0.50**	-10.56**	-1283.28**	5.48**
7. Pusa jwala	-3.08**	-.69**	11.94**	2822.62**	0.77**
8. California wonder	-4.91**	-2.59**	-24.66**	-2600.96**	-6.68**
9. Purple cluster	-9.17**	-.26**	2.42**	-1690.31**	-9.54**
S.E. $(\hat{g}_i)$	0.29	0.09	0.40	101.61	0.30
S.E. $(\hat{g}_i - \hat{g}_j)$	0.44	0.14	0.60	152.42	0.45

*Significent at 5 per cent level
**Significent at 1 per cent level

continued...

Table 25 continued

Parents	Days taken for blooming	Number of fruits	Weight of fruit	Length of fruit	Girth of fruit
1. CA 960	3.33**	4.96**	-.54**	0.30**	-.93**
2. CA 1068	3.77**	-7.58**	-1.33**	0.19**	-1.09**
3. G4	1.90**	3.63**	-1.58**	-.08**	-1.12**
4. Purple round	6.63**	16.35**	-.27**	-1.94**	0.97**
5. Vella notchi	-2.79**	5.31**	2.30**	0.66**	1.03**
6. Pant C-1	-1.50**	28.39**	-1.65**	-.23**	-1.03**
7. Puse jwala	1.26**	8.69**	-1.20**	1.02**	-1.04**
8. California wonder	-10.97**	-37.27**	6.04**	1.04**	4.14**
9. Purple cluster	-1.52**	-23.01**	-1.77**	-1.46**	-.95**
S.E. ($\hat{g}_i$)	0.16	1.07	0.04	0.02	0.02
S.E.($\hat{g}_i$-$\hat{g}_j$)	0.24	1.61	0.06	0.03	0.04

*Significant at 5 per cent level
**Significant at 1 per cent level

continued..

Table 25 continued

Parents	Size of fruit	Number of seeds/ fruit	Total yield	Life span	Vitamin A
1. CA 960	-1.13**	16.16**	22.55**	-4.44**	449.22**
2. CA 1068	-1.22**	-1.00**	-36.62**	-2.59**	-1183.14**
3. G4	-1.33**	-7.55**	-41.20**	6.82**	786.35**
4. Purple round	0.41**	-28.34**	79.50**	18.31**	-781.76**
5. Vella notchi	2.96**	23.37**	126.20**	-6.71**	153.20**
6. Pant C-1	-1.50**	-9.39**	-13.16*	-2.28**	546.53**
7. Pusa jwala	-1.21**	-4.48**	-55.50*	1.95**	-306.58**
8. California wonder	5.58**	27.60**	1.99	-17.64**	-1311.49**
9. Purple cluster	-1.73**	-16.37**	-103.46**	6.50**	1647.73**
S.E. ($\hat{g}_i$)	0.15	0.25	5.46	0.25	13.68
S.E.($\hat{g}_i - \hat{g}_j$)	0.22	0.36	9.69	0.37	20.53

*Significant at 5 per cent level
**Significant at 1 per cent level

Table 25 continued

Parents	Vitamin C	Capsaicin	Oleoresin
1. GA 960	-23.60**	-.07**	1.04**
2. GA 1068	-27.20**	-.15**	1.37**
3. G4	-37.42**	0.08**	0.40**
4. Purple round	-2.21**	0.21**	-.71**
5. Vella notchi	34.69**	-.26**	-2.48**
6. Pant C-1	-5.44**	0.23**	1.95**
7. Pusa jwala	2.11*	0.22**	1.21**
8. California wonder	71.76**	-.25**	-3.71**
9. Purple cluster	-12.59**	-.02*	0.92**
S.E.($\hat{g}_i$)	0.83	0.01	0.15
S.E.($\hat{g}_i - \hat{g}_j$)	1.24	0.01	0.22

*Significant at 5 per cent level
**Significant at 1 per cent level

Table 26. Estimates of g.c.a. effects of parents and F_1 hybrids.

Parents and F_1 hybrids	Height	Primary branches	Secondary branches	Number of leaves	Spread
1	13.31**	-5.03**	-46.92**	264.11	-2.57**
2	9.92**	-4.76**	-26.59**	-9264.43**	0.51
3	1.26	-2.75**	-32.91**	5013.14**	17.98**
4	-27.45**	-7.68**	-37.25**	-7445.70**	45.82**
5	-1.10	-0.84**	-32.37**	1072.92**	-10.06**
6	-15.81**	-4.36**	-20.22**	-363.67	-20.82**
7	-0.87	-2.27**	-33.45**	1253.92**	-4.62**
8	1.92*	-0.77**	2.98*	1363.21**	-4.45**
9	-6.69**	-4.10**	-40.32**	-504.72	-9.13**
1 x 2	-20.54**	7.86**	-15.76**	-388.23	-10.03**
1 x 3	-.82	0.89**	30.67**	-212.06	9.25**
1 x 4	-18.53**	-2.10**	-22.84**	-4019.92**	-12.06**
1 x 5	-.80	1.70**	37.87**	1762.05**	7.04**
1 x 6	2.60**	-0.91**	-9.27**	161.57	-14.59**
1 x 7	6.02**	1.98**	36.20**	628.92	8.09**
1 x 8	1.54	-1.21**	-1.14	1052.94**	5.78**
1 x 9	3.90**	1.85**	38.11**	486.40	11.67**

continued..

Table 26 continued

Parents and F_1 hybrids	Height	Primary branches	Secondary branches	Number of leaves	Spread
2 x 3	1.90*	-1.30**	-18.33**	-4987.19**	-5.57**
2 x 4	6.35**	3.95**	5.86**	28219.23**	2.15*
2 x 5	-6.65**	1.55**	47.73**	-3121.18**	4.99**
2 x 6	2.28*	-1.93**	-13.14**	-4676.40**	-15.56**
2 x 7	-2.90**	0.45	33.40**	11736.40**	6.45**
2 x 8	-3.30**	-1.53**	-7.94**	-3857.28**	1.32
2 x 9	1.05	0.30	21.38**	-4396.46**	12.74**
3 x 4	0.92	2.60**	-2.08	-4324.09**	2.80**
3 x 5	-8.96**	-1.43**	-4.34**	471.58	-12.82**
3 x 6	5.62**	1.43**	-2.35	1237.01**	35.70**
3 x 7	2.18**	2.82**	37.22**	-4372.06	4.40*
3 x 8	3.57**	1.26**	-2.61*	1701.78**	1.76
3 x 9	-6.92**	-0.77*	27.64**	461.66	-1.57
4 x 5	19.56**	0.26	9.02**	-992.75**	26.50**
4 x 6	36.48**	6.35**	47.71**	-574.00	59.53**
4 x 7	13.91**	-2.13**	-2.52	-4948.40**	20.21**
4 x 8	-19.71**	0.11	0.55	-2924.79**	-18.48**
4 x 9	13.89**	6.31**	38.70**	4456.12**	10.98**

continued..

Table 26 continued

Parents and F_1 hybrids	Height	Primary branches	Secondary branches	Number of leaves	Spread
5 x 6	-6.56**	-0.62**	-8.25**	653.11*	-4.94**
5 x 7	-5.49**	-0.66*	-1.58	-2583.66**	-17.12**
5 x 8	6.95**	2.18**	5.39**	1295.85**	9.01**
5 x 9	4.15**	-1.09**	-21.10**	369.04	7.46**
6 x 7	-5.85**	1.20**	5.05**	1422.99**	-2.87**
6 x 8	-2.92**	-0.70*	1.08	663.17*	-6.65**
6 x 9	-0.04	4.07**	19.63**	1839.82**	-9.01**
7 x 8	3.28**	2.50**	0.72	-1220.03**	9.38**
7 x 9	-2.49**	-1.60**	-41.60**	-3160.07**	-19.78**
8 x 9	6.74**	-1.07**	-2.10	561.83	5.76**
S.E. ($\hat{s}_{ii}$)	0.83	0.26	1.14	289.20	0.86
S.E. ($\hat{s}_{ii}-\hat{s}_{jj}$)	1.15	0.36	1.59	403.27	1.20
S.E. ($\hat{s}_{ij}$)	0.94	0.29	1.29	326.91	0.97
S.E.($\hat{s}_{ij}-\hat{s}_{ik}$)	1.38	0.43	1.90	482.00	1.45
S.E.($\hat{s}_{ij}-\hat{s}_{kl}$)	1.31	0.41	1.80	457.26	1.36

*Significant at 5 per cent level
**Significant at 1 per cent level

Table 26 continued

Parents and F_1 hybrids	Number of days taken for blooming	Number of fruits	Weight of fruit	Length of fruit	Girth of fruit
1	1.11	0.42	1.45**	2.90**	0.44**
2	-15.06**	-12.74**	1.69**	2.30**	0.59**
3	3.42**	-41.49**	1.25**	2.05**	0.34**
4	3.99**	-78.95**	1.28**	1.17**	0.74**
5	0.10	-68.82**	-0.37**	0.47**	0.16*
6	1.61**	-59.78**	0.59**	0.41**	-0.13
7	1.00	4.44	1.50**	2.51**	-0.18
8	0.49	0.21	8.45**	-0.68**	4.99**
9	-1.44**	-6.32*	1.68**	0.28**	0.98**
1 x 2	-3.56**	-35.31**	-0.33*	-1.43**	0.27**
1 x 3	2.95**	11.45**	-0.23	-0.21**	0.10
1 x 4	2.49**	-88.05**	0.04	-0.62**	-0.71**
1 x 5	-6.16**	13.90**	-1.61**	-0.45**	-0.80**
1 x 6	-6.09**	19.75**	1.25**	-1.96**	0.18*
1 x 7	-0.78	63.36**	1.10**	-0.85**	0.21*
1 x 8	11.55**	11.92**	-2.85**	0.70**	0.00
1 x 9	-2.63**	2.15	-0.24	-1.00**	-0.13

continued..

Table 26 continued

Parents and F_1 hybrids	Number of days taken for blooming	Number of fruits	Weight of fruit	Length of fruit	Girth of fruit
2 x 3	-4.92**	-41.75**	0.29*	-1.55**	-0.40**
2 x 4	9.88**	4.42	-.51**	0.04	-0.59**
2 x 5	-0.10	3.50	-1.78**	-0.32**	-0.42**
2 x 6	10.24**	20.02**	0.50**	-1.33**	0.21*
2 x 7	7.16**	36.26**	0.56**	-0.71**	0.43**
2 x 8	14.05**	32.35**	-3.13**	0.33**	-0.87**
2 x 9	-6.63**	5.99	0.98**	-0.14*	-0.20*
3 x 4	-0.28	51.81**	-0.21	-0.15*	-0.19*
3 x 5	2.48**	-10.84**	-1.60**	0.85**	-0.27**
3 x 6	-0.22	-10.05**	1.31**	0.14	0.32**
3 x 7	-7.64**	10.26**	0.49**	-1.22**	0.34**
3 x 8	-2.08**	18.28**	-3.58**	-0.18	-0.97**
3 x 9	2.87**	53.82**	1.04**	-0.06	0.41**
4 x 5	-6.79**	233.93**	0.41**	-1.08**	2.29**
4 x 6	-9.58**	58.72**	0.31*	0.32**	0.34**
4 x 7	-1.14*	-42.41**	-0.51**	-1.17**	0.15
4 x 8	-6.41**	-8.99*	-1.37**	0.21**	-2.57**
4 x 9	3.84**	-51.52**	-0.72**	0.11	-0.19*

continued..

Table 26 continued

Parents and F_1 hybrids	Number of days taken for blooming	Number of fruits	Weight of fruit	Length of fruit	Girth of fruit
5 x 6	3.81**	-11.80**	-0.66**	0.66**	-0.15
5 x 7	-0.85	-47.36**	-1.66**	-0.55**	0.10
5 x 8	-0.12	-16.77**	8.98**	-0.53**	-0.10
5 x 9	7.53**	-26.93**	-1.19**	1.97**	-0.97**
6 x 7	-0.81	12.96**	1.29**	1.33**	0.28**
6 x 8	2.52**	-29.55**	-5.96**	0.22**	-1.57**
6 x 9	-1.10*	59.52**	0.99**	-0.43**	0.65**
7 x 8	-7.71**	-9.61**	-4.50**	-0.40**	-1.92**
7 x 9	11.75**	-32.34**	0.26*	-1.46**	0.05
8 x 9	-12.76**	1.95	-4.48**	0.46**	-1.98**
S.E. ($\hat{s}_{ii}$)	0.45	3.05	0.11	0.06	0.07
S.E. ($\hat{s}_{ii}-\hat{s}_{jj}$)	0.63	4.26	0.16	0.09	0.10
S.E. ($\hat{s}_{ij}$)	0.51	3.45	0.13	0.07	0.08
S.E.($\hat{s}_{ij}-\hat{s}_{ik}$)	0.75	5.09	0.19	0.11	0.11
S.E. ($\hat{s}_{ij}-\hat{s}_{kl}$)	0.71	4.83	0.18	0.10	0.11

*Significant at 5 per cent level
**Significant at 1 per cent level

Table 26 continued

Parents and F_1 hybrids	Size of fruit	Number of seeds/ fruit	Total yield	Life span	Vitamin A
1	1.50**	8.99**	62.36**	-27.30**	2801.27**
2	1.66**	8.33**	27.91	-34.30**	148.33**
3	0.98*	10.20**	-11.52	-44.01**	1357.68**
4	-0.78	28.97**	-235.32**	-48.53**	1738.22**
5	-1.64**	2.49**	-346.18**	-27.02**	401.63**
6	0.95*	13.04**	-68.92**	-41.87**	4503.12**
7	1.06*	9.17**	-16.77	-48.77**	-564.12**
8	8.46**	51.83**	-99.31**	-39.52**	849.02**
9	1.43**	9.64**	41.35*	-26.18**	227.35**
1 x 2	0.76	-15.69**	-109.58**	17.08**	-1605.75**
1 x 3	0.65	-9.37**	-30.26	15.91**	526.02**
1 x 4	-0.59	-17.78**	-254.01**	-2.18**	450.95**
1 x 5	-1.46**	40.24**	-40.34	-31.52**	-1335.30**
1 x 6	-0.22	2.67**	48.40*	18.28**	-4873.91**
1 x 7	0.14	-12.50**	200.96**	16.38**	1231.47**
1 x 8	-3.8 **	6.58**	-92.54**	14.27**	87.13
1 x 9	0.30	-12.12**	-32.42	5.56**	818.66**

continued..

Table 26 continued

Parents and F_1 hybrids	Size of fruit	Number of seeds/ fruit	Total yield	Life span	Vitamin A
2 x 3	-.02	-17.95**	-69.83**	10.56**	1717.85**
2 x 4	-.47	-6.96**	-81.90**	-.33	-1049.97**
2 x 5	-1.31**	17.83**	-41.69*	-33.38**	239.05**
2 x 6	0.19	6.52**	8.70	21.20**	-3352.68**
2 x 7	0.41	-7.28**	79.02**	17.17**	2906.96**
2 x 8	-3.35**	10.13**	121.89**	38.95**	-1632.31**
2 x 9	0.47	-3.26**	37.61	-2.66**	2480.09**
3 x 4	0.25	-2.95**	-5.04	10.59**	1143.18**
3 x 5	-1.18*	-1.92*	-62.89**	28.98**	-1028.45**
3 x 6	0.57	-2.03*	-24.00	-1.71*	-2051.25**
3 x 7	0.35	6.00**	36.62	17.99**	-499.28**
3 x 8	-3.46**	-18.79**	71.22**	1.75**	-594.99**
3 x 9	0.89	26.59**	107.25**	2.94**	-1928.55**
4 x 5	2.22**	-19.23**	1054.58**	38.39**	2061.08**
4 x 6	1.42**	4.42**	114.83**	24.26**	-894.46**
4 x 7	0.10	-.95	-130.43**	19.37**	-968.72**
4 x 8	-1.02*	-18.73**	-92.74**	2.39**	-1930.75**
4 x 9	-.35	4.24**	-134.67**	4.58**	-1385.96**

continued..

Table 26 continued

Parents and F_1 hybrids	Size of fruit	Number of seeds/fruit	Total yield	Life span	Vitamin A
5 x 6	-1.45**	-25.52**	-54.55*	10.45**	-234.45**
5 x 7	-0.80	16.65**	-164.60**	17.49**	-1489.65**
5 x 8	8.42**	-2.37**	125.15**	8.48**	1433.39**
5 x 9	-1.15*	-27.66**	-125.29**	15.14**	-449.05**
6 x 7	1.71**	-4.43**	37.70	0.56	810.04**
6 x 8	-5.59**	-25.75**	-88.64**	0.95	950.32**
6 x 9	1.02*	19.03**	95.40**	9.74**	639.56**
7 x 8	-4.43**	-23.22**	-11.96	1.79*	177.52**
7 x 9	0.42	7.39**	-13.77	6.78**	-440.28**
8 x 9	-4.45**	-33.50**	-18.82**	10.47**	-189.05**
S.E.($\hat{s}_{ii}$)	0.41	0.71	18.38	0.71	38.95
S.E.($\hat{s}_{ii}$-$\hat{s}_{jj}$)	0.58	0.99	25.63	0.99	54.31
S.E.($\hat{s}_{ij}$)	0.47	0.80	20.77	0.80	44.03
S.E.($\hat{s}_{ij}$-$\hat{s}_{ik}$)	0.69	1.19	30.63	1.19	64.91
S.E.($\hat{s}_{ij}$-$\hat{s}_{kl}$)	0.65	1.24	29.06	1.12	61.58

*Significant at 5 per cent level
**Significant at 1 per cent level

Table 26 continued

Parents and F_1 hybrids	Vitamin C	Capsaicin	Oleoresin
1	-107.12**	-.21**	-3.12**
2	-81.96**	-.05*	-3.85**
3	-82.15**	-.42**	-2.25**
4	-110.33**	-.76**	-2.53**
5	-126.70**	0.07**	-.51
6	-92.41**	-.45**	-4.95**
7	-83.13**	-.25**	-5.40**
8	-206.53**	0.03	0.95*
9	-135.98**	-.24**	3.99**
1 x 2	11.08*	0.19**	0.29
1 x 3	-34.33**	0.09**	2.54**
1 x 4	2.04	-.27**	1.56**
1 x 5	-54.70**	0.00	1.42**
1 x 6	18.18**	0.24**	2.60**
1 x 7	29.19**	0.11**	3.83**
1 x 8	44.50**	-0.08**	-.40
1 x 9	202.25**	0.16**	2.89**

continued.....

Table 26 continued

Parents and F_1 hybrids	Vitamin C	Capsaicin	Oleoresin
2 x 3	18.05**	0.15**	4.29**
2 x 4	30.97**	-.16**	2.45**
2 x 5	-47.69**	0.04*	-.93
2 x 6	31.75**	-.09**	2.58**
2 x 7	-36.41**	-.19**	-2.34**
2 x 8	58.01**	0.00	-.74
2 x 9	98.15**	0.15**	2.68**
3 x 4	12.61**	0.38**	-4.04**
3 x 5	81.14**	-.15**	1.19*
3 x 6	30.30**	0.46**	3.32**
3 x 7	32.96**	-.11**	4.10**
3 x 8	44.32**	-.18**	1.05**
3 x 9	-20.73**	0.23**	-2.86**
4 x 5	52.26**	0.45**	5.12**
4 x 6	-41.33**	0.39**	-.36
4 x 7	18.39**	0.31**	-2.62**
4 x 8	117.00**	0.49**	0.37
4 x 9	32.79**	-0.07**	2.59**

continued..

Table 26 continued

Parents and F_1 hybrids	Vitamin C	Capsaicin	Oleoresin
5 x 6	100.83**	-.15**	-1.68**
5 x 7	26.38**	-.37**	-.84
5 x 8	86.22**	0.07**	0.72
5 x 9	6.90**	-.04*	-1.13*
6 x 7	63.57**	0.46**	2.54**
6 x 8	46.47**	-.17**	-1.16*
6 x 9	-65.01**	-.28**	2.05**
7 x 8	16.51**	-.11**	-.59
7 x 9	15.67**	0.42**	2.81**
8 x 9	-.07	-.09**	1.05*
S.E.$(\hat{s}_{ii})$	2.36	0.02	0.42
S.E.$(\hat{s}_{ii}-\hat{s}_{jj})$	3.29	0.02	0.59
S.E.$(\hat{s}_{ij})$	2.67	0.02	0.48
S.E.$(\hat{s}_{ij}-\hat{s}_{ik})$	3.93	0.03	0.70
S.E.$(\hat{s}_{ij}-\hat{s}_{kl})$	4.12	0.03	0.67

*Significant at 5 per cent level
**Significant at 1 per cent level

(i) Height of plant

Out of the nine parents, only three namely, CA-1063 (2), Purple round (4), Pant C-1 (6), showed significant g.c.a. effects for increased height of plant, Purple round (4) and Pant C-1 (6), having the highest and the lowest g.c.a. effects respectively. There was significant difference between the g.c.a. effects of parents. For this character g.c.a. effects in the negative direction were also examined. The remaining six parents showed significant g.c.a. effects for lower plant height. Purple cluster (9) had the lowest g.c.a. effects.

Out of the 36 F_1 hybrids, fourteen showed significant $\hat{s}_{ij}$ effects for increased plant height and thirteen for reduced plant height at 0.01 level of significance. Only two parents namely CA-960 (1) and CA-1063 (2) entering the diallel displayed $\hat{s}_{ii}$ effects for increased height of plant while three parents namely, purple round (4), Pant C-1 (6) and Purple cluster (9) showed significant $\hat{s}_{ii}$ effects for lower plant height at 0.01 level of probability.

(ii) Primary branches

The parents CA 960 (1), CA-1063 (2), Purple round (4) and Pant C-1 (6) manifested significant g.c.a. effects for increased number of primary branches while parents 04 (3), Vella natchi (5), Pusa jwala (7), California wonder (8) and Purple cluster (9) exhibited significant g.c.a. effects for reduced number of primary branches. Between the two parents, Purple round (4) and Pant C-1 (6) which displayed maximum and

minimum positive g.c.a. effects, there was significant difference. Similarly there was significant difference between the parents which exhibited the maximum and minimum g.c.a. effects, for reduced number of primary branches.

Seventeen hybrid combinations showed significant $\hat{s}_{ij}$ effects for increased number of primary branches and twelve for reduced number of primary branches at 0.01 level of significance. None of the parents entering the diallel cross for this character showed significant $\hat{s}_{ii}$ effects for increased number of primary branches, while all manifested $\hat{s}_{ii}$ effects for reduced number of primary branches.

(iii) Secondary branches

Six parents displayed significant g.c.a. effects for increased number of secondary branches, the maximum and minimum being Fusa jwala (7) and G4 (3) respectively. These two parents possessed significant difference between them. The remaining three parents showed significant g.c.a. effects for decreased number of secondary branches and the maximum was manifested by California wonder (6) and minimum, Purple round (4).

Sixteen F_1 hybrids showed significant $\hat{s}_{ij}$ effects for enhanced number of secondary branches and ten for reduced number of secondary branches. Only one parent, California wonder (6) manifested significant $\hat{s}_{ii}$ effect in the positive direction. All the remaining eight parents showed significant $\hat{s}_{ii}$ effects, although in the negative direction.

(iv) Number of leaves

Three parental lines namely, CA-1068 (2), Purple round (4) and Pusa jwala (7) manifested significant g.c.a. effects for this character in the order mentioned. Pusa jwala (7) differed significantly from the former two parents. Out of the remaining six parents only five showed significant g.c.e. effects in the negative direction. The maximum and minimum g.c.a. effects for the decreased number of leaves were displayed by California wonder (8) and G4 (3) respectively, and the difference was statistically significant.

Among the 36 hybrids, 10 displayed significant $\hat{s}_{ij}$ effects towards positive direction while 14 were on negative direction. Only four parental lines exhibited significant $\hat{s}_{ii}$ effects for increased number of leaves, while only 2 lines showed significant $\hat{s}_{ii}$ effects for decreased number of leaves.

(v) Spread

Among the 9 parental lines only Purple round (4), Pant C-1 (6) and Vella notchi (5) exhibited significant positive g.c.a. effects in the order mentioned. The difference among them was statistically significant. Five parents showed significant g.c.a. effects in the negative direction. The maximum by Purple cluster (9) and minimum G4 (3); the difference being statistically significant.

Eighteen hybrid combinations showed significant positive $\hat{s}_{ij}$ effects while 13 displayed significant $\hat{s}_{ij}$ effects, but in the negative direction. None of the parental lines

exhibited significant positive $\hat{s}_{ii}$ effects while 8 parents displayed significant effects in the negative direction.

(vi) Number of days taken for blooming

Five parental lines showed significant positive g.c.a. effects for this character. The maximum and minimum g.c.a. effects were shown by Purple round (4) and Pusa jwala (7) respectively. The difference between the two was statistically significant. Four parents displayed significant negative g.c.a. effects. The maximum was shown by California wonder (8) and minimum by Pant C-1 (6), and the difference was statistically significant.

Among the 36 hybrid combinations, 14 displayed significant positive $\hat{s}_{ij}$ effects while 13 had significant negative $\hat{s}_{ij}$ effects. Only 3 parents showed significant positive $\hat{s}_{ii}$ effects, while 2 parents displayed significant $\hat{s}_{ii}$ effects in the negative direction. The maximum $\hat{s}_{ii}$ effect towards the negative direction was registered by the parent CA-1060 (2).

(vii) Number of fruits

Significant g.c.a. effects for increased number of fruits were found in six parental lines. The maximum and minimum g.c.a. effects were manifested by Pant C-1 (6) and G4 (3) respectively. There was significant difference betwden these two parents. The remaining 3 parents registered g.c.a. effects towards the negative direction.

The maximum significant negative g.c.a. effect was exhibited by California wonder (8).

None of the parental lines displayed significant $\hat{s}_{ii}$ effects for increased number of fruits, while 5 parents showed significant $\hat{s}_{ii}$ effects towards the negative direction, maximum being purple round (4).

Among the hybrids, 16 showed significant $\hat{s}_{ij}$ effects for increased number of fruits, while 14 for decreased number of fruits.

(viii) Weight of fruits

Only two parental lines, California wonder (8) and Vella notchi (5) registered statistically significant g.c.a. effects for weight of fruits, maximum being the former. The remaining seven parents exhibited significant g.c.a. effects in the negative direction.

All the parents except Vella notchi (5) exhibited significant $\hat{s}_{ii}$ effects for increased weight of fruits. Out of the 36 hybrid combinations, 12 showed significant $\hat{s}_{ij}$ effects for increased weight of fruits.

(ix) Length of fruit

Five parents exhibited significant g.c.a. effects for this character. These five parents, CA-960 (1), CA-1068 (2), Vella notchi (5) Pusa jwala (7) and California wonder (8) were statistically on par.

All the parental lines except California wonder (8) registered significant $\hat{g}_{ii}$ effects for increased length of fruit. Nine of the hybrids also exhibited significant positive $\hat{s}_{ij}$ effects for this character.

(x) Girth of fruit

California wonder (8) exhibited maximum g.c.a. effect for girth of fruit, followed by Vella matchi (5) and Purple round (4). The remaining 6 parents registered significant negative g.c.a. effects for this character.

All parental lines except Pant C-1 (6) and Pusa jwala (7) displayed significant positive $\hat{g}_{ii}$ effects. Although statistically not significant the two parents, showed negative $\hat{g}_{ii}$ effects, for the character. Further, nine hybrids exhibited significant positive $\hat{s}_{ij}$ effects.

(xi) Size of the fruit

The three parental lines, California wonder (8), Vella matchi (5) and Purple round (4) showed significant positive g.c.a. effects according to the order mentioned. The difference among these three were statistically significant. Vella matchi (5) alone displayed significant negative $\hat{g}_{ii}$ effects while Purple round (4) displayed the effect in the same direction although statistically not significant. Among the hybrids only 4 showed significant positive $\hat{s}_{ij}$ effects while 9 exhibited significant negative $\hat{s}_{ij}$ effects.

(xii) Number of seeds/fruit

Significant g.c.a. effects for increased number of seeds/fruit was seen in California wonder (8) followed by Vella mothi (5) and CA-960 (1). California wonder (8) registered maximum g.c.a. effect and the three parents differed significantly.

All the parental lines entering the diallel cross showed significant positive $\hat{g}_{ii}$ effects, maximum being California wonder (8). Thirteen of the 36 hybrid combinations showed significant positive $\hat{s}_{ij}$ effects while 20 exhibited significant negative $\hat{s}_{ij}$ effects.

(xiii) Total yield

All the nine parental lines except five showed negative g.c.a. effects for this character, while 3 displayed statistically significant positive g.c.a. effects, the maximum being Vella mothi (5) and minimum, California wonder (8) respectively.

For increased total yield, only one parent showed statistically significant $\hat{g}_{ii}$ effect, while among the hybrids, 10 exhibited significant positive $\hat{s}_{ij}$ effects.

(xiv) Life span

Purple round (4), G4 (3), Purple cluster (9) and Pusa jwala (7) registered significant positive g.c.a. effects according to the order mentioned. The difference between G4 (3) and Purple cluster (9) was not statistically significant.

None of the parents displayed positive $\hat{g}_{ii}$ effects while 26 hybrids showed significant $\hat{s}_{ij}$ effects.

(xv) Vitamin A content

Five parents possessed highly significant g.c.a. effects for increased Vitamin A content. The maximum and minimum was registered by Purple cluster (9) and Vella notchi (5) respectively. The difference between the two was statistically significant.

All parents except Pusa jwala (7) displayed significant $\hat{g}_{ii}$ effects for enhanced Vitamin A content. Out of the 36 hybrids 14 had significant positive $\hat{s}_{ij}$ effects.

(xvi) Vitamin C content

Among the nine parents, California wonder (6) manifested maximum significant positive g.c.a. effects followed by Vella notchi (5) and Pusa jwala (7). The difference among the three parents was statistically significant. The remaining six parents displayed significant g.c.a. effects in the negative direction. The maximum and minimum effects were shown by G4 (3) and Purple round (4) respectively, the difference being statistically significant.

None of the parents exhibited significant positive $\hat{g}_{ii}$ effects while, 26 hybrids out of 36 hybrid combinations possessed significant positive $\hat{s}_{ij}$ effects.

(xvii) Carotein content

Pant C-1 (6), Pusa jwala (7), Purple round (4) and

G4 (3) exhibited significant positive g.c.a. effects according to the order mentioned. The difference among these parents was statistically on par. The remaining five parents showed significant g.c.a. effects for decreased capsaicin content. The maximum and minimum g.c.a. effects towards the negative direction was manifested by Vella matchi (5) and Purple cluster (9) respectively. The difference between the two was statistically significant.

Among the parents, only one variety, Vella matchi (5) possessed significant positive $\hat{g}_{ii}$ effects while among the hybrids, 17 had significant $\hat{s}_{ij}$ effects.

(xviii) Oleoresin content

Six parents exhibited significant g.c.a. effects for increased oleoresin content. The maximum g.c.a. effect for this character was displayed by Pant C-1 (6) and minimum by G4 (3). The difference between the two was statistically significant.

Only one parent showed statistically significant $\hat{g}_{ii}$ effect for increased oleoresin content at 0.05 level of probability. While, 15 out of 36 hybrids exhibited significant $\hat{s}_{ij}$ effects for increased oleoresin content.

8. Gene action

The nine parent diallel was done for all the characters under study. The results are presented character-wise.

Table 27. Estimates of b, sb, (b-0)/sb and (1-b)/sb for the different characters.

Characters	Statistics			
	b	sb	(b-0)/sb	(1-b)/sb
1. Height				
Complete diallel	0.254	0.229	1.109	3.25*
Sub-diallel excluding parents 6 and 8	0.819	0.332	2.466*	0.543
2. Number of primary branches				
Complete diallel	0.082	0.078	1.039	11.667**
Sub-diallel excluding parents 2,6 and 8	0.158	0.161	0.984	5.229**
3. Number of secondary branches				
Complete diallel	0.088	0.079	1.109	11.423**
Sub-diallel excluding parents 2, 3 and 8	0.224	0.224	0.998	3.455*
4. Number of leaves				
Complete diallel	0.029	0.040	0.741	24.131**
Sub-diallel excluding parents 2,4 and 3	0.884	0.173	5.116**	0.672
Sub-diallel excluding parents 2,4 and 7	1.066	0.110	9.674**	-.604
5. Spread				
Complete diallel	0.012	0.031	0.409	31.471**
Sub-diallel excluding parents 3, 4 and 8	0.556	0.216	2.565*	2.048

continued..

Table 27 continued

Characters	Statistics			
	b	sb	(b-o)/sb	(1-b)/sb
6. Number of days taken for blooming				
Complete diallel	0.499	0.211	2.360	2.370*
Sub-diallel excluding parent 3	0.595	0.197	3.017*	2.049
7. Number of fruits/plant				
Complete diallel	-.092	0.037	2.471*	29.360**
Sub-diallel excluding parents 4 and 6	0.635	0.162	3.926**	2.262
8. Weight of fruit				
Complete diallel	0.764	0.077	9.868**	3.044*
Sub-diallel excluding parent 5	0.962	0.073	13.192**	0.522
Sub-diallel excluding parent 8	0.915	0.058	15.561**	1.444
9. Length of fruit				
Complete diallel	0.755	0.132	5.718**	1.852
10. Girth of fruit				
Complete diallel	0.951	0.077	12.348**	0.628
11. Size of fruit				
Complete diallel	0.749	0.075	9.696**	3.311*
Sub-diallel excluding parent 5	0.950	0.077	12.303**	0.647
12. Number of seeds/fruit				
Complete diallel	0.906	0.082	10.980**	1.136

continued

Table 27 continued

Characters	Statistics			
	b	sb	(b-o)/sb	(1-b)/sb
13. Total yield/ plant				
Complete diallel	-0.189	0.015	-1.248	67.286**
Sub-diallel excluding parents 2, 4 and 5	0.668	0.227	3.034*	1.372
14. Life span				
Complete diallel	0.351	0.186	1.690	3.486**
Sub-diallel excluding parent 5	0.793	0.165	4.785**	1.244
15. Vitamin A				
Complete diallel	0.156	0.145	1.071	5.790**
Sub-diallel excluding parents 6 and 7	0.820	0.160	5.111**	1.117
16. Vitamin C				
Complete diallel	0.022	0.185	0.119	5.267**
Sub-diallel excluding parents 1, 8 and 9	0.279	0.348	0.803	2.069
17. Capsaicin				
Complete diallel	0.195	0.093	2.094	8.632**
Sub-diallel excluding parents 1,2 and 6	0.519	0.407	1.2756	1.178
18. Oleoresin				
Complete diallel	0.280	0.072	3.883**	9.964**
Sub-diallel excluding parents 2, 6 and 8	0.445	0.190	2.340	2.915*

Table 23. Estimates of components of variation and some statistical parameters.

	Height	Number of primary branches	Number of secondary branches
$\hat{D}$	251.846**	1.024	136.694
	±37.197	±5.456	±239.348
$\hat{F}$	21.129	-2.992	205.695
	±137.215	±15.328	±584.727
$\hat{H}_1$	707.450**	41.465*	4020.840**
	±137.701	±15.650	±607.607
$\hat{H}_2$	461.438**	56.024**	3851.136**
	±121.334	±12.373	±542.790
$\hat{h}^2$	51.827	473.710**	47157.237**
	±31.493	±8.327	±365.334
$\hat{E}$	1.435	0.133	2.581
	±20.222	±2.062	±90.465
$(\hat{H}_1/\hat{D})^{\frac{1}{2}}$	1.676	6.365	5.423
$\hat{H}_2/4\hat{H}_1$	0.163	0.217	0.238
$\frac{(4\hat{D}\hat{H}_1)^{\frac{1}{2}}+\hat{F}}{(4\hat{D}\hat{H}_1)^{\frac{1}{2}}-\hat{F}}$	1.051	0.625	1.318
$\hat{h}^2/\hat{H}_2$	0.112	15.149	12.308
$\hat{v}^2$	0.114	7.328	2.776
r	-.657	-.476	-.261
$V_0 I_0$	253.282	1.156	139.275
$V_0 I_1$	119.295	2.375	30.891
$(M_{L1}-M_{L0})^2$	13.132	116.446	11769.674

continued

Table 28 continued

	Number of leaves	Spread	Number of days taken for blooming
$\hat{D}$	11308597.00**	82.148*	128.112**
	±408561.12	±26.159	±20.071
$\hat{F}$	8809044.80**	54.509	50.453
	±998115.20	±63.908	±47.415
$\hat{H}_1$	5174121.60**	410.034**	248.359**
	±1037169.40	±66.408	±46.129
$\hat{H}_2$	3242302.40*	387.624**	201.450**
	±926529.44	±59.324	±40.132
$\hat{h}^2$	2896761.60**	733.508**	34.118
	±623615.36**	±39.929	±26.914
$\hat{E}$	1686.347	0.512	0.647
	±154421.520	±9.887	±6.688
$(\hat{H}_1/\hat{D})^{\frac{1}{2}}$	0.674	2.234	1.392
$\hat{H}_2/4\hat{H}_1$	0.157	0.236	0.203
$\frac{(4\hat{D}\hat{H}_1)^{\frac{1}{2}}+\hat{F}}{(4\hat{D}\hat{H}_1)^{\frac{1}{2}}-\hat{F}}$	3.692	1.349	1.329
$\hat{h}^2/\hat{H}_2$	0.893	1.892	0.169
t^2	0.714	1.347	1.087
x	0.929**	-.405	0.028
$V_0 I_0$	11390295.00	82.659	128.759
$V_0 I_1$	1127985.90	12.554	31.182
$(M_{I,1}-M_{I0})^2$	724424.64	183.448	8.600

continued...

Table 28 continued

	Number of fruits	Weight of fruit	Length of fruit
$\hat{D}$	1255.144**	59.385**	7.081**
	±203.427	±2.346	±0.420
$\hat{F}$	147.046	62.003**	4.885**
	±488.018	±5.545	±0.980
$\hat{H}_1$	3344.874**	34.509**	6.675**
	±499.745	±5.395	±0.927
$\hat{H}_2$	3170.638**	18.079**	4.429**
	±431.554	±4.693	±0.797
$\hat{h}^2$	10432.538**	229.999**	71.549**
	±289.638	±3.147	±0.534
$\hat{E}$	9.592	0.014	0.097
	±71.922	±0.783	±0.133
$(\hat{H}_1/\hat{D})^{\frac{1}{2}}$	1.632	0.762	0.971
$\hat{H}_2/4\hat{H}_1$	0.237	0.151	0.166
$\frac{(4\hat{D}\hat{H}_1)^{\frac{1}{2}}+\hat{F}}{(4\hat{D}\hat{H}_1)^{\frac{1}{2}}-\hat{F}}$	1.085	5.346	2.102
$\hat{h}^2/\hat{H}_2$	3.290	12.721	16.152
t^2	2.083	0.086	1.554
r	0.823**	0.996**	0.804**
V_0L_0	1264.735	59.399	7.087
V_0L_1	321.269	3.454	1.111
$(M_{L1}-M_{L0})^2$	2609.309	57.502	17.887

continued..

Table 28 continued

	Girth of fruit	Size of fruit	Number of seeds/fruit
$\hat{D}$	24.715**	55.774**	1839.449**
	±0.665	±2.38	±111.606
$\hat{F}$	17.625**	61.637**	818.875*
	±1.552	±5.637	±260.356
$\hat{H}_1$	7.953**	34.777**	1641.392**
	±1.468	±5.484	±246.335
$\hat{H}_2$	4.319*	17.375**	1292.572**
	±1.262	±4.772	±211.759
$\hat{h}^2$	37.682**	173.782**	11168.842**
	±0.845	±3.20	±141.859
$\hat{E}$	0.007	0.010	0.817
	±0.210	±0.795	±35.293
$(\hat{H}_1/\hat{D})^{\frac{1}{2}}$	0.567	0.789	0.944
$\hat{H}_2/4\hat{H}_1$	0.136	0.125	0.197
$\frac{(4\hat{D}\hat{H}_1)^{\frac{1}{2}}+\hat{F}}{(4\hat{D}\hat{H}_1)^{\frac{1}{2}}-\hat{F}}$	4.385	5.661	1.616
$\hat{h}^2/\hat{H}_2$	8.724	10.000	8.641
t^2	0.118	0.159	0.631
r	0.948**	0.987**	0.964**
V_0L_0	24.732	55.784	1840.265
V_0L_1	2.681	2.885	342.394
$(M_{L1}-M_{L0})^2$	9.421	43.447	2792.289

Table 28 continued

	Total yield	Life span	Vitamin A
$\hat{D}$	8554.758**	404.383**	6030091.20**
	±2076.422	±71.562	±583492.96
$\hat{F}$	-457.192	128.090	1388011.90
	±5072.704	±169.094	±1399787.90
$\hat{M}_1$	20127.520**	1620.472**	9032702.40**
	±5271.190	±164.510	±1404743.10
$\hat{M}_2$	19446.144**	1551.876**	8142319.60**
	±4708.684	±143.124	±1237775.80
$\hat{n}^2$	54783.968**	65997.920**	39442304.00**
	±3169.390	±95.985	±831346.88
$\hat{E}$	19.849	1.014	2399.998
	±784.815	±23.954	±206296.00
$(\hat{M}_1/\hat{D})^{\frac{1}{2}}$	1.534	2.002	1.224
$\hat{M}_2/4\hat{M}_1$	0.242	0.239	0.225
$\frac{(4\hat{D}\hat{M}_1)^{\frac{1}{2}}+\hat{F}}{(4\hat{D}\hat{M}_1)^{\frac{1}{2}}-\hat{F}}$	0.965	1.172	1.207
n^2/M_2	2.167	42.527	4.844
t^2	0.495	0.365	0.379
r	0.443	-.832**	-.264
V_0L_0	8574.609	405.397	6032494.4
V_0L_1	2424.985	86.289	1383209.3
$(M_{L1}-M_{L0})^2$	13698.759	16499.595	9860876.8

continued..

Table 28 continued

	Vitamin C	Capsaicin	Oleoresin
$\hat{D}$	1527.064	0.058*	3.304
	±1189.944	±0.023	±1.761
$\hat{F}$	-1344.901	-.009	-2.570
	±2907.055	±0.056	±4.302
$\hat{H}_1$	16523.237**	0.557**	40.345**
	±3020.779	±0.058	±4.470
$\hat{H}_2$	15358.190**	0.389**	37.325**
	±2698.539	±0.053	±3.994
$\hat{h}^2$	366244.000**	2.948**	257.265**
	±1816.295	±0.035	±2.688
$\hat{E}$	10.357	0.0005	0.025
	±449.757	±0.008	±0.665
$(\hat{H}_1/\hat{D})^*$	3.528	3.038	3.494
$\hat{H}_2/4\hat{H}_1$	0.232	0.181	0.231
$\frac{(4\hat{D}\hat{H}_1)^{\frac{1}{2}}+\hat{F}}{(4\hat{D}\hat{H}_1)^{\frac{1}{2}}-\hat{F}}$	0.749	0.948	0.799
$\hat{h}^2/\hat{H}_2$	23.846	7.563	6.892
t^2	0.394	0.006	2.979
r	-.323	0.575	0.899**
$V_0 I_0$	1337.421	0.058	3.329
$V_0 I_1$	960.118	0.054	2.225
$(u_{L1}-u_{L0})^2$	91562.496	0.737	64.319

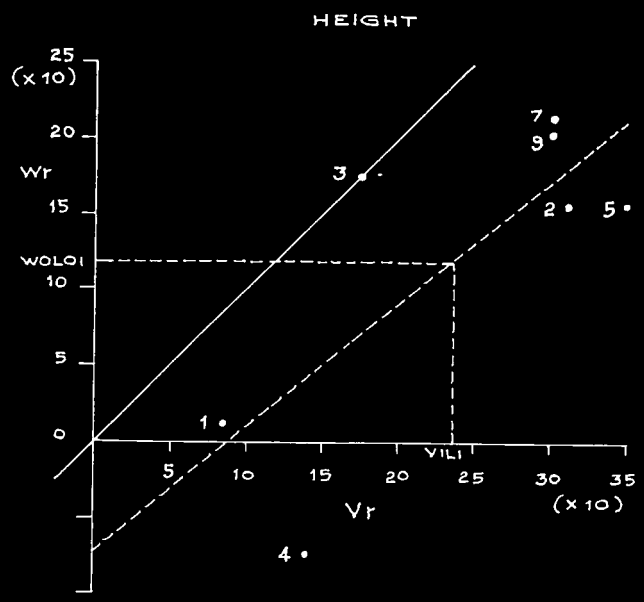


FIG.9.A. Vr, Wr GRAPH

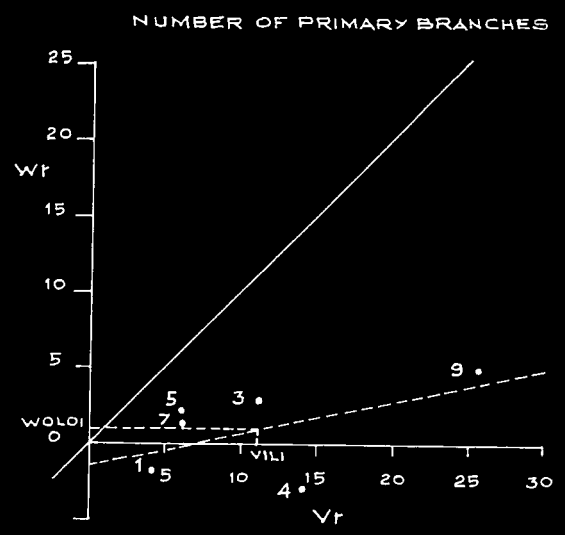


FIG.10A, Vr, Wr GRAPH

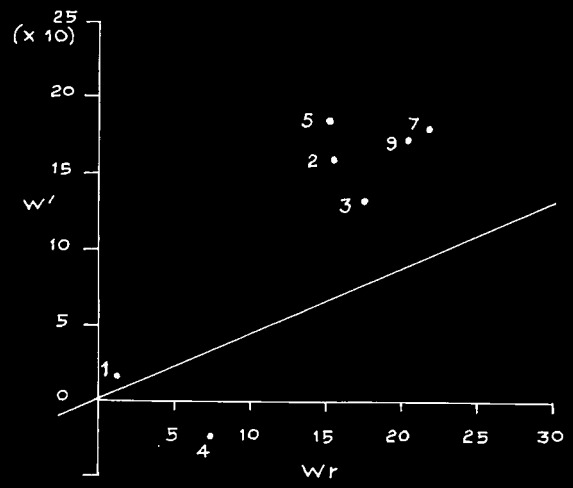


FIG.9.B. Wr, W' GRAPH

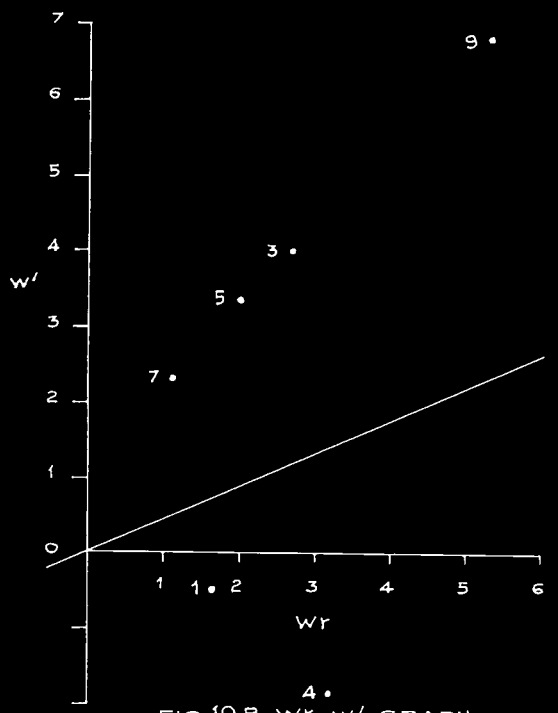


FIG.10.B. Wr, W' GRAPH

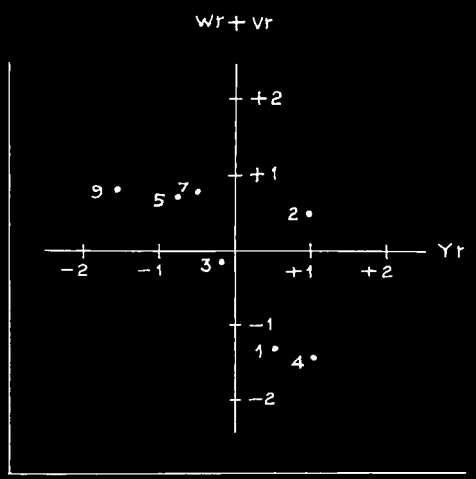


FIG.9.C, STANDARDIZED DEVIATION
Yr, Wr+Vr GRAPH

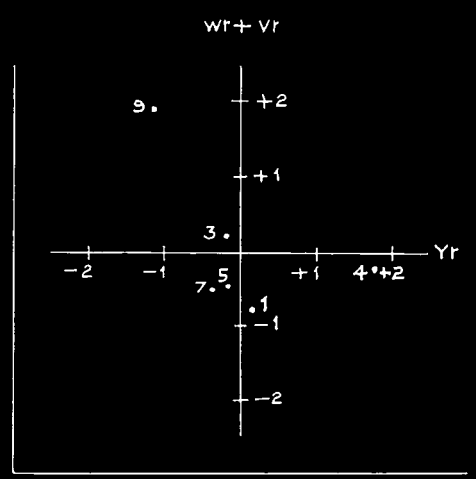


FIG.10 C, STANDARDIZED DEVIATION
Yr, Wr+Vr GRAPH

(i) Height of plant

The nine parent diallel analysis indicated the failure of the hypotheses. The sub-diallel omitting parents 6 (Pant C-1) and 8 (California wonder) satisfied the assumptions (Table 27).

The regression line W_r on V_r showed significant deviation from zero; but not from the unit slope (Table 27). The V_r, W_r graph (Fig.9A) showed that the regression line had cut the W_r-axis below the point of origin, indicating presence of over-dominance. Wide scattering of array points revealed genetic diversity among the parents. The arrays 7 (Pusa jwala), 9 (Purple cluster), 5 (Vella notchi), 2 (CA-1068) in that order, had predominance of recessive genes while in the arrays 4 (Purple round) and 1 (CA-960) dominant genes predominated. The array point 3 (G4) was on the line of unit slope. All the array points except 3 (G4) were lying below the line of unit slope suggesting the presence of epistasis. In the W_r, W' graph (Fig.9B) all the array points except 4 shifted above the line of ¼ slope indicating presence of a complementary type of gene action in them.

The correlation coefficient between Y_r and $W_r + V_r$ was negative and not significant. The standardised deviation graph of Y_r and $W_r + V_r$ (Fig. 9C) showed that the arrays 1 and 4 had predominance of dominant genes for increased height of plant while parents corresponding to arrays 9, 5

and 7 had recessive genes for decreased height of plant. The parent corresponding to array 2 displayed more number of recessive genes for increased height of plant while parent 3 possessed dominant and recessive genes in almost equal proportions for medium height of plant.

The estimates of three components of variation namely $\hat{D}$, $\hat{H}_1$ and $\hat{H}_2$ were significant while those of $\hat{F}$, $\hat{h}^2$ and $\hat{E}$ were not (Table 28). The positive sign of $\hat{F}$ indicated that in parents dominant genes were more than the recessive ones. The proportion of dominant and recessive genes in the parents was 1.051. The value of $\hat{H}_1$ was greater than that of $\hat{D}$ suggesting the presence of over-dominance, which was also confirmed by the average degree of dominance (1.676). The ratio $\hat{H}_2/4\ \hat{H}_1$ (0.163) suggested that there was some asymmetry at the loci showing dominance. The ratio $\hat{h}^2/\hat{H}_2$ (0.112) implied that atleast one gene or one group of genes controlling plant height exhibited some degree of dominance.

(ii) Number of primary branches

The full diallel analysis of nine parental set indicated significance of "t^2" and failure of hypotheses. None of the sub-diallel analyses excluding different parents satisfied the assumptions. The sub-diallel excluding parents 2, 6 and 8 was near the satisfactory proposition and hence the same was selected for further studies (Table 27).

The regression line had cut the W_r-axis below the point of origin in the V_r, W_r graph (Fig. 10A) suggesting the

presence of over-dominance. The array points are widely scattered indicating genetic diversity among the parents. Parent 9 possessed an excess of recessive genes for the character while in other parents dominant genes predominated. All the array points were lying below the line of unit slope, displaying epistatic gene action. In the W_r, W' graph (Fig. 10B) parents 7, 5, 3 and 9 had shifted above the line of $\frac{1}{2}$ slope, which suggested complementary type of gene action in them.

The correlation coefficient between V_r and $W_r + V_r$ was negative and not significant. The standardized deviation graph of V_r and $W_r + V_r$ (Fig. 10C) revealed that parent 9 possessed more recessive genes for lower number of primary branches, while in parent 4 dominant and recessive genes were in almost equal proportion for greater number of primary branches. In the remaining parents both dominant and recessive genes were in almost equal proportion for medium number of primary branches.

The estimates of three components of variation $\hat{H}_1$, $\hat{H}_2$, $\hat{h}^2$ were significant (Table 28). The presence of more number of recessive genes in the parents were revealed from the negative sign of $\hat{F}$. The value of $\hat{D}$ was lower than that of $\hat{H}_1$ indicating the presence of over-dominance which was confirmed by the average degree of dominance (6.365). The proportion of dominant and recessive genes in parents was 0.626. Some asymmetry existed at loci showing dominance

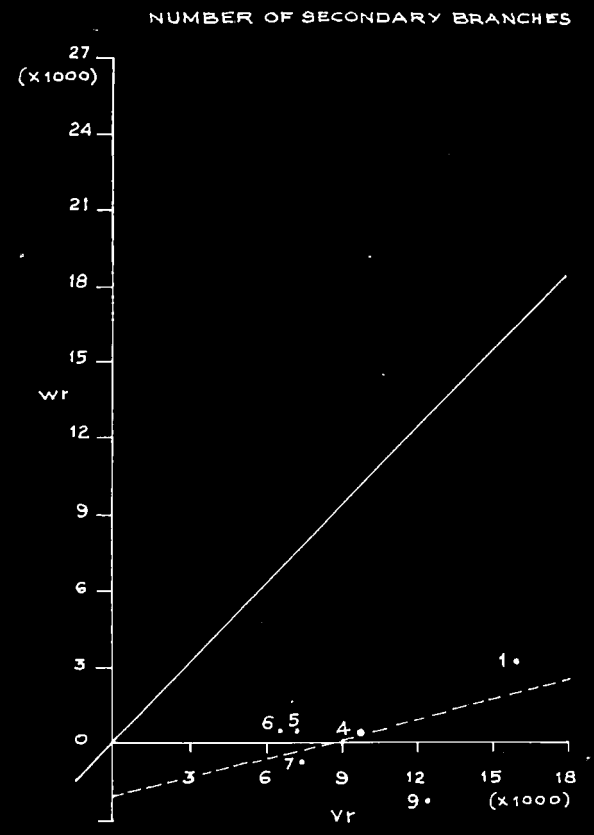


FIG.11.A, Vr, Wr GRAPH

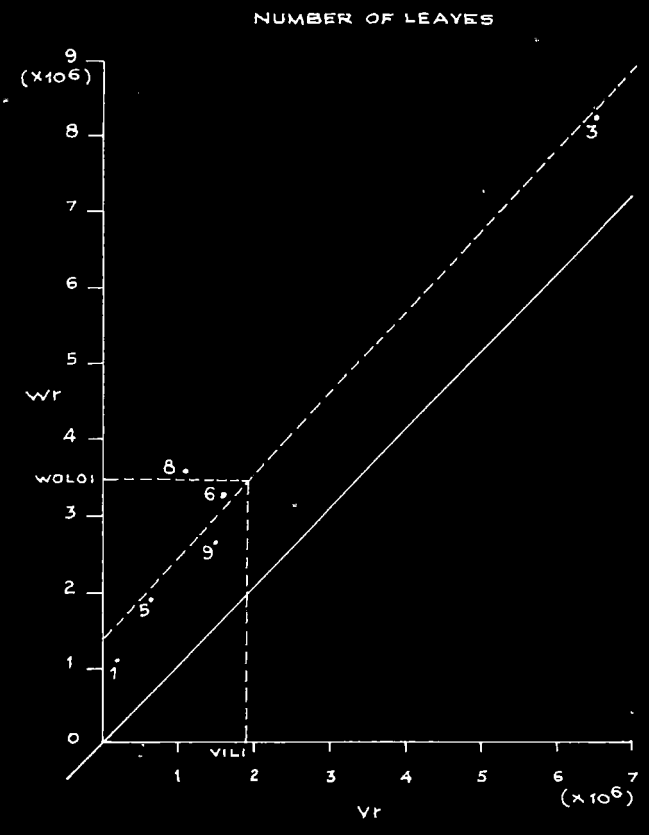


FIG.12.A, Vr, Wr GRAPH

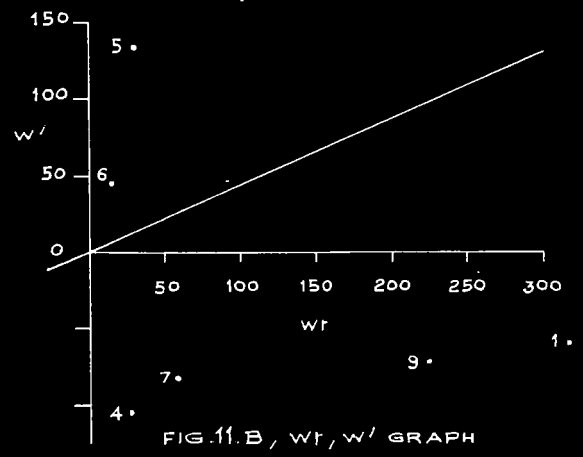


FIG.11.B, Wr, W' GRAPH

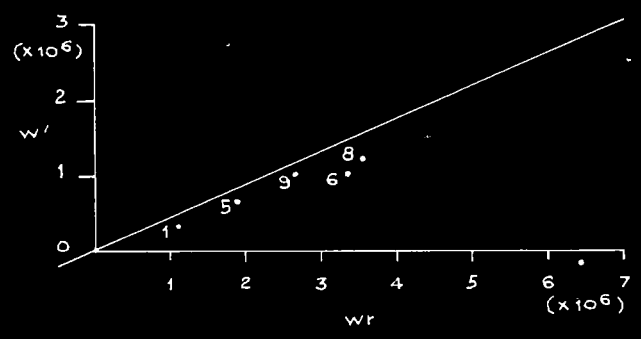


FIG.12.B, Wr, W' GRAPH

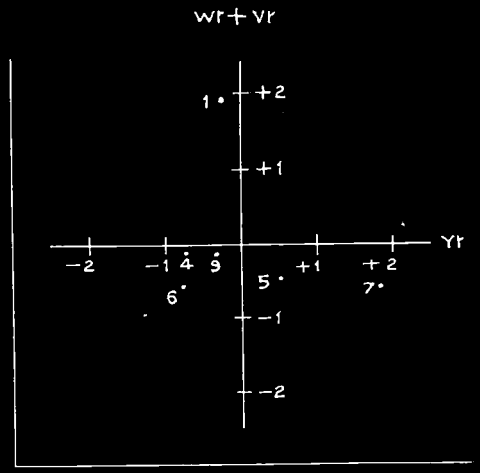


FIG 11.C, STANDARDIZED DEVIATION
Yr, Wr+Vr GRAPH

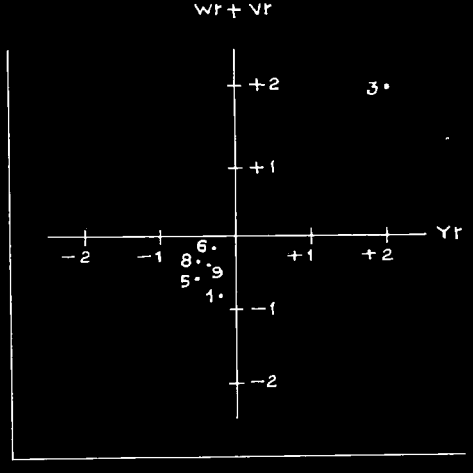


FIG.12 C, STANDARDIZED DEVIATION
Yr, Wr+Vr GRAPH

which was indicated by the ratio $\hat{H}_2/4\ \hat{H}_1$ (0.217). The number of genes or groups of genes which exhibited dominance for the character was 14.

(iii) Number of secondary branches

The "t^2" testing the uniformity of W_r-V_r was significant in the original nine parent full diallel analysis. None of the sub-diallel omitting different parents satisfied the assumptions. But the sub-diallel without parents 2, 3 and 8 was almost near the satisfactory conditions and as such the same was selected for further studies (Table 27).

The regression line W_r, on V_r showed significant deviation from zero (Table 27). In the V_r, W_r graph (Fig. 11A), the regression line had cut the W_r-axis below the point of origin indicating the presence of over-dominance. Wide scattering of arrays exhibited genetic diversity among parents. Parent 1 predominated in recessive genes for this character while in the remaining parents dominant genes were in excess. Epistatic gene action among parents was revealed by the fact that all the arraypoints were lying below the line of unit slope. In the W_r, V' graph (Fig. 11B) 2 parents namely 6 and 5 were lying above the line of $\frac{1}{4}$ slope, which indicated complementary type of gene action in them.

The correlation coefficient between Y_r and $W_r + V_r$ was negative and not significant. The standardised deviation

graph of Y_r and $W_r + V_r$ (Fig. 11C) suggested that in parents 5 and 7 dominant genes predominated for greater number of secondary branches while parent 1 possessed excess of recessive genes for medium number of secondary branches. In parent 6 dominant genes predominated for lower number of secondary branches. Both dominant and recessive genes were in almost equal proportion in parents 4 and 9 for medium number of secondary branches.

The three estimates of components of variation namely $\hat{H}_1$, $\hat{H}_2$ and $\hat{h}^2$ were significant (Table 28). The positive sign of $\hat{F}$ suggested the presence of more number of dominant genes in the parents. The value of $\hat{H}_1$ was greater than that of $\hat{D}$, which indicated the presence of over-dominance and the same was confirmed by the average degree of dominance (5.423). The proportion of dominant and recessive genes in parents was 1.318. The ratio $\hat{H}_2/4\ \hat{H}_1$ suggested that some asymmetry existed at loci showing dominance. The ratio $\hat{h}^2/\hat{H}_2$ indicated that atleast 13 genes or groups of genes controlling the character displayed some degree of dominance.

(iv) Number of leaves

The 't^2' testing the uniformity of W_r-V_r was significant in the nine parent diallel; but the two sub-diallelles omitting parents 2, 4 and 3, and 2, 4 and 7 satisfied the assumptions. The latter was selected for further studies (Table 27). The regression line W_r on V_r showed significant

deviation from zero; but not from the unit slope (Table 27).

The V_r, W_r graph (Fig.12A) showed that, the regression line had cut the W_r-axis above the point of origin indicating partial dominance. The arraypoints were scattered widely revealing the genetic diversity among the parents. The parent corresponding to array 3 possessed an excess of recessive over dominant genes for number of leaves while the remaining parents possessed an excess of dominant over recessive genes. All the arrays were lying above the line of unit slope thereby revealing the presence of additive effects among them for this character. In the W_r, V_r graph (Fig.12B) all the arraypoints were lying below the line of ¼ slope.

The correlation coefficient between Y_r and $W_r + V_r$ was positive and significant. The standardised deviation graph of Y_r and $W_r + V_r$ (Fig. 12C) showed that the parent corresponding to the array 1 possessed an excess of dominant genes for medium number of leaves while those corresponding to arrays 6, 8, 9 and 5 had equal proportion of dominant and recessive genes for medium number of leaves. The parent 3 had predominance of recessive genes for increased number of leaves.

All the estimates of components of variation except $\hat{E}$ were significant (Table 28). The positive sign of $\hat{F}$ showed that dominant genes were more frequent in the parents.

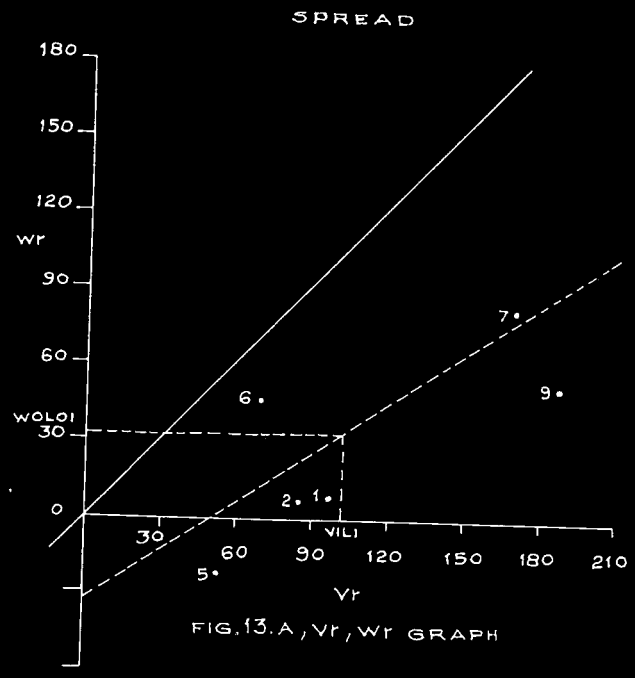


FIG.13.A, Vr, Wr GRAPH

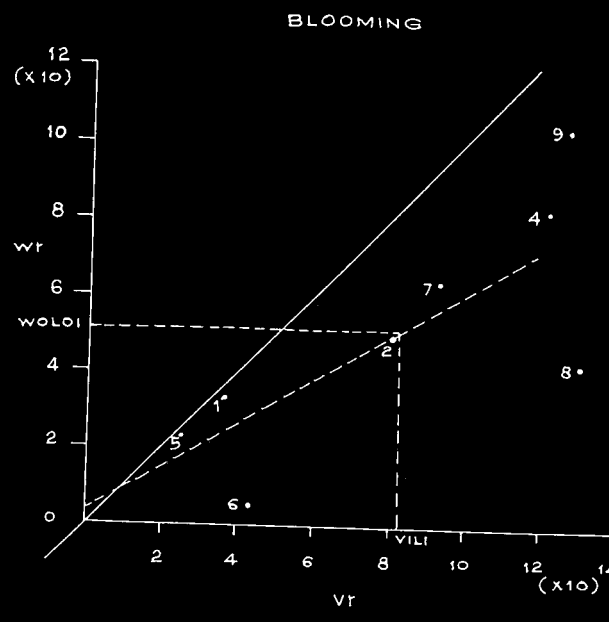


FIG.14 A, Vr, Wr GRAPH

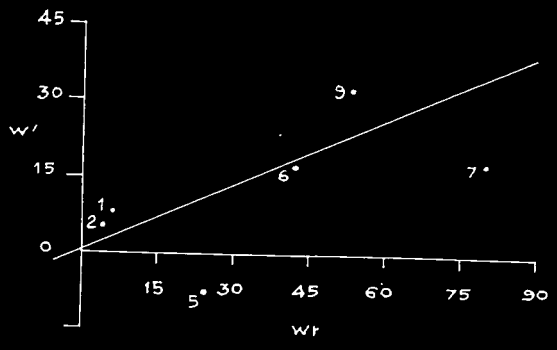


FIG.13.B, Wr, W' GRAPH

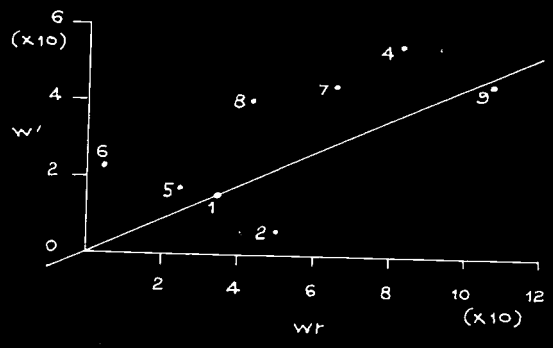


FIG.14 B, Wr, W' GRAPH

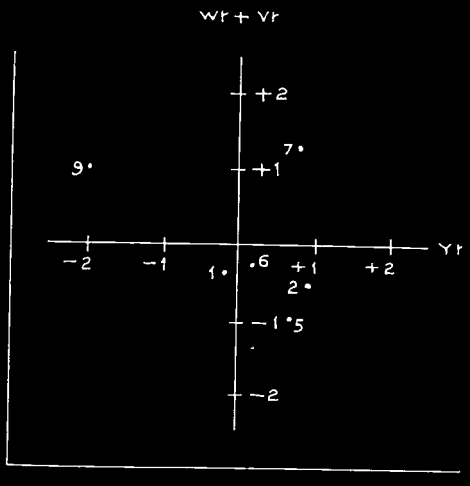


FIG 13.C, STANDARDIZED DEVIATION

Yr, Wr + Vr GRAPH

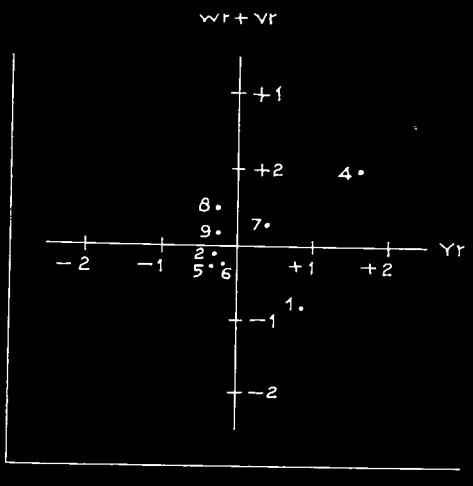


FIG 14 C, STANDARDIZED DEVIATION

Yr, Wr + Vr GRAPH

The proportion of dominant and recessive genes in the parents was 3.692. The value of $\hat{H}_1$ was smaller than that of $\hat{D}$ indicating the presence of partial dominance which was also confirmed by the mean degree of dominance (0.674). The ratio $\hat{H}_2/4\hat{H}_1$ (0.157) indicated that there was some asymmetry at the loci showing dominance. The ratio $\hat{h}^2/\hat{H}_2$ (0.693) suggested that at least one gene or one group of genes controlling the number of leaves exhibited some degree of dominance.

(v) Spread

The 't^2' was significant in the nine parent diallel, but the sub-diallel omitting parents 3, 4 and 8 satisfied the assumptions (Table 27).

The regression line W_r on V_r showed significant deviation from zero; but not from the unit slope (Table 27). The V_r, W_r graph (Fig. 13A) showed that the regression line had cut the W_r-axis below the point of origin revealing the presence of over-dominance. The array points were widely scattered indicating the presence of genetic diversity among the parents. The parents 7 and 9 in that order had predominance of recessive genes while in the remaining parents dominant genes were in excess. All the array points were lying below the unit slope indicating epistatic gene action. The V_r, W' graph (Fig. 13B) suggested complementary type of gene action for the parents 9, 7 and 2 as they were lying above the line of $\frac{1}{4}$ slope.

The correlation between V_r and $W_r + V_r$ was negative and not significant. The standardized deviation graph of V_r and $W_r + V_r$ (Fig. 130) indicated that the parents corresponding to arrays 2 and 5 had dominant genes for increased spread of the plant while the parent 7 possessed predominance of recessive genes for increased spread of the plant. The parent 9 dominated in recessive genes for decreased spread of plant while parents 1 and 6 possessed dominant and recessive genes in almost equal proportion for medium spread of the plant.

The estimates of four components of variation $\hat{D}$, $\hat{H}_1$, $\hat{H}_2$ and $\hat{h}^2$ were significant (Table 28). The positive sign of $\hat{F}$ revealed that dominant genes were more frequent in parents than the recessive ones. The proportion of dominant and recessive genes in the parents was 1.349. The value of $\hat{H}_1$ was greater than that of $\hat{D}$ indicating the presence of over-dominance, which was also confirmed by the average degree of dominance (2.234). The ratio $\hat{H}_2/4\hat{H}_1$ (0.236) indicated some asymmetry at loci showing dominance. The ratio $\hat{h}^2/\hat{H}_2$ was 1.892 suggesting that at least 2 genes or 2 groups of genes controlling this character exhibited some degree of dominance.

(vi) Number of days taken for blooming

The nine parent diallel did not satisfy the hypotheses, but the sub-diallel omitting parent 3 satisfied the assumptions (Table 27).

The regression line W_r on V_r showed significant deviation from zero; but not from the unit slope (Table 27). The V_r, W_r graph (Fig. 14A) showed that the regression line had cut the W_r axis just above the point of origin indicating partial or no dominance. All the array points were widely scattered revealing genetic diversity among the parents. The parents 9, 4, 7 and 8 in that order had predominance of recessive genes, while in the remaining parents dominant genes were in excess. All the array points were lying below the line of unit slope indicating the presence of epistasis. The arrays 4, 7, 8, 5 and 6 were lying above the line of ¼ slope in the W_r, W' graph (Fig. 14B) revealing a complementary type of gene action in them.

The correlation coefficient between Y_r and $W_r + V_r$ was positive but not significant. The standardised deviation graph of Y_r and $W_r + V_r$ (Fig. 14C) showed that the parent 1 possessed dominant genes for lateness in blooming while parent 4 had recessive genes for late blooming. All the remaining parents had dominant and recessive genes in equal proportions for medium number of days taken for blooming.

Three estimates of components of variation, $\hat{D}$, $\hat{H}_1$, and $\hat{H}_2$ were significant, but not those of $\hat{F}$, $\hat{h}^2$ and $\hat{E}$ (Table 28). The positive sign of $\hat{F}$ revealed that more dominant genes were present in the parents. The proportion of dominant and recessive genes in parents was 1.329.

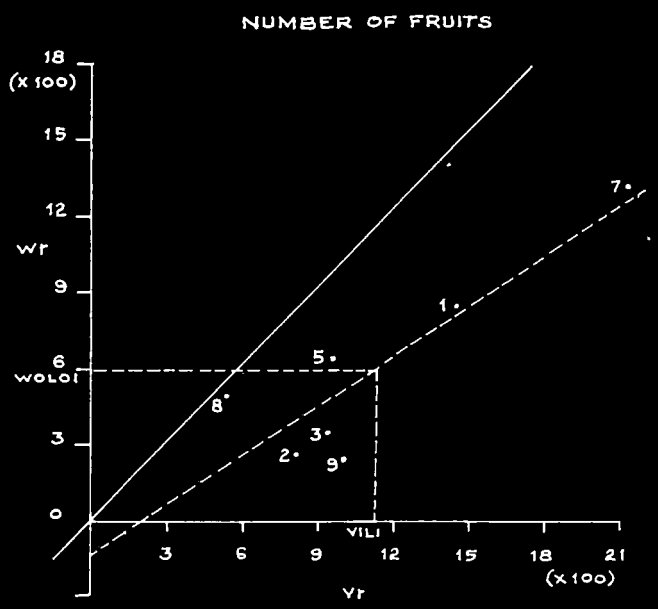


FIG. 15. A, Vr, Wr GRAPH

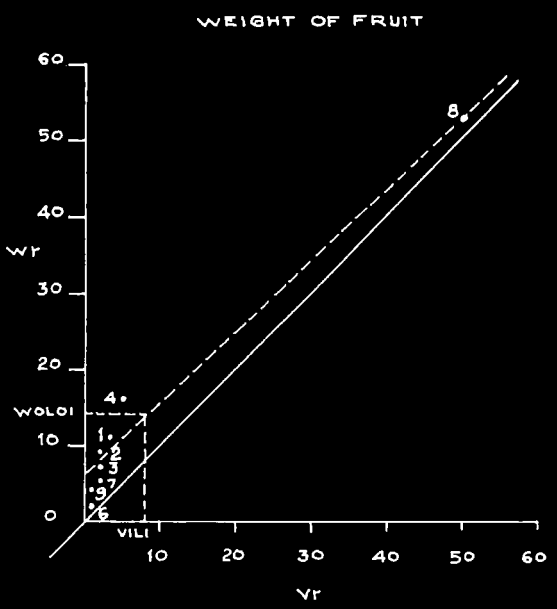


FIG. 16. A, Vr, Wr GRAPH

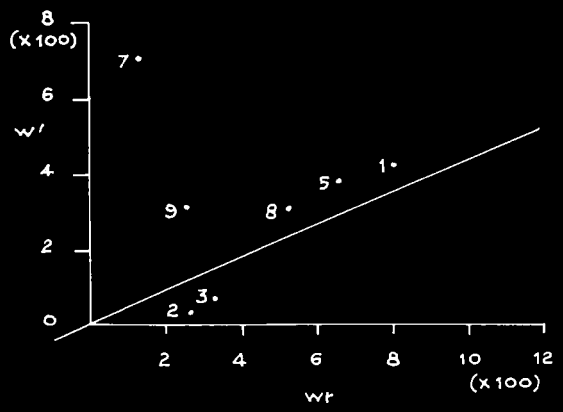


FIG. 15. B, Wr, W' GRAPH

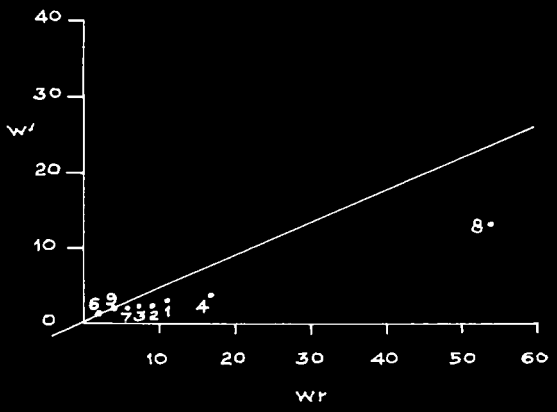


FIG. 16. B, Wr, W' GRAPH

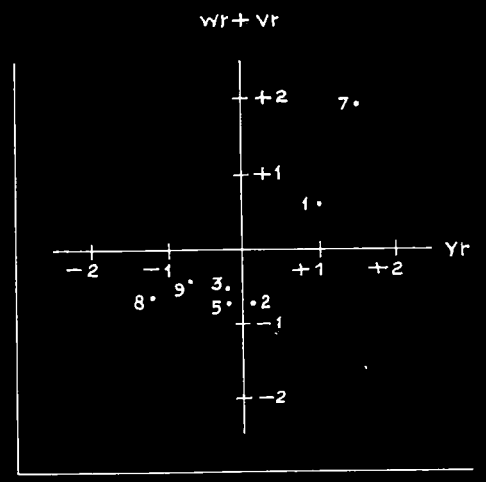


FIG. 15. C, STANDARDIZED DEVIATION
Yr, Wr + Vr GRAPH

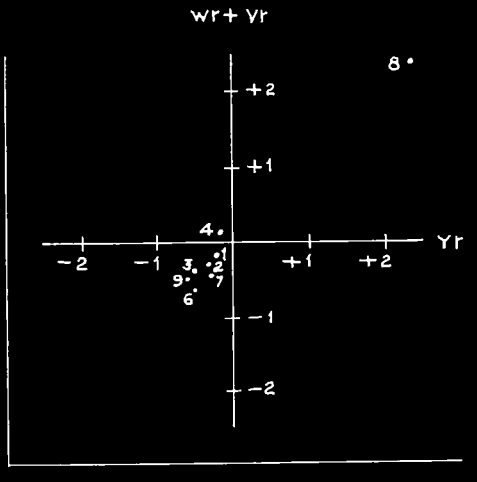


FIG. 16. C, STANDARDIZED DEVIATION
Yr, Wr + Vr GRAPH

The value of $\hat{H}_1$ was greater than that of $\hat{D}$ indicating the presence of over-dominance, which was also confirmed by the average degree of dominance (1.392). The ratio $\hat{H}_2/4\hat{H}_1$ (0.203) suggested the presence of asymmetry at loci showing dominance. The ratio $\hat{h}^2/\hat{H}_2$ (0.169) indicated that at least one gene or one group of genes controlling the character exhibited dominance.

(vii) Number of fruits

The 't^2' value was significant in the nine parent diallel set thereby indicating the failure of the assumptions. The sub-diallel set omitting parents 4 and 6 satisfied the assumptions (Table 27).

The regression line, W_r on V_r showed significant deviation from zero, but not from the unit slope (Table 27). The V_r, W_r graph (Fig. 15A) showed that the regression line had cut the W_r axis below the point of origin indicating the presence of over dominance. The array points were scattered widely revealing genetic diversity among the parents. The parents 7 and 1 in that order had predominance of recessive genes, while in the remaining parents dominant genes were in excess. All the array points were lying below the line of unit slope indicating presence of epistasis. All the arrays except 2 and 3 were lying above the line of ¼ slope in the W_r, W' graph (Fig. 15B) revealing a complementary type of gene action in them.

The correlation coefficient between Y_r and $W_r + V_r$ was positive and significant. The standardized deviation graph of Y_r and $W_r + V_r$ (Fig. 15C) showed that the arrays 9 and 8 had dominant genes for lower number of fruits while parents 2, 3 and 5 possessed dominant and recessive genes in almost equal proportion for medium number of fruits. The arrays 1 and 7 predominated in recessive genes for higher number of fruits.

The estimates of components of variation namely $\hat{D}$, $\hat{H}_1$, $\hat{H}_2$ and $\hat{h}^2$ were significant (Table 28). The positive sign of $\hat{F}$ suggested that more dominant genes were present in parents than recessive ones. The proportion of dominant and recessive genes in the parents was 1.075. The value of $\hat{H}_1$ was greater than that of $\hat{D}$ indicating presence of over-dominance which was also confirmed by the average degree of dominance (1.652). The ratio $\hat{H}_2/4\hat{H}_1$ (0.237) suggested that there was some asymmetry at loci showing dominance. The number of groups of genes showing dominance was 3.29 implying that at least 4 genes or 4 groups of genes controlling number of fruits exhibited dominance.

(viii) Weight of fruit

The 't^2' value testing the uniformity of W_r-V_r was significant in the nine parent diallel, thereby indicating failure of the assumptions. Sub-diallel sets omitting parents 5 and 8 satisfied the assumptions. The former was selected for further studies (Table 27).

The regression line W_r on V_r showed significant deviation from zero but not from the unit slope (Table 27). The V_r, W_r graph (Fig. 16A) showed that the regression line had cut the W_r axis above the point of origin indicating partial dominance. The array points except 8 were not lying scattered indicating very little genetic diversity among the parents for this character. The array point 8 had predominance of recessive genes while in the rest of the parents dominant genes were in excess. All the array points were lying above the line of unit slope suggesting that additiveness played a greater role for this character. In the W_r, W' graph (Fig. 16B) the array points were lying just below the line of $\frac{1}{4}$ slope.

The correlation coefficient between Y_r and $W_r + V_r$ was positive and significant. The standardised deviation graph of Y_r and $W_r + V_r$ (Fig. 16C) showed that the parent 8 had an excess of recessive genes for increased weight of fruit. The remaining parents possessed an almost equal proportion of dominant and recessive genes for medium weight of fruit.

All the estimates of components of variation except $\hat{F}$ were significant. The positive sign of $\hat{F}$ suggested that in parents more dominant genes were present than recessive ones. The proportion of dominant and recessive genes in the parents was 5.346. The value of $\hat{H}_1$ was smaller than that of $\hat{D}$ indicating the presence of partial dominance, which

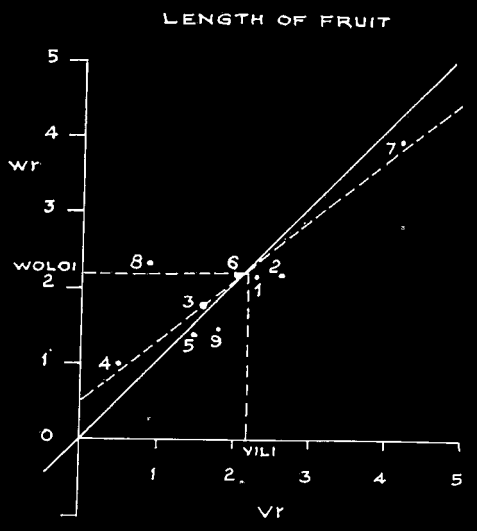


FIG.17.A, Vr, Wr GRAPH

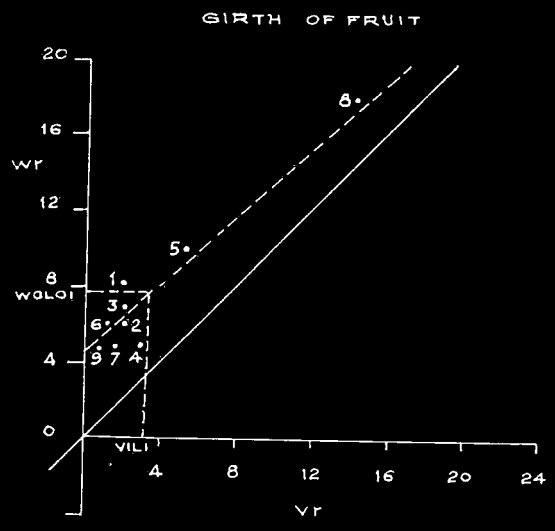


FIG.18.A, Vr, Wr GRAPH

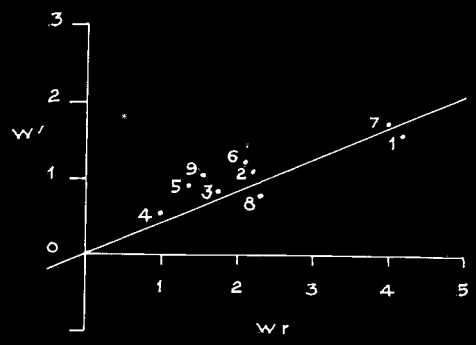


FIG 17 B, Wr, W' GRAPH

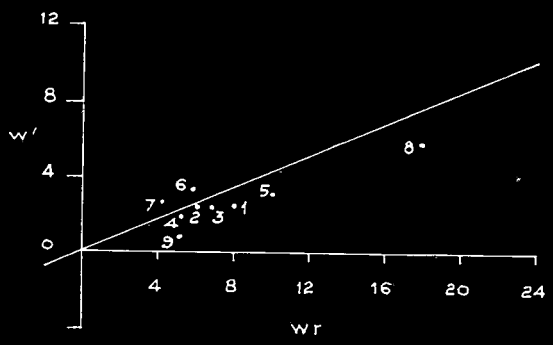


FIG.18.B, Wr, W' GRAPH

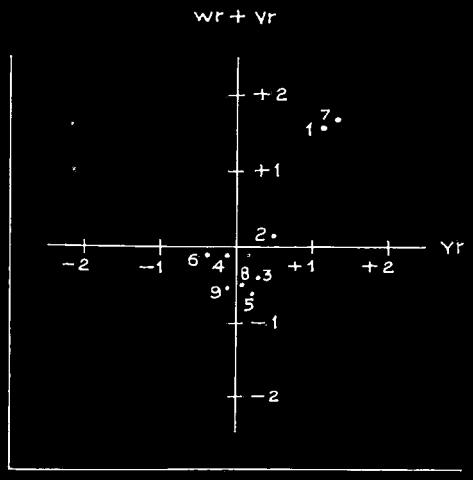


FIG.17.C, STANDARDIZED DEVIATION
Yr, Wr + Vr GRAPH

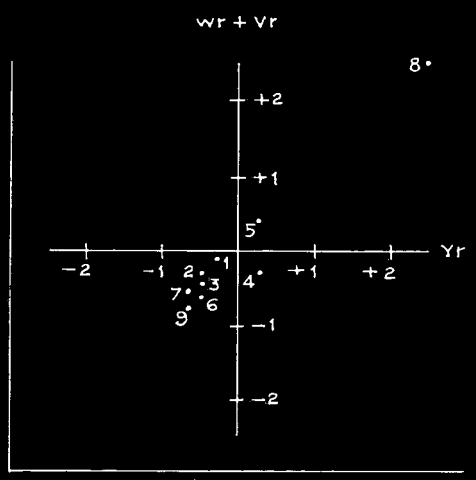


FIG.18.C, STANDARDIZED DEVIATION
Yr, Wr + Vr GRAPH

was also confirmed by the average degree of dominance (0.762). The ratio $\hat{H}_2/4\hat{H}_1$ (0.131) indicated that there was some asymmetry at loci showing dominance. The ratio $\hat{h}^2/\hat{H}_2$ was 12.721 which suggested that at least 13 genes or groups of genes controlling fruit weight exhibited dominance.

(ix) Length of fruit

The nine parent diallel set satisfied the hypotheses (Table 27).

The regression line W_r on V_r showed significant deviation from zero; but not from the unit slope (Table 27). The V_r, W_r graph (Fig. 17A) showed that the regression line had cut the W_r axis above the point of origin indicating the presence of partial dominance. Widely scattered array points revealed genetic diversity among parents. The parents 7 and 2 had predominantly recessive genes. Five arrays 1, 7, 2, 5 and 9 were lying below the line of unit slope indicating epistasis. The remaining arrays suggested additive type of gene action. In the W_r, W' graph (Fig. 17B) arrays 2, 3, 4, 5, 6, 7 and 9 were lying above the line of ¼ slope revealing a complementary type of gene action in them.

The correlation coefficient between Y_r and $W_r + V_r$ was positive and significant. The standardized deviation graph of Y_r and $W_r + V_r$ (Fig. 17C) showed that the parent 1 and 7 had an excess of recessive genes for longer fruits. The remaining parents possessed dominant and recessive genes in almost equal proportion for medium length of fruit.

All the estimates of components of variation except $\hat{E}$ were significant (Table 28). The positive sign of $\hat{F}$ showed the presence of more dominant genes in the parents. The proportion of dominant and recessive genes in parents was 2.102. The value of $\hat{H}_1$ was less than that of $\hat{D}$ indicating the presence of partial dominance which was also confirmed by the average degree of dominance (0.97). The ratio $\hat{H}_2/4\hat{H}_1$ (0.166) suggested that there was some asymmetry at loci showing dominance. The number of genes or groups of genes showing dominance for this character was at least 17.

(x) Girth of fruit

The nine parent diallel analysis satisfied the assumptions (Table 27).

The regression line W_r on V_r showed significant deviation from zero; but not from the unit slope (Table 27). The V_r, W_r graph (Fig. 18A) revealed that the regression line had cut the W_r axis above the point of origin indicating the presence of partial dominance. Only the parents 8 and 5 displayed wide genetic diversity. The parents 8 and 5 in that order possessed an excess of recessive genes, while the remaining parents had dominant genes for the character. All the array points were lying above the line of unit slope suggesting additive type of gene action. The arrays 6 and 7 were lying above the line of $\frac{1}{4}$ slope in the W_r, W' graph (Fig. 18B) displaying complementary type of gene action in them.

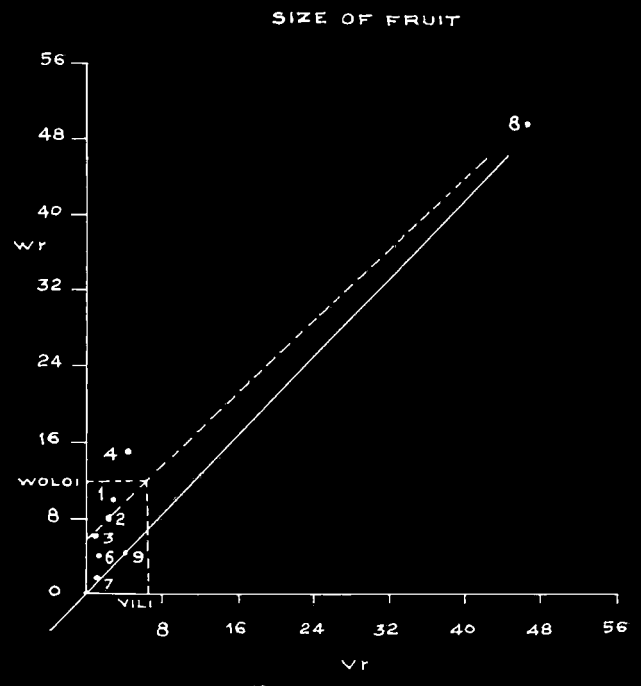


FIG 19 A, Vr, Wr, GRAPH

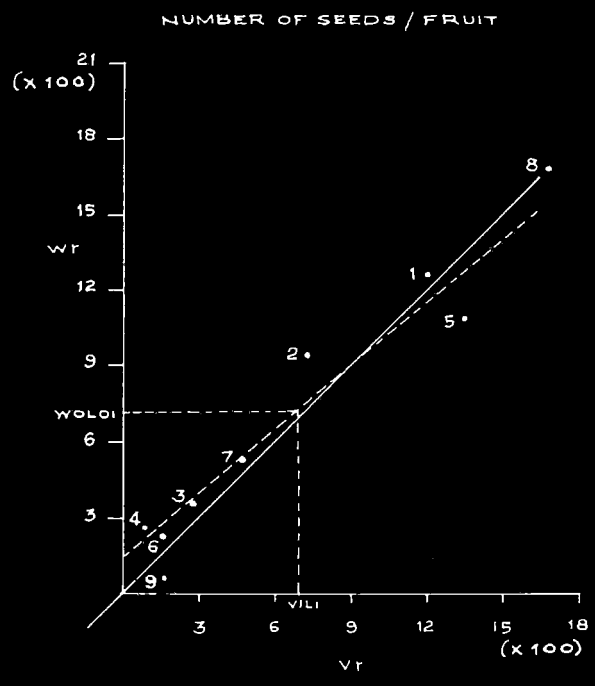


FIG.20 A, Vr, Wr, GRAPH

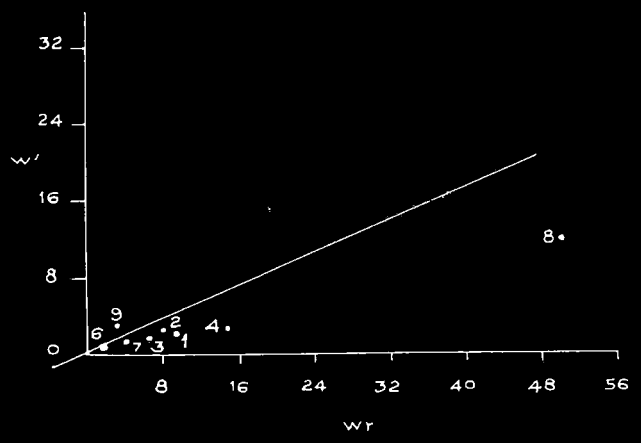


FIG 19 B, Wr, Wr' GRAPH

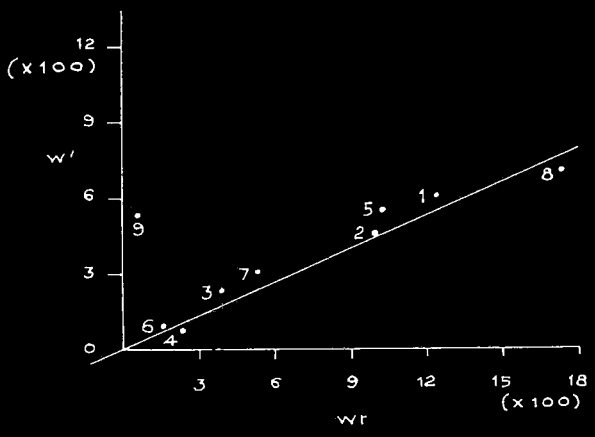


FIG 20.B, Wr, Wr' GRAPH

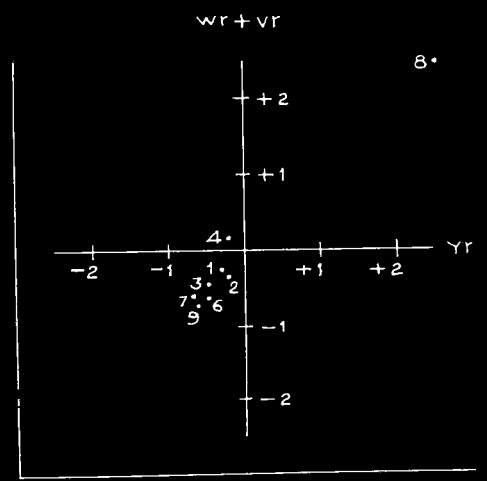


FIG 19 C, STANDARDIZED DEVIATION
Yr, Wr+Vr GRAPH

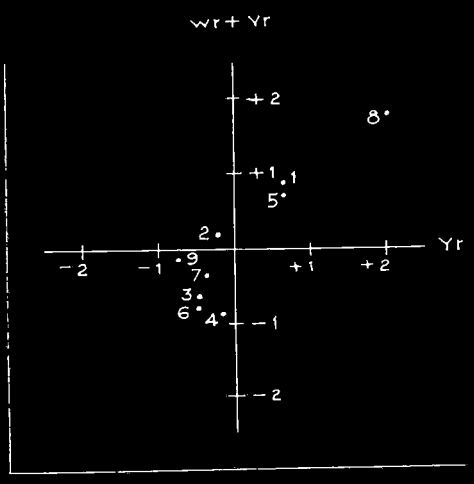


FIG 20 C, STANDARDIZED DEVIATION
Yr, Wr+Vr GRAPH

The correlation coefficient between V_p and $W_r + V_r$ was positive and significant. The standardised deviation graph of V_r and $W_r + V_r$ (Fig. 18C) revealed that the parent 8 possessed an excess of recessive genes for increased girth of fruit while the remaining parents had dominant and recessive genes in almost equal proportion for medium girth of fruit.

All the estimates of components of variation except $\hat{E}$ were significant (Table 28). The positive sign of $\hat{F}$ showed the presence of more dominant genes in the parents. The proportion of dominant and recessive genes in parents was 4.385. The value of $\hat{H}_1$ was less than that of $\hat{D}$ indicating the presence of partial dominance which was also confirmed by the average degree of dominance (0.567). The ratio $\hat{H}_2/4\hat{H}_1$ (0.136) implied that there was some asymmetry at loci showing dominance. The ratio $\hat{h}^2/\hat{H}_2$ (0.724) indicated that at least 9 genes or 9 groups of genes controlling this character exhibited dominance.

(xi) Size of fruit

The "t^2" value testing the uniformity of W_r-V_r was significant in the nine parent diallel, thereby indicating failure of the hypotheses. The sub-diallel omitting parent 5 satisfied the assumptions (Table 27).

The regression line W_r on V_r showed significant deviation from zero; but not from unit slope (Table 27). The V_r, W_r graph (Fig. 19A) indicated that the regression line had cut the W_r axis above the point of origin suggesting partial dominance. All the array points remained above the

line of unit slope indicating additive type of gene action in parents. The parents 8 and 4 showed wide genetic diversity between them. The parent 8 possessed an excess of recessive genes for the character and in the remaining parents dominant genes predominated. The parent 9 was lying above the line of 1 slope in W_r, W' graph indicating complementary type of gene action in that parent (Fig. 19B).

The correlation coefficient between Y_r and $W_r + V_r$ was positive and significant. The standardized deviation graph of Y_r and $W_r + V_r$ (Fig. 19C) showed that in parent 8 recessive genes dominated for larger size of fruit while in the remaining parents both dominant and recessive genes appeared in almost equal proportions for medium size of fruit.

All the estimates of components of variation except $\hat{E}$ was significant (Table 28). The positive sign of $\hat{F}$ suggested the presence of more dominant genes in the parents. The proportion of dominant and recessive genes in the parents was 5.661. The value of $\hat{D}$ was greater than that of $\hat{H}_1$, indicating the presence of partial dominance which was also confirmed by the average degree of dominance (0.789). The ratio $\hat{H}_2/4\hat{H}_1$ (0.125) suggested that there was some asymmetry at loci showing dominance. The number of genes or number of groups of genes showing dominance for size of fruit was at least 10.

(xii) Number of seeds/fruit

The 9 parent diallel analysis satisfied the hypotheses (Table 27).

The regression line W_r on V_r showed significant deviation from zero; but not from unit slope (Table 27). In the V_r, W_r graph (Fig. 20A) the regression line had cut the W_r axis above the point of origin indicating the presence of partial dominance. The wide scattering of array points suggested genetic diversity among parents. The array point 8 was lying along the line of unit slope. The parents 5 and 9 remained below the line of unit slope indicating epistasis, while in the remaining parents additive gene action was present. In the parents 8, 1, 5 and 2, in that order possessed an excess of recessive genes, and in the rest of the parents dominant genes predominated for the expression of the character concerned. In the V_r, W' graph (Fig. 20B) the array points except 4 and 6 were lying above the line of $\frac{1}{2}$ slope indicating complementary type of gene action in them.

The correlation coefficient between V_r and $W_r + V_r$ was positive and significant. The standardized deviation graph of V_r and $W_r + V_r$ (Fig. 20C) suggested that in parents 1, 5, 8 recessive genes dominated for increased number of seeds/fruit while in parents, 3, 4 and 6 dominant genes predominated for decreased number of seeds/fruit. With respect to the parents 2, 7 and 9 both dominant and

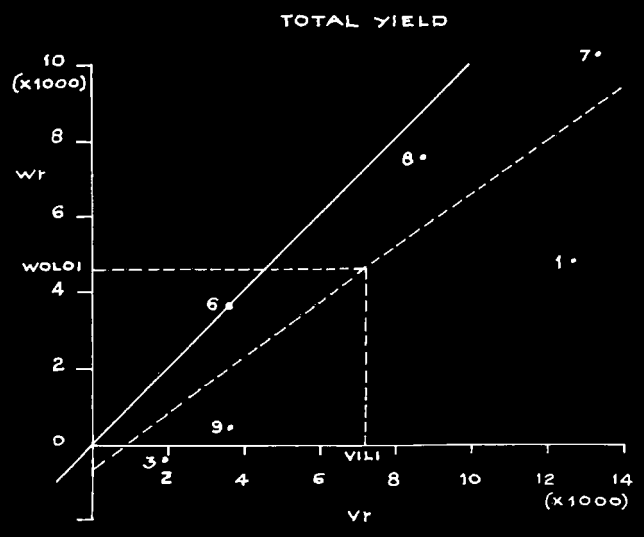


FIG. 21 A, Vr, Wr GRAPH

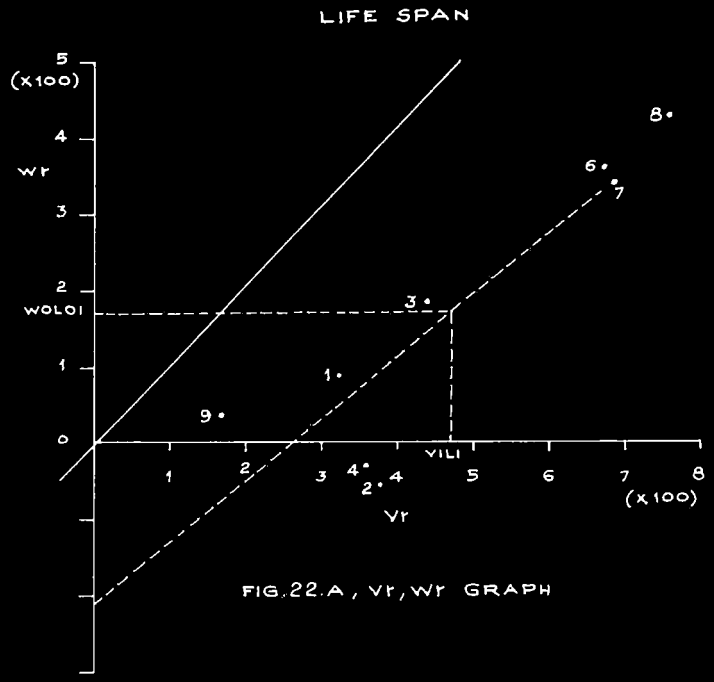


FIG. 22.A, Vr, Wr GRAPH

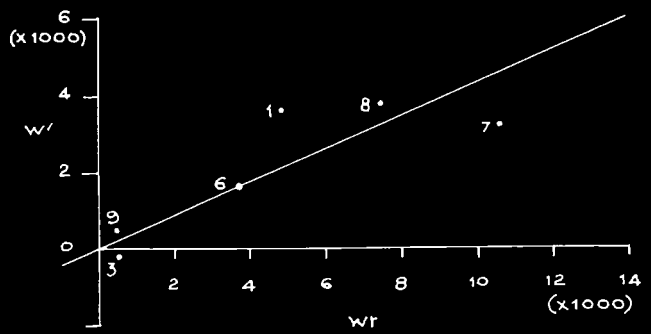


FIG. 21.B, Wr, W' GRAPH

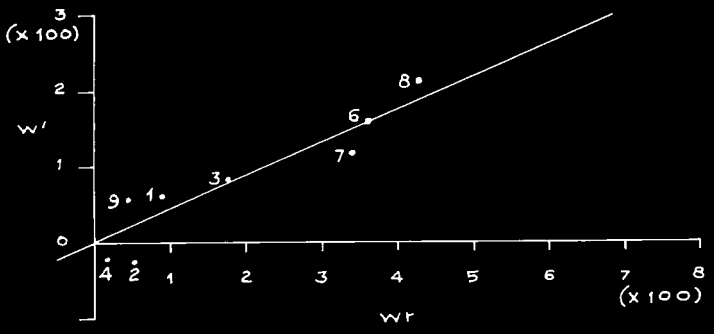


FIG 22.B, Wr, W' GRAPH

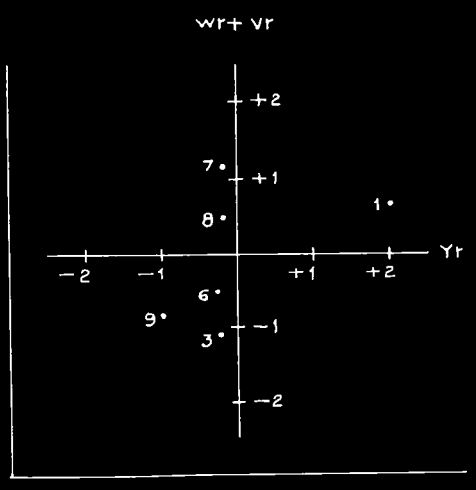


FIG. 21.C, STANDARDIZED DEVIATION
Yr, Wr+Vr GRAPH

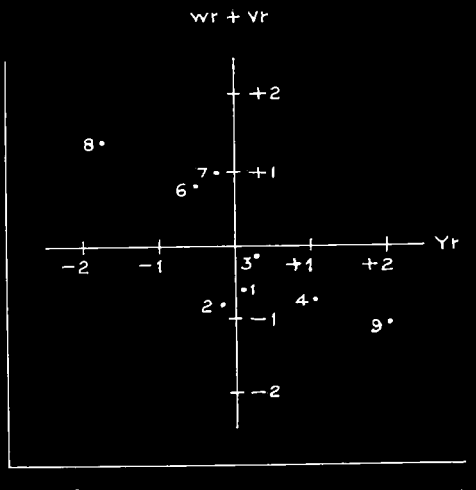


FIG.22.C, STANDARDIZED DEVIATION
Yr, Wr+Vr GRAPH

recessive genes had an equal proportion for medium number of seeds/fruit.

All the estimates of components of variation except $\hat{E}$ were significant (Table 26). The presence of more number of dominant genes were revealed by the positive sign of $\hat{F}$. The value of $\hat{H}_1$ was less than that of $\hat{D}$ suggesting the presence of partial dominance which was also confirmed by average degree of dominance (0.944). The proportion of dominant and recessive genes in parent was 1.616. The ratio $\hat{H}_2/4\hat{H}_1$ (0.197) indicated that there was some asymmetry at loci showing dominance. At least 9 genes or 9 groups of genes were showing dominance for the character concerned.

(xiii) Total yield

The 't^2' testing the uniformity of W_r-V_r was significant in the nine parent diallel, but the sub-diallel omitting parents 2, 4 and 5 satisfied the hypotheses (Table 27).

The regression line W_r on V_r showed significant deviation from zero; but not from the unit slope (Table 27). The regression line had cut the W_r axis, in the V_r, W_r graph (Fig. 21A) below the point of origin displaying over-dominance. Wide scattering of the arrays indicated rich genetic diversity among the parents. The parents corresponding to the array points 7, 8 and 1 in that order had an excess of recessive genes for the character concerned, while in the remaining parents dominant genes predominated.

All the array points were lying below the line of unit slope exhibiting epistatic gene action in them. In the W_r, V_r graph (Fig. 21B) the parents 1, 8 and 9 were lying above the line of 1 slope suggesting complementary type of gene action in them.

The correlation coefficient between V_r and $W_r + V_r$ was positive but not significant. The standardised deviation graph of V_r and $W_r + V_r$ (Fig. 21C) indicated that parents 3 and 9 possessed an excess of dominant genes for lower yield. While in parent 7 recessive genes predominated for medium yield. In parent 1 recessive genes predominated, for the production of higher yield. The array points corresponding to parents 6 and 8 possessed dominant and recessive genes in almost equal proportion for medium yield.

Among the estimates of components of variation $\hat{F}$ and $\hat{E}$ were not significant (Table 28). The negative sign of $\hat{F}$ indicated the presence of more recessive genes in the parents. The value of $\hat{H}_1$ was higher than that of $\hat{D}$ indicating the presence of over-dominance, which was also confirmed by the average degree of dominance (1.534). The ratio $\hat{H}_2/4\hat{H}_1$ (0.242) suggested some asymmetry at the loci showing dominance. The proportion of dominant and recessive genes in parents was 0.965. The ratio $\hat{h}^2/\hat{H}_2$ (2.917) indicated that the number of genes or groups of genes controlling dominance in this attribute was 3.

(xiv) Life span

The original nine parent diallel did not satisfy the hypotheses. But the sub-diallel omitting parent 9 satisfied the assumptions (Table 27).

The regression line W_r on V_r showed significant deviation from zero; but not from the unit slope (Table 27). The regression line had cut the W_r axis in the V_r, W_r graph (Fig. 22A) below the point of origin, indicating the presence of over dominance. High genetic diversity among parents was revealed from the wide scattering of array points. The parents 8, 6 and 7 in that order had an excess of recessive genes for the character. In the remaining parents dominant genes predominated. All the array points were lying below the line of unit slope suggesting epistatic gene action. In the W_r, W' graph (Fig. 22B) all the parents except 2, 4, 6 and 7 were lying above the line of $\frac{1}{4}$ slope indicating complementary type of gene action in them. The parent 7 was lying just below the line of $\frac{1}{4}$ slope while the parent 6 lies in the line of $\frac{1}{4}$ slope.

The correlation coefficient between V_r and $W_r + V_r$ was negative but significant. The standardised deviation graph of V_r and $W_r + V_r$ (Fig. 22C) indicated that in parents 4 and 9 dominant genes predominated for long life span while parents 6 and 8 possessed an excess of recessive genes for short life span. Parent 7 had predominated in recessive genes for medium life span. Dominant and recessive genes

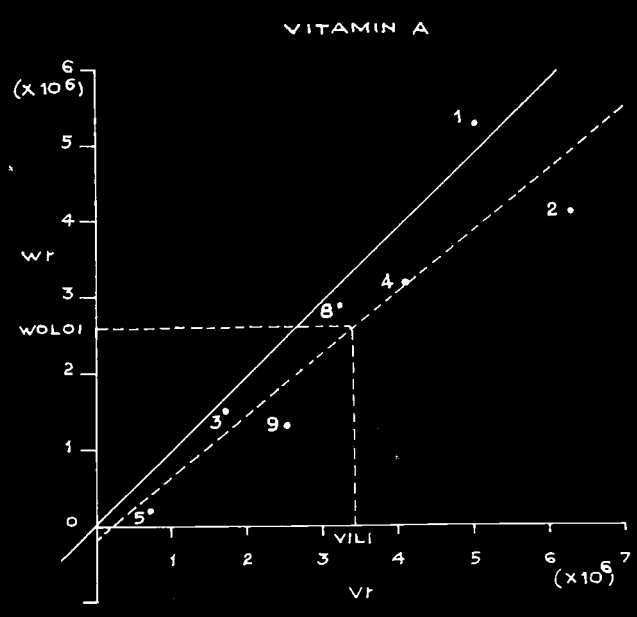


FIG. 23.A, Vr, Wr GRAPH

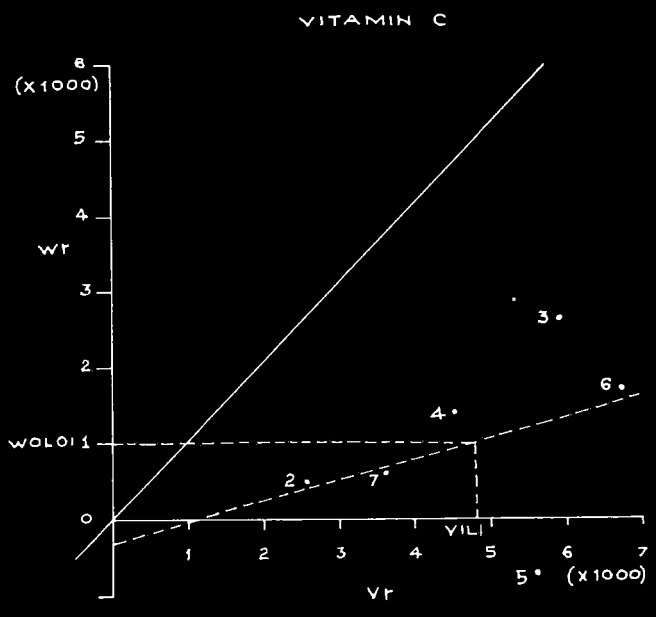


FIG. 24.A, Vr, Wr GRAPH

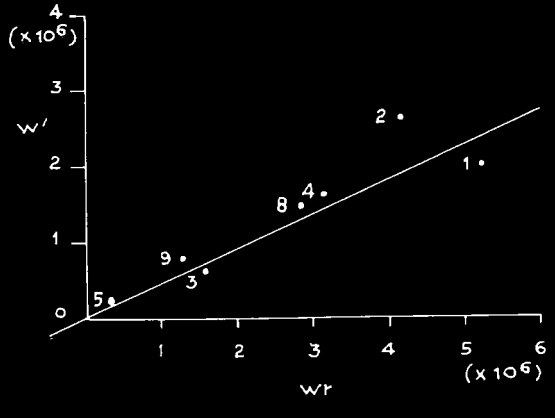


FIG. 23.B, Wr, W' GRAPH

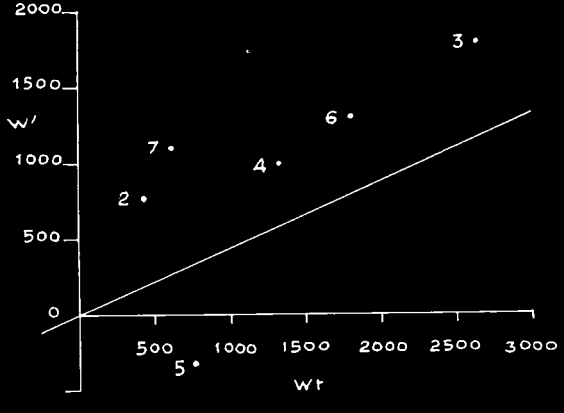


FIG. 24.B, Wr, W' GRAPH

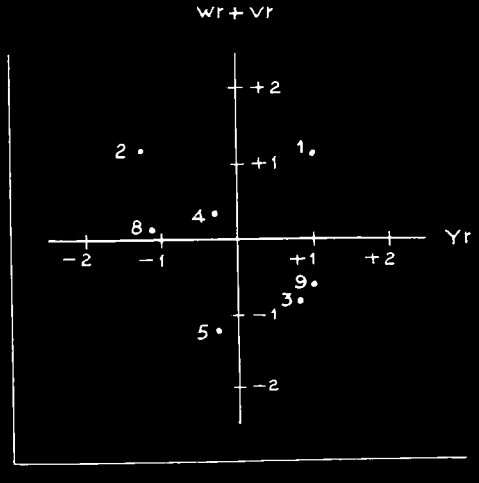


FIG. 23.C, STANDARDIZED DEVIATION
Yr, Wr + Vr GRAPH

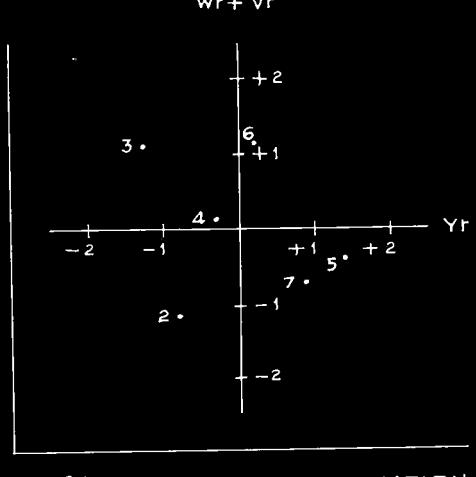


FIG. 24.C, STANDARDIZED DEVIATION
Yr, Wr + Vr GRAPH

were in almost equal proportion with respect to the parents 1, 2 and 3 for medium life span.

Except $\hat{F}$ and $\hat{E}$, other estimates of components of variation were significant (Table 28). The presence of more number of dominant genes in the parents were indicated by the positive sign of $\hat{F}$. The value of $\hat{H}_1$ was greater than that of $\hat{D}$ indicating the presence of over-dominance which was also confirmed by the average degree of dominance (2.002). The proportion of dominant and recessive genes in parents was 1.172 which also supported the above proposition. There was some asymmetry at loci showing dominance, which was indicated by the ratio $\hat{H}_2/4\hat{H}_1$ (0.239). The number of genes or groups of genes showing dominance, for the concerned character was 43.

(xv) Vitamin A

Original full-diallel analysis with nine parents indicated failure of the hypotheses. But the sub-diallel omitting parents 6 and 7 satisfied the assumptions (Table 27).

The regression line W_r, on V_r showed significant deviation from zero but not from unit slope (Table 27). The V_r, W_r graph (Fig. 23A) revealed that the regression line had cut the W_r axis below the point of origin indicating over-dominance. Wide scattering of the arrays suggested rich genetic diversity among parents for the character. All the arrays except 1 remained below the line of unit slope indicating epistatic gene action in them, while the

parent corresponding to array 1 displayed additiveness. The parents 1, 2, 4 and 8 in that order exhibited predominance of recessive genes for the character concerned while in the rest of the parents there was an excess of dominant genes. All the parents except 1 and 3 were lying above the line of $\frac{1}{4}$ slope in the W_r, W' graph (Fig. 23B) suggesting complementary type of gene action in them.

The correlation coefficient between Y_r and $W_r + V_r$ was negative and not significant. The standardised deviation graph of Y_r and $W_r + V_r$ (Fig. 23C) indicated that parents 3 and 9 had an excess of dominant genes for higher Vitamin A content, while in the parent 1 recessive genes dominated for higher Vitamin A content. In parent 2 recessive genes were in excess for lower Vitamin A content, but parent 4 possessed dominant and recessive genes in almost equal proportions for medium Vitamin A content. Parent 8 also had dominant and recessive genes in almost equal proportion for lower Vitamin A content while in parent 5 dominant genes predominated for medium Vitamin A content.

The estimates of 4 components of variation namely $\hat{D}$, $\hat{H}_1$, $\hat{H}_2$ and $\hat{h}^2$ were significant (Table 28). The positive sign of $\hat{F}$ suggested the presence of more dominant genes in the parents. The value of $\hat{H}_1$ was greater than that of $\hat{D}$ indicating the presence of over-dominance which was also confirmed by the average degree of dominance (1.224). The proportion of dominant and recessive genes in parents was

1.207. The ratio $\hat{H}_2/4\hat{H}_1$ indicated that some asymmetry existed at loci showing dominance. The number of genes or groups of genes showing dominance for the character was 5.

(xvi) Vitamin C

In the nine parent diallel set 't^2' testing the uniformity of W_r-V_r was significant indicating the failure of hypotheses. None of the sub-diallel omitting different parents fully satisfied the assumptions. The sub-diallel excluding parents 1, 8 and 9 was almost near the satisfactory proposition and as such the same was selected for further studies (Table 27).

The regression line W_r on V_r showed significant deviation from zero (Table 27). The regression line in the V_r, W_r graph (Fig. 24A) had cut the W_r axis below the point of origin indicating over-dominance. Ample genetic diversity among parents was evident from the wide scattering of arrays. All the array points were lying below the line of unit slope suggesting epistatic gene action in parents for the character. The parents 3, 6 and 4 in that order had an excess of recessive genes while in the other parents dominant genes predominated. In the W_r, W' graph (Fig. 24B) all the parents except 5 were lying above the line of ¼ slope displaying complementary type of gene action in them.

The correlation coefficient between Y_r and $W_r + V_r$ was negative and not significant. The standardised

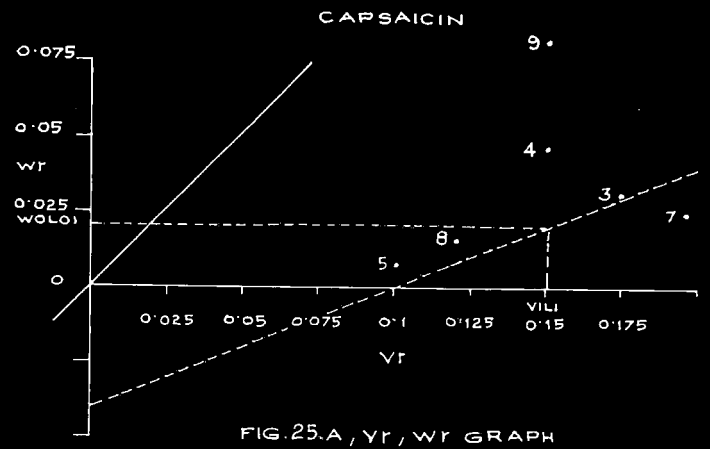


FIG.25.A, Yr, Wr GRAPH

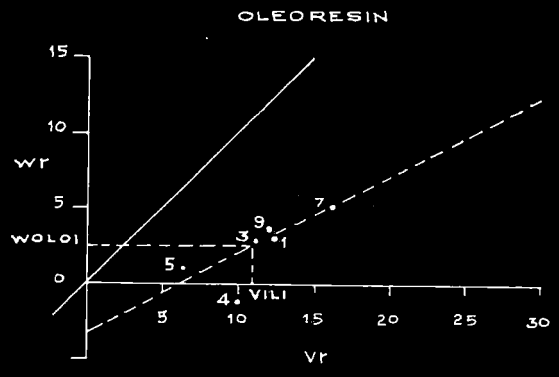


FIG.26.A, Vr, Wr GRAPH

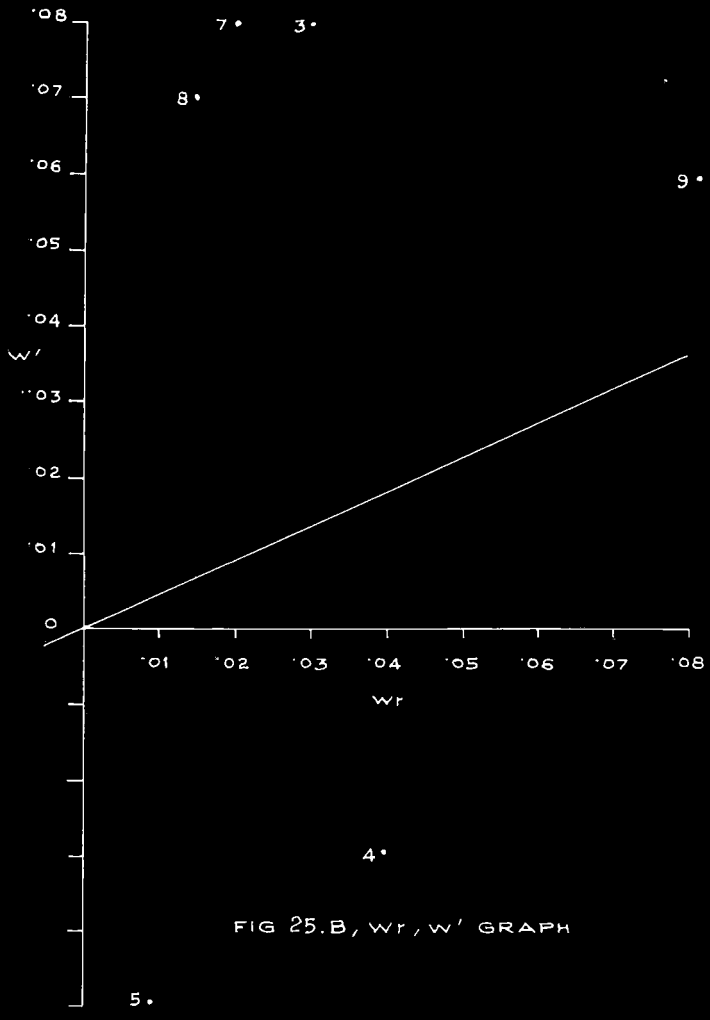


FIG 25.B, Wr, W' GRAPH

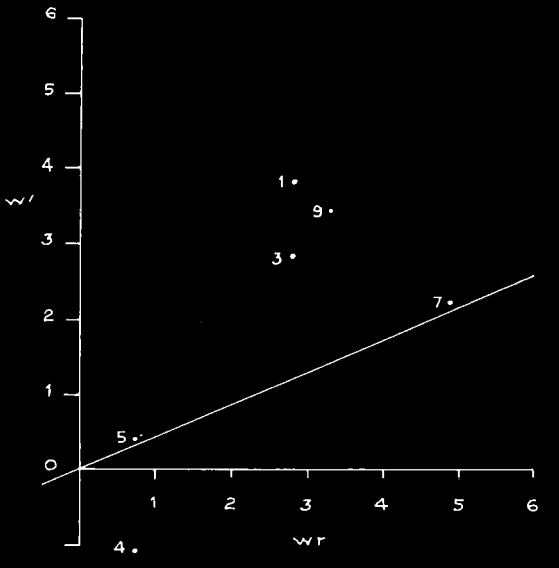


FIG.26 B, Wr, W' GRAPH

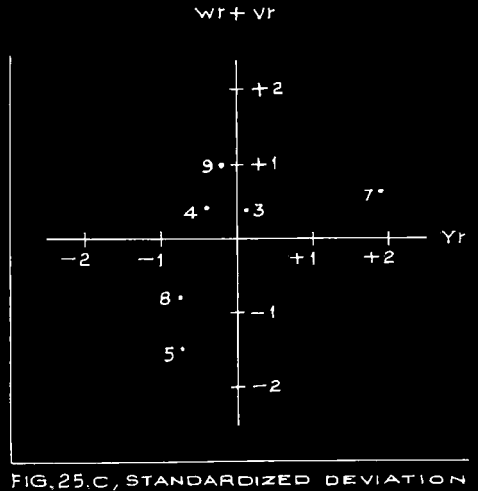


FIG.25.C, STANDARDIZED DEVIATION
Yr, Wr+Vr GRAPH

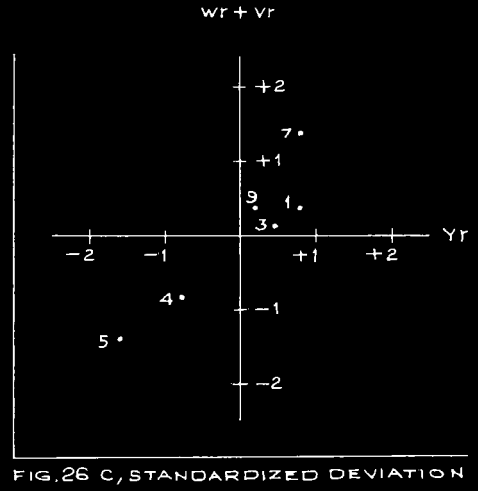


FIG.26 C, STANDARDIZED DEVIATION
Yr, Wr+Vr GRAPH

deviation graph of V_r and $W_r + V_r$ (Fig. 240) revealed that in parent 5 and 7 dominant genes predominated for higher Vitamin C content while parent 6 possessed an excess of recessive genes for medium Vitamin C content. Parent 2 had an excess of dominant genes for lower Vitamin C content while in parent 3 recessive genes predominated for the character. But in parent 4 dominant and recessive genes were in almost equal proportion for medium Vitamin C content.

The estimates of 3 components of variation namely $\hat{H}_1$, $\hat{H}_2$ and $\hat{h}^2$ were significant (Table 28). The negative sign of $\hat{F}$ indicated the presence of more number of recessive genes in the parents. The value of $\hat{H}_1$ was greater than that of $\hat{D}$ suggesting the presence of over-dominance which was also confirmed by the average degree of dominance (3.528). The proportion of dominant and recessive genes in parents was 0.749. There was some asymmetry at loci showing dominance, which was revealed by the proportion of $\hat{H}_2/4\hat{H}_1$ (0.232). The proportion of $\hat{h}^2/\hat{H}_2$ (23.846) implied that the number of genes or groups of genes exhibiting dominance for the character was at least 24.

(xvii) Capsaicin

The analysis of full diallel set indicated the significance of "t^2" suggesting the failure of hypotheses. None of the sub-diallel omitting different parents fully satisfied the assumptions. The sub-diallel excluding

parents 1, 2 and 6 was almost satisfying the assumptions and as such the same was selected for further studies (Table 27).

The regression line W_r, on V_r showed significant deviation from zero (Table 27). The V_r, W_r graph (Fig. 25A) showed that the regression line had cut the W_r axis below the point of origin indicating over-dominance. Wide scattering of the arrays exhibited genetic diversity among the parents. All the array points remained below the line of unit slope displaying epistatic gene action. The parents 9, 4, 3 and 7 had an excess of recessive genes while in the remaining parents dominant genes predominated. In the W_r, W' graph (Fig. 25B) four parents namely, 7, 3, 8 and 9 were lying above the line of $\frac{1}{4}$ slope revealing complementary type of gene action in them.

The correlation coefficient between Y_r and $W_r + V_r$ was positive but not significant. The standardized deviation graph of Y_r and $W_r + V_r$ (Fig. 25C) indicated that in parents 8 and 5 dominant genes predominated for lower capsaicin content while parent 4 had an excess of recessive genes for lower capsaicin content. Further, in parent 9 recessive genes predominated for medium capsaicin content. Recessive genes were in excess in parent 7 for higher capsaicin content while parent 3 possessed dominant and recessive genes in almost equal proportion for medium expression of the character.

Four estimates of components of variation $\hat{D}$, $\hat{H}_1$, $\hat{H}_2$, $\hat{h}^2$, were significant (Table 28). The negative sign of $\hat{F}$ suggested the presence of more number of recessive genes for the character. The value of $\hat{H}_1$ was greater than that of $\hat{D}$ indicating the presence of over-dominance which was also confirmed by the average degree of dominance (3.038). The proportion $\hat{H}_2/4\hat{H}_1$ (0.181) suggested some asymmetry at the loci showing dominance. The proportion of dominant and recessive genes in parents was 0.948. The number of genes or groups of genes showing dominance for the character was 8.

(xviii) Oleoresin

The "t^2" testing the uniformity of W_r-V_r was significant in the original nine parent diallel analysis indicating failure of the hypotheses (Table 27). None of the sub-diallel omitting different parents satisfied the assumptions. The sub-diallel excluding parents, 2, 6 and 8 was almost near the satisfactory assumptions and as such the same was selected for further studies.

The regression line W_r on V_r showed, significant deviation from zero (Table 27). The regression line had cut the W_r axis below the point of origin in the V_r, W_r graph (Fig. 26A) indicating the presence of over-dominance. Wide genetic diversity among parents was revealed from the scattering of array points. All the array points were below the line of unit slope suggesting epistasis gene

action. In parents 7, 9, 1 and 3 recessive genes had predominated while the remaining parents possessed an excess of dominant genes. In the W_r, W' graph (Fig. 26B) parents 5, 7, 3, 9 and 1 were lying above the line of 1 slope revealing complementary type of gene action in them.

The correlation coefficient between Y_r and $W_r + V_r$ was positive and significant. The standardized deviation graph of Y_r and $W_r + V_r$ (Fig. 26C) suggested that parents 4 and 5 had an excess of dominant genes for lower oleoresin content while in parents 1 and 7 recessive genes predominated for higher oleoresin content.

Parents 3 and 9 possessed dominant and recessive genes in almost equal proportion for medium oleoresin content. The three estimates of components of variation namely $\hat{H}_1$, $\hat{H}_2$ and $\hat{h}^2$ were significant (Table 28). The presence of more number of recessive genes in the parents was revealed by the negative sign of $\hat{F}$. The value of $\hat{D}_1$ was lower than that of $\hat{H}_1$ suggesting the presence of over-dominance which was confirmed by the average degree of dominance (3.494). The proportion of dominant and recessive genes in parents was 0.799. The ratio $\hat{H}_2/4\hat{H}_1$ (0.231) indicated the existance of some asymmetry at loci showing dominance. The number of genes or groups of genes showing dominance for the character was revealed as 7 from the ratio $\hat{h}^2/\hat{H}_2$.

DISCUSSION

DISCUSSION

Chilli, (*Capsicum annuum*) is richly endowed with Capsaicin, Oleoresin and other qualities in addition to nutritive attributes. However, the various yield components and contributing characteristics of this crop are scattered in different varieties (Nair and George, 1973). Although positive heterosis has been reported in chilli as early as 1933 (Deepende) commercial production of hybrids has not become popular. One of the reasons for this could be the lack of systematic studies to understand the genetic architecture determining the various quantitative traits. Another reason could be the ineffective methodology adopted which stand in the way of realising the revealed potential. With a view to examine the manifestation and magnitude of heterosis in the hybrid combinations and to estimate the combining abilities and gene action of the characters a nine-parent diallel experiment was carried out at the College of Agriculture, Vellayani. Before resorting to the diallel cross, as an imperative pre-requisite, genetic divergence among the selected varieties from the base material was estimated by Mahalanobis' D^2 statistic. Prior to that, the cause-effect relationship of yield and it's components were unveiled by path analysis. As a prelude to path coefficient analysis genetic parameters were computed. The parents entering the diallel cross were

selected on the basis of the results of D^2 analysis and also as per the procedure enunciated by Singh and Choudhary (1979).

Although, chilli is considered as a self pollinated crop, some amount of variation in the progenies is noticed consequent on cross pollination effected through the activities of bees. The difference in style length is also found to be a contributing factor. Proximity of different lines also adds to the problem. In order to provide homozygous lines, the selected parents were selfed and the inbreds crossed in all possible combinations. In addition to the four nutritive and quality attributes namely Vitamin A, Vitamin C, Capsaicin and Oleoresin, fourteen other characteristics including yield contributing traits were studied. The results obtained are discussed in the succeeding pages.

1. Genetic parameters

A perusal of the estimates of genetic parameters of different characters indicated that the environmental coefficient of variation was minimum, suggesting that the characters were less influenced by environmental factors. The phenotypic and genotypic coefficients of variation were higher for number of fruits, weight of fruit, total yield and capsaicin content. This indicates the possibility for further improvement of these characters through combination breeding. Other characters have comparatively less genetic

variability. The results provide an index of the variability present in the base population. These observations are in agreement with the findings of Arya (1979).

A strong positive association between the genotypic coefficient of variation and the genetic advance due to selection was noticed. Number of fruits, with the highest genotypic coefficient of variation, has the highest estimate of genetic advance, while life span with the least genetic variability, has also the least genetic advance. This phenomenon suggests that the more the genetic variability in the population for a particular character, the higher would be the genetic advance i.e. the response to selection for that character.

High heritability was observed for all the characters under study, indicating the presence of a large number of fixable additive factors. The heritability values ranged from 99.92 for girth of fruit to 70.91 for number of primary branches. High estimates of heritability in chillies for various characters were reported by several other workers (Sethupathi Ramalingam and Muruga Rajendran, 1977; Hiremath and Mathapathi, 1977; Arya, 1979). All the characters, however did not show high genetic advance. In the case of the number of secondary branches, number of fruits, weight of fruit, number of seeds, girth of fruit, total yield, Vitamin A and Capsaicin content, high heritability was accompanied by high genetic advance.

High heritability followed by low genetic advance attributable to non-additive gene action was noticed in characters like number of days taken for blooming, height, spread, number of primary branches, life span and Vitamin C content. This was again reflected and confirmed in V_r, W_r graphs. Height of plant, number of branches and weight of fruits were found to combine high heritability with high genetic advance(Sethupathi Ramalingam and Muruga Rajendran, 1977), while Hiremath and Mathapathi (1977) noticed low genetic advance for length of fruit, number of branches and number of fruits, inspite of the fact that the character exhibited comparatively high degree of heritability. The difference in these findings might be due to the difference in the varieties studied. The results state that the high estimates of heritability is not always an indication of high genetic gain (Johnson et al., 1955). High heritability indicates that these characters are less influenced by environmentalfactors. High heritability accompanied by high genetic advance is attributable to additive gene effects, while low heritability with low genetic advance is ascribed to non additive gene effects. Selection based on the characters having high estimates of both heritability and genetic advance would be rewarding in chillies for genetic improvement.

2. Association of characters and path analysis

The genotypic correlation coefficients were of higher magnitude than the phenotypic correlation coefficients in general. Wherever both phenotypic and genotypic correlations were significant they were both of the same sign (either positive or negative). The number of fruits exhibited significant positive correlation with the number of primary branches, secondary branches and total yield, while it showed significant negative correlation with number of seeds, weight and girth of fruit. Vitamin C content exhibited significant positive correlation with weight of fruit, number of seeds, length and girth of fruit but exhibited significant negative correlation with number of days taken for blooming and life span. Capsaicin content manifested significant negative correlation with number of seeds, weight of fruit and Vitamin C content. Similar results have been recorded by Arya and Saini (1976) and Chang (1977). The capsaicin and Vitamin C content showed significant negative correlation which was in conformity with the earlier findings of Nair and George (1973). Capsaicin content also displayed a nonsignificant correlation with Vitamin A content, as indicated by Lee et al. (1973).

Path coefficient analysis indicated that the number of fruits was the principal yield attribute. Yield in

chilli can be considered as the effect of five first order components namely, number of fruits, number of secondary branches, girth and weight of individual fruit and life span which accounted for 68% of the variability in yield. The number of primary branches and spread accounted for 42% of the variability in the number of secondary branches. Similar results were observed by Nandapuri et al. (1979); Mishra et al. (1976); Singh and Singh (1976c) and Chang (1977). Based on correlation and multiple regression analysis Rochetta et al. (1976) showed that yield mainly depended on the number and weight of fruits, and that the other characters contributed to the yield through the number of fruits. Their study thus indicated that selection of high yielding lines should be based on these characters, which is in conformity with the findings of Lee (1976) and Gill et al. (1976).

There was no significant association between girth of fruit, weight of individual fruit and life span with yield. This was apparent in big fruited varieties like California wonder, where although girth of the fruit and weight of individual fruit were high they contributed little towards total yield. Further, varieties like purple round have a long life span, but it did not contribute to appreciable increase in yield. The direct effect of the girth of fruit was negative and the effect through number of fruits was also negative. When girth increased, the

number of fruits decreased.

3. Genetic divergence

The multivariate analysis done by using Mahalanobis' D^2 statistic enabled the assessment of the statistical distance between varieties. The D^2 values ranged from 25.48 to 47713.04. Out of the 435 comparisons one value (D^2 between variety 25 and 26) was significant only at 5% level, while all the remaining values were significant at 1% level also. This clearly indicated the presence of appreciable amount of genetic divergence between the varieties studied. The 30 varieties selected from the base material which in turn constituted 63 varieties, were grouped into 16 clusters including four with single variety. The varieties Jrong, Red slender, Gundu Mulaku and Byrwa, stood out singly with intra-cluster distance of '0'. The average intra-cluster distance was least, while the inter-cluster distances were more reflecting the genetic diversity of the varieties. The larger number of constellations indicated the high genetic diversity available in the species. The significance of all the D^2 values also confirmed this inference.

The intra-cluster D values ranged from '0' to 43.494 while the inter-cluster D values ranged from 17.238 to 213.172. The intra-cluster distance for groups 13, 14, 15 and 16 was '0' because they constituted only one variety each. The average intra-cluster distance (D) was the low

in the remaining clusters which indicated that the variability within clusters was low and between clusters high. In otherwords clusters are sets of varieties which are genetically homogenous within the heterogenous between. The importance of close genetic relationship within clusters and lack of such relationship between clusters was emphasised by George (1976) in arecanut. By D^2 analysis and canonical analysis he grouped 17 cultivars into 6 clusters including 4 single clusters. The major contributors in the present study for divergence was number of seeds, total yield, girth of fruit, Vitamin A content, Capsaicin content and number of fruits per plant. Number of seeds and number of primary branches had contributed to maximum and minimum divergence respectively. The results are in agreement with the findings of Singh and Singh (1976b) in Capsicum annuum. They observed that number of branches, thickness of fruits, number of fruits per plant and yield per plant contributed more towards divergence. They further, grouped forty five Indian lines of Capsicum annuum into 10 clusters based on the similarities of D^2 values.

The grouping of varieties into clusters by Tocher's method was confirmed by canonical analysis. The first two canonical roots together contributed 73.7% of the total variation which again reflected on the grouping of varieties based on genetic divergence. This was emphasised by George (1976) in Arecanut and Peter and Rai (1976) in tomato.

The clustering pattern was found to be following geographical distribution of the varieties, which is in agreement with the results of Singh and Singh (1976b) and contrary to the findings of Peter and Rai (1976) in tomato. In general, considerable genetic diversity was present in the varieties as revealed by D^2 analysis. With respect to each of the characters studied, this was reflected in V_r, W_r graphs, by the wide scattering of array points. This phenomenon was responsible for the manifestation of heterosis in many of the characters studied. In the hybridisation programme of Solanum melongena, Vijay et al. (1978) observed that it would be desirable to reserve a place for the parents of genetically diverse origin to locate the best combiners. The cross I.I.H.R.2-1 x Supreme, which proved to be the best general combiners in respect of all characters was named Arka Navaneet and released for commercial cultivation.

The varieties studied represent a broad spectrum of variability when their mean performance for different traits were examined. Therefore in addition to the manifestation of hybrid vigour in the F_1 generation, desirable recombinants in the segregating generations are also expected. The study has shown that number of seeds, total yield, girth of fruit, Vitamin A content, Capsaicin content and number of fruits per plant had profound impact on the observed diversity. Hence selection of parents differing in these attributes may be worthwhile as divergent material for

heterosis breeding in Capsicum annuum.

4. Combining ability and heterosis

All the attributes studied manifested heterosis over the mid parental values, though there was wide variation for different traits in different cross combinations. Maximum heterosis was exhibited for number of primary branches and Vitamin C content. Positive heterosis was less in characters like weight, length, girth and size of fruits and number of seeds per fruit. All crosses were significantly heterotic in two traits namely number of primary branches and Vitamin C content when heterosis was computed over mid parental value. 1488.94 per cent and 1366.51 per cent positive heterosis were manifested with respect to the characters, number of leaves (CA 1068 x Purple cluster) and total yield (Purple round x Vella notchi) respectively. Popova and Mikhailov (1978) reported similar results in red pepper (Capsicum annuum). They further noticed that the embryos of the hybrid seeds were larger than those of the parents and thereby heterosis became apparent immediately after fertilization. However, Novak and Chmela (1979) recorded heterosis of 50 per cent and above for total yield and attributed the phenomenon to over-dominance.

The maximum heterosis for Vitamin C and Capsaicin content was displayed by CA 960 x Purple cluster (498.15 per cent) and Purple round x California wonder (980.46 per cent)

respectively. An analysis of the performance of hybrids revealed that Purple round x Vella notchi (4 x 5) was the best with respect to number of fruits, total yield and life span. It is interesting to note that the same hybrid was the most heterotic one for number, girth and size of fruit, total yield and oleoresin content. The mean number of fruits and total yield per plant were 334 and 1443.8 grammes respectively. This hybrid is also endowed with the other desirable attributes like high Vitamin A (6761 I.U), Vitamin C (307.6 mg%) and Capsaicin content (0.897%). The mean number of seeds per fruit in this hybrid is only 26.7. This is an added advantage. The rind of the fruit is thick and as such it is ideally suited as a fresh vegetable.

An examination of the general combining abilities of varieties revealed that Purple round was the best for height, number of primary branches, spread and life span in addition to being the second best for total yield, number of fruits and number of leaves. It was third in respect of characters like girth and size of fruit and Capsaicin content. Vella notchi, the second parent involved in the cross exhibited the highest gvc.s. for total yield. Further, it was the second best general combiner for weight, girth and size of fruit and Vitamin C content.

As regards Vitamin C content, Vella notchi x California wonder (5 x 8) was the best hybrid. This was

also the most heterotic hybrid for weight of fruit. These parents were better general combiners than others for the character concerned. California wonder x Purple cluster (6 x 9) was the best hybrid for early blooming and bearing. The same hybrid was the best heterotic F_1 for early blooming and low number of seeds per fruit. California wonder was the best general combiner for early blooming character as well.

Another promising hybrid was Pant C-1 x Purple cluster (6 x 9). The mean number of fruits and yield per plant were 142.6 and 162.3 g respectively. Since both the parents had erect fruiting habit, the hybrid also produced erect fruits, which enabled uniform maturity and early ripening. This hybrid has also reasonable quantities of Vitamin A, Vitamin C, Capsaicin and Oleoresin. The rind is thin and hence the fruits are suited as dry chilli. The pollen parent had fruits in clusters, and determinate growth habit. The former trait was partially inherited while the latter was fully dominant. In the hybrid Pant C-1 which is known for its resistance to leaf curl disease, was the best general combiner for number of fruits, Capsaicin and Oleoresin content. This variety along with different parental combinations produced the best hybrids for the characters like, height, number of primary branches, spread and Capsaicin content. Further, Pant C-1, along

with other varieties produced the most heterotic hybrid for characters like height, secondary branches and spread. The variety, Purple cluster showed the highest g.c.a. for Vitamin A content and along with different combinations produced the best F_1 with respect to early blooming and low number of seeds. In addition, purple cluster produced the most heterotic F_1's in different combinations for length of fruit, Vitamin C content, early blooming and low seeds per fruit. The lower Capsaicin content in hybrids might be due to the higher Vitamin C content. Such inverse relationship was earlier reported by Nair and George (1973). The apparent reduction of Vitamin A in hybrids can be ascribed to the higher pungency as suggested by Lee et al. (1973). The very low increase of carotene in hybrids was in agreement with the observations of Duczek, et al. (1970). The two hybrids namely, Purple round x Vella mothi and Pant C-1 x Purple cluster had an added advantage of not being susceptible to leaf curl complex virus disease which is one of the menaces faced by chilli growers.

The analysis of variance for combining ability indicated that the variances due to both g.c.a. and s.c.a. effects were significant for all the eighteen characters studied. However, the g.c.a. component of variance was higher than the s.c.a. component indicating that the additive type of gene action was more predominant than the non additive type for those characters. This observation

is in conformity with the findings of Milkova (1978); Singh and Singh (1976a) and Soh et al. (1976). Singh and Singh (1976) after an elaborate study of 8 Capsicum annuum lines for two years observed that both general and specific combining ability effects were significant for the characters, the g.c.a. effect however was larger. Singh and Singh (1978) in a cross involving sixteen widely variable lines with four pollen parents recorded that specific combining ability variances were greater than that for g.c.a. for the characters studied, except fruit yield. They further suggested that reciprocal recurrent selection be adopted for yield improvement. The inconsistency in the results may be attributable to the difference in the varieties investigated. The present study enabled to identify best general combiners for each of the eighteen characters investigated. Purple round was the best general combiner for height, primary branches, spread and life span, while California wonder was the best general combiner for six attributes namely weight, length, girth and size of fruit, number of seeds per fruit and Vitamin C content. As regards total yield Vella notchi was the best general combiner. Pant C-1 which is tolerent to leaf curl complex was found to be the best general combiner with respect to three traits namely number of fruits, capsaicin and oleoresin content. As far as secondary branches are concerned Pusa jwala was found to be the best general

combiner.

An examination of the results indicate that the best performing F_1's are not always the most heterotic ones as reported by Balachandran (1976) in tomatoes. However a critical perusal of the results reveal that in many instances one or both the parents involved in the best performing F_1's topped the list in the g.c.a. analysis for the character in question. High yielding parents were found to have high general combining abilities as indicated by Gill et al. (1973). Reports wherein good general combiners have given rise to best performing F_1 hybrids have been made by Singh (1971) and Mohanakumaran et al. (1973) in Cauliflower and Balachandran (1976) in tomato. For attaining high s.c.a. values the parents involved should have high g.c.a. values as suggested by Singh et al. (1972) in tomatoes. Earlier, Hays and Johnson (1939) had observed such beneficial effects of selecting good general combiners in a heterosis breeding programme in sweet corn. In certain hybrid combinations the s_{ij} effects have contributed to the maximum heterosis observed. This can be expected and such observation have been reported by Singh and Singh (1978) in Gossipium arnuum and Khalf-allah (1970) Svanosino and Vendoni (1974) and Milkova (1976) in tomatoes.

5. Gene action

The diallel analysis revealed a clear case of over dominance in eleven characters and partial dominance in six

characters and one character exhibiting partial or no dominance. As advocated by Jinks and Hayman (1953) the interacting arrays were omitted to satisfy the hypotheses. In five characters, namely, number of primary branches, number of secondary branches, Vitamin C, Capsaicin and Oleoresin content, even after omitting a maximum of 3 parents none of the sub-diallel analyses satisfied the assumptions and as such the one which was nearer to the satisfactory proposition was selected for further studies. However, the results of graphical analysis were found to agree with the results of numerical approach. In cases where over-dominance was observed in the V_r, W_r graph, the same was confirmed by the higher magnitude of components of variation, $\hat{H}_1$ and also by the value of average degree of dominance. Likewise, the partial dominance was confirmed by the higher magnitude of components of variation, $\hat{D}$ and also by the value of average degree of dominance.

Epistatic gene effects were observed in eleven characters while four characters displayed additive gene action. In three characters, both additive and non-additive type of gene effects were prominent. The role of epistatic gene action in major characteristics of chilli was emphasised by Scossiroli et al. (1974). Where additive and non-additive gene action were noticed they were reflected in higher g.c.a. and s.c.a. effects, respectively. These observations were in agreement with the earlier findings that both g.c.a.

and s.c.a. effects were significant indicating the importance of both additive and non-additive variances (Singh and Singh, 1976; 1976). The inheritance of characters involving non additive gene action possessing high estimated values for specific combining ability was reported by Gill et al. (1973). Complementary type of gene action was revealed in most of the characters under study.

The graphical analysis was helpful in identifying the parents with excess of dominant genes for the various characters under study. The parent, Purple round (4) which was a good general combiner has predominance of dominant genes for height, number of primary branches, long life span, medium Vitamin A and C contents. Vella notchi (5) another good general combiner possessed an excess of dominant genes for larger number of secondary branches, medium number of fruits, medium Vitamin A and higher Vitamin C content. California wonder (8) possessed dominant genes for medium number of leaves and medium yield while Purple cluster (9) had predominance of dominant genes for medium number of leaves, life span, higher Vitamin A, and medium Oleoresin content. Dominant genes for medium number of leaves, medium spread and medium yield predominated in Pant C-1.

6. Genetic improvement through heterosis exploitation

It is evident from the above discussion that the varieties Purple round (4), Vella notchi (5), Pant C-1 (6)

and Purple cluster (9) show considerable promise in the heterosis breeding programme. The hybrid combination Purple round x Vella notchi (4 x 5) has proved to be the best with respect to many characteristics. Further, Vella notchi (5) in combination with California wonder (8) has given to best hybrid for Vitamin C content. Although the hybrid combinations Pant C-1 x Purple cluster (6 x 9) did not figure in any of the best performing ones it deserves mention because of its desirable traits described earlier.

Since considerable heterosis was evident for most of the important vegetative, fruiting, nutritive and quality attributes, heterosis breeding may be a worthwhile proposition in Capsicum annuum. A review of literature available on the subject has revealed identical opinions from various quarters (Deshpande, 1953; Greenleaf, 1947; Gill et al., 1973; Bak et al., 1975; Allah et al., 1975; Lippert, 1975; Alpatev and Khrenova, 1976; Singh and Singh, 1976; Popova and Mikhailov, 1976 and Studentsova, 1976. However in a self pollinated crop like Capsicum annuum the production of F_1 hybrid seeds poses obvious problems. One of the problems leading to the high cost of production of F_1 seeds is the labour involved in hand emasculation and hand pollination. Another difficulty could be the poor setting percentage in artificial pollinations. But all these difficulties are negligible when the high yield potential of the hybrid crop is considered.

The task of hand emasculation and hand pollination can be obviated by employing male-sterile lines. Novak and Betlach (1973), Shifriss (1973), Dikii (1976), Dackaloff (1974), Hirose and Fujima (1975) have reported the occurrence of male sterility in Capsicum annuum. This may be taken advantage of to produce hybrid seeds in large scale with a competitive reduction in the cost of seeds. Promising heterotic hybrids in Capsicum annuum were produced by Dackalov (1973) and Dekii (1976) by employing male sterile lines.

Summing up, high heritability was observed with respect to most of the traits under study which suggested more number of fixable genes for the characters concerned. High heritability, followed by low genetic advance indicating epistatic gene action was evident in some characters and in six instances this was confirmed and reflected clearly in high s.c.a. effects.

The cause effect relationship as exploited by path coefficient analysis emphasised that the primary traits influencing yield in Capsicum annuum directly and indirectly are number of fruits, number of secondary branches, girth of fruit, weight of individual fruit and life span. This was clearly reflected in the best performing hybrid namely

Purple round x Vella mothi. High genetic diversity was present between the clusters of varieties as indicated by D^2 values. The nine parent diallel attempted to, has unveiled considerable amount of heterosis in many of the vegetative, fruiting, nutritive and quality attributes. Ample diversity was evident between the parents, with regard to each of the eighteen characters studied, as revealed by the wide scattering of array points in the graphical analysis. Epistatic gene action of a complementary type was evident in many of the characters examined. Four general combiners of economic importance were identified. The possibilities of commercial exploitation of two hybrids, namely Purple round x Vella mothi (4 x 5) and Pant C-1 x Purple cluster (6 x 9) deserve to be explored further. These two hybrids are endowed with desirable yield potential coupled with nutritive attributes namely higher Vitamin A, Vitamin C, Capsaicin and Oleoresin content. The former can be utilised as a fresh vegetable while the latter is suited for dry chilli.

The present study enabled to identify best general combiners for each of the eighteen characters investigated. Purple round was the best general combiner for height, primary branches, spread and life span while California wonder was the best general combiner for six attributes

like weight, length, girth, size of fruit, number of seeds and Vitamin C content. As regards total yield, Vella notchi was the best general combiner. Pant C-1 which is tolerent to leaf curl complex was the best general combiner with respect to three traits namely number of fruits, Capsaicin and Oleoresin contents. As far as secondary branches are concerned Pusa jwala was the best general combiner.

An examination of the results indicate that the best performing F_1's are not always the most heterotic ones as reported by Balachandran (1978) in tomatoes. However a critical perusal of the results reveal that in many instances one or both of the parents involved in the best performing F_1's topped the list in the g.c.a. analysis for the character in question. High yielding parents were found to have high general combining abilities as indicated by Gill et al. (1973).

SUMMARY

SUMMARY

Comprehensive genetic studies including the estimation of genetic parameters, cause effect relationship by path coefficient analysis and genetic divergence by Mahalanobis' D^2 statistic were undertaken in Capsicum annuum. A nine parent diallel analysis was also attempted to assess the combining ability of varieties, the pattern of inheritance and the degrees of heterosis manifested by eighteen economic characters including four nutritive and quality attributes namely Vitamin A, Vitamin C, Capsaicin and Oleoresin content. The study was conducted in the Department of Agricultural Botany, College of Agriculture, Vellayani, during 1976-'79.

Sixty three varieties collected from the different agroclimatic regions of the country formed the base material of the study. Based on their adaptation, performance and disease tolerance, thirty varieties were selected for further studies. The cause effect relationship was estimated by path analysis. Genetic divergence among the varieties was computed by Mahalanobis' D^2 statistic. Height, spread, number of primary branches, number of secondary branches, number of days taken for blooming, number of fruits, weight of fruits, life span, number of seeds, length of fruit, girth of fruit, total yield,

Vitamin A, Vitamin C and Capsaicin content were taken into account for the estimation of genetic divergence.

Estimation of the genetic parameters indicated that the environmental coefficient of variability was minimum, suggesting that the characters were less influenced by environmental factors. The phenotypic and genotypic coefficients of variation were higher for number of fruits, weight of fruit, total yield and capsaicin content. This suggests the possibility of further improvement of these characters through combination breeding. A strong positive association between the genotypic coefficient of variation and genetic advance to selection was noticed. Number of fruits with the highest genotypic coefficient of variation, has the highest estimate of genetic advance, while life span with the least genetic variability has also the least genetic advance. The phenomenon indicates that the more genetic variability present in the population, the higher will be the response to selection. The heritability values ranged from 99.92 for girth of the fruit to 70.91 for number of primary branches. High heritability was observed in all the characters studied indicating the presence of large number of fixable additive factors. In six instances, high heritability was accompanied by low genetic advance indicating non-additive gene action.

The genotypic correlation coefficients were of higher magnitude than the phenotypic correlation coefficients

in general. The number of fruits exhibited significant positive correlation with the number of primary branches, secondary branches and total yield, while it displayed significant negative correlation with number of seeds, weight and girth of fruit. The cause effect relationship elucidated by path analysis indicated that the number of fruits was the principal yield attribute. Yield in chilli can be considered as the effect of five first order components namely, number of fruits, number of secondary branches, girth and weight of individual fruit and life span which accounted for 68% of the variability in yield. The number of primary branches and spread accounted for 42% of the variability in the number of secondary branches.

There was considerable divergence between the thirty varieties selected. Out of the 435 comparisons all values except one were significant at 1% level, and the remaining one being significant at 5% level only. The thirty varieties were grouped into 16 clusters including four single variety clusters. The larger number of constellations suggested high magnitude of genetic diversity available between the varieties. Closer genetic reletionship was prevalent within clusters, while between clusters the relationship was wider. The grouping was confirmed by canonical analysis. The genetic diversity was found to agree with the geographical distribution of varieties. Based on the informations unveiled from these analysis,

nine varieties were selected and selfed. The inbreds were crossed in all possible combinations and a diallel set without reciprocals obtained. Eighteen characters such as height, number of primary branches, number of secondary branches, number of leaves, spread, number of days taken for blooming, number of fruits, weight of fruit, length of fruit, girth of fruit, size of fruit, number of seeds per fruit, total yield, life span, Vitamin A, Vitamin C, Capsaicin and Oleoresin content were studied for the estimation of heterosis, combining abilities and gene action.

Hybrid vigour was manifested in respect of thirteen traits out of the eighteen vegetative, fruiting, nutritive and quality characters studied. The phenomenon of positive heterosis was negligible in five characters namely, weight, length, girth and size of fruit and number of seeds per fruit. There was wide variation in the range of heterosis. As much as 1488.04 per cent positive heterosis was observed with respect to number of leaves while as regards to total yield, maximum hybrid vigour observed was 1366.51 per cent (Purple round x Vella notchi). Appreciable amount of hybrid vigour was present in respect of Vitamin C, Capsaicin and Oleoresin content. The reduction in Vitamin C content in certain hybrid combinations is ascribed to the higher Capsaicin content. Likewise an inverse relationship of Capsaicin and Vitamin A content was also observed. The studies thus revealed that heterosis breeding is of paramount importance in the genetic improvement of this crop.

The varieties which showed maximum g.c.a. for the different characters were identified. Purple round was the best general combiner for height, number of primary branches, spread and life span. Further it was the second best general combiner for number of leaves, number of fruits and total yield. Vella notchi, topped in g.c.a. for total yield in addition to its being the second best for weight, girth and size of fruit and Vitamin C content. Pant C-1 which is known for its resistance to leaf curl disease was the best general combiner for number of fruits, Capsaicin and Oleoresin content. It was the second best general combiner for spread of plant. Pant C-1 and Purple cluster both with erect fruiting habit produced the second best hybrid. California wonder was the best general combiner for six traits namely weight, length, girth and size of fruit, number of seeds and Vitamin C content.

In most of the characters studied the varieties with high g.c.a. effects gave rise to the best performing F_1's. But the best performing F_1's were not always the most heterotic F_1's.

Over dominance was exhibited by eleven out of eighteen characters studied. Epistasis was pronounced in eleven characters and it was mostly of complementary type. Additive gene effects were noticed in weight, girth and size of fruits and number of leaves, suggesting the possibility for improving these characters by selection.

Graphical analysis has revealed that the variety Purple round which was a good general combiner has predominance of dominant genes for height, number of primary branches, long life span, medium Vitamin A and C content. While Vella notchi, another good general combiner possessed an excess of dominant genes for number of secondary branches, number of fruits, Vitamin A and Vitamin C content. California wonder possessed dominant genes for medium number of leaves and medium yield while purple cluster had predominance of dominant genes for medium number of leaves, life span, higher Vitamin A and medium Oleoresin content. Dominant genes for medium number of leaves, medium spread and medium yield predominated in Pant C-1.

Summing up, the study revealed that heterosis breeding programme can go a long way in bringing about improvements in Capsicum annuum. It further points towards the possibilities of commercial exploration of hybrids with high yield potential coupled with nutritive and quality attributes. Purple round and Vella notchi, both good general combiners for total yield have produced the hybrid with highest yield of 1443.8 g of fruits per plant (The hybrid vigour over better parent was 1246.83 per cent). Besides, this hybrid is bestowed with desirable economic attributes like enhanced number of fruits (334), less number of seeds (26.7), long life span (230.2 days),

higher Vitamin C (307.6 mg per cent) and Capsaicin (0.80 per cent) content. This hybrid having thick rind is ideal for use as fresh vegetable. The second promising hybrid combination is Pant C-1 x Purple cluster, which produced a total number of 142.8 fruits, yield of 162.5 g with a life span of 194.3 days. Other highlights of this hybrid include 8162.9 I.U. of Vitamin A and 139.7 mg per cent, Vitamin C, 0.426 per cent Capsaicin and 14.9 per cent Oleoresin content. An added advantage of this variety is the erect fruiting habit similar to its parents which enables uniform maturity and ripening. Since the rind is thin, unlike the former one, this hybrid is suited for use as dry chilli. Both these hybrids were found to be tolerant to the dreadful disease of leaf curl which has been posing a formidable problem to the chilli growers. The percentage of fruit set would be more when the method of hand emasculation and pollination are standardised and perfected. The high cost of hybrid seed production will be offset by the high yield potential of hybrid progeny. Exploration of functional male sterile lines with good general combining abilities is worthtrying.

Single plant selection employing pedigree method of breeding is suggested from the cross combinations of Purple round x Vella notchi, Pant C-1 x Purple cluster, CA-1068 x Vella notchi, G4 x Pusa jwala, Purple round x Pant C-1 and Vella notchi x Pusa jwala. Since additive and

non additive components of variation were found significant, a recurrent selection would provide ample improvements to the characters concerned. These are suggested as future lines of work.

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*Original not seen

APPENDIX

Appendix I

D^2 values between different varieties

	V_1	V_2	V_3	V_4	V_5	V_6	V_7	V_8	V_9	V_{10}	V_{11}	V_{12}	V_{13}	V_{14}	V_{15}	V_{16}	V_{17}	V_{18}
V_1		13105.9	4828.2	8609.5	3231.9	1585.1	2528.8	3619.2	7770.0	1128.0	3472.1	4036.7	3698.5	4470.9	3457.8	21682.5	17976.8	2647.9
V_2			9473.2	10192.7	6427.4	16970.3	14082.1	7982.3	8779.6	16543.2	6400.5	6886.7	7807.2	7423.8	11518.0	47713.0	45171.6	10231.6
V_3				4941.1	3376.6	9543.7	6206.2	1192.1	3378.4	8656.9	5726.4	3118.3	4658.3	699.9	963.4	37452.1	33932.4	11454.8
V_4					9153.5	11557.5	11169.8	3053.7	6572.2	11476.6	9685.7	4295.0	11976.8	5301.4	3795.5	36304.2	33915.9	14894.6
V_5						5680.5	4510.5	3321.8	6819.5	5553.5	1436.6	4042.2	582.8	2742.7	4842.1	32692.0	28454.3	6209.9
V_6							3271.3	7839.1	12557.9	805.4	5274.0	7585.6	6535.6	9373.9	7366.6	19068.1	11686.4	657.9
V_7								6096.8	12324.9	3675.8	7094.3	8897.9	5501.9	8096.5	5514.2	16329.6	14089.3	4463.9
V_8									5326.2	7281.8	4813.2	1919.2	4701.6	765.2	836.6	36170.6	32803.2	10854.7
V_9										11205.5	5795.0	1891.6	7031.5	2198.4	3488.9	45707.2	40947.3	15151.8
V_{10}											4356.1	6154.9	5668.9	6042.9	6467.2	17007.0	13522.2	1248.3
V_{11}												2578.7	1371.9	3966.1	6383.5	33432.0	28249.0	5459.4
V_{12}													4607.2	1691.4	2607.6	30246.8	25324.9	9507.6
V_{13}														3399.9	6165.5	35153.6	30367.7	6755.2
V_{14}															1236.4	40096.7	35960.9	11574.0
V_{15}																32557.6	29423.0	9993.4
V_{16}																498.1	14369.5	
V_{17}																	10765.2	
V_{18}																		
V_{19}																		
V_{20}																		
V_{21}																		
V_{22}																		
V_{23}																		
V_{24}																		
V_{25}																		
V_{26}																		
V_{27}																		
V_{28}																		
V_{29}																		
V_{30}																		

*Significant at 5% level

All other values are significant at 1% level

V_{19}	V_{20}	V_{21}	V_{22}	V_{23}	V_{24}	V_{25}	V_{26}	V_{27}	V_{28}	V_{29}	V_{30}
2302.8	2572.8	2862.2	2051.8	5506.4	14029.0	945.4	857.5	5191.0	4049.3	4213.0	5392.0
9222.3	9036.3	6579.2	13067.3	7470.0	14679.1	15917.0	15360.9	6127.8	6560.0	6822.4	6843.7
4467.2	5269.4	2829.9	5332.8	6057.5	10043.6	7080.2	7370.1	2967.4	3401.4	3674.8	3693.6
11664.8	10104.8	7644.8	8344.1	10950.3	15696.3	10000.6	10369.3	8736.2	10316.0	10769.3	10276.9
625.7	787.8	477.6	4040.2	1358.4	10712.3	4090.3	4604.9	352.6	348.2	326.0	223.4
4290.8	4863.8	5248.2	2265.2	4919.9	13589.3	575.4	531.6	6229.9	7377.8	7258.2	6158.7
3134.9	2752.0	3137.5	1301.8	6852.3	10211.5	5567.6	5129.3	5273.5	5163.5	5417.0	5001.8
4697.9	3813.4	2520.9	5161.8	5440.29	12478.5	6774.9	6978.8	2828.3	3595.50	4070.32	3878.2
6331.7	7408.7	6598.6	10038.0	6669.1	10611.6	10553.2	10220.6	4895.5	6843.5	7043.1	6974.5
4401.7	4286.7	5457.6	2148.6	4217.3	16035.2	217.6	231.1	5702.3	6940.4	7012.6	5812.9
2170.6	2509.3	2425.8	4969.9	138.8	12462.3	4166.4	3955.1	1194.2	2079.2	1951.3	1496.3
5526.6	4816.8	4016.3	5974.4	3321.0	13894.9	5960.2	5795.6	5111.2	4704.5	4910.8	4957.5
795.7	764.3	1256.2	4640.5	1094.9	12522.3	5552.2	5158.1	769.9	520.3	542.9	409.4
4006.9	2945.7	2426.1	5726.6	4499.8	10906.5	7659.8	7215.9	2032.1	2645.5	3045.2	3026.2
5590.7	4245.1	3824.1	4383.2	6903.2	11953.6	5948.0	5594.9	4218.6	5212.2	5670.8	5340.9
20477.5	20495.4	30577.7	16361.8	32809.5	33721.9	16846.5	16857.0	34421.2	33510.6	33406.9	33601.6
24384.3	24717.3	26874.1	15492.8	27586.8	31556.2	13301.3	13362.9	30053.5	31278.7	31078.9	29233.8
4648.07	5518.1	6575.3	3373.5	4878.8	16979.8	890.6	884.8	7017.6	7973.1	7648.4	6478.2
	498.72	858.1	3508.1	1759.4	10760.9	3884.7	3524.5	877.2	736.3	678.3	514.0
		774.2	2467.7	2049.3	9276.6	4028.7	3568.5	950.6	797.8	835.3	720.9
			2894.3	2401.2	9263.6	5037.9	4565.3	796.8	722.2	841.6	748.70
				4852.2	10002.4	2372.7	1971.6	4746.5	5150.2	5316.3	4619.1
					12578.9	3987.0	3769.1	1196.6	1900.9	1692.6	1242.6
						15373.9	14518.9	9891.2	10524.9	10466.4	11012.0
							25.48°	5096.7	6376.7	6338.4	5217.8
								4746.2	5921.4	5891.7	4858.9
									503.4	523.4	258.4
										54.7	139.41
											82.94

PLATE NO. I

Purple round - Best general combiner for height, number of primary branches, spread and life span. Also second best general combiner for total yield, number of fruits and number of leaves.

PLATE NO. I

Purple round - Best general combiner for height, number of primary branches, spread and life span. Also second best general combiner for total yield, number of fruits and number of leaves.

PLATE NO. II

Vella notchi - The best general combiner for total yield and the second best general combiner for weight, girth and size of fruit and Vitamin C content.

PLATE NO. III

Purple round x Vella notchi - The most heterotic
number of fruits, girth and size of fruit, total
and Oleoresin content.

PLATE NO. V

Purple cluster - The best general combiner for Vitamin A content.

PLATE NO. IV

Pant C-1 - Resistant to leaf curl disease. Best general combiner for number of fruits, Capsaicin and Oleoresin content.

PLATE NO. VI

Pant C-1 x Purple cluster - The hybrid with erect fruiting habit.

ABSTRACT

Sixty three varieties of Capsicum annuum representing different agroclimatic regions of the country constituted the base material of the study. Based on yield potential, adaptability and tolerance to leaf curl complex disease, thirty varieties were selected for subsequent studies.

Comprehensive genetic studies including estimation of genetic parameters, cause effect relationship by path coefficient analysis, genetic divergence by Mahalanobis' D^2 statistic and a nine parent diallel analysis to assess the combining ability, to unravel the pattern of inheritance and also to examine the level of heterosis manifested with respect to eighteen economic characters including four nutritive and quality attributes namely Vitamin A, Vitamin C, Capsaicin and Oleoresin content were conducted during the year 1976-'79.

Analysis of plot means exhibited highly significant differences among varieties except for Capsaicin content. The high degree of variability in economic attributes offers scope for recombining desirable genes from different varieties.

The number of fruits exhibited significant positive correlation with primary branches, secondary branches and total yield, while it showed significant negative correlation with number of seeds, weight and girth of fruit. Vitamin C content displayed significant positive correlation with weight of fruit, number of seeds, length and girth of fruit but exhibited significant negative correlation with number of

days taken for blooming and life span. Capsaicin content manifested significant negative correlation with number of seeds, weight of fruit and Vitamin C content. Path coefficient analysis revealed that the number of fruits, number of secondary branches, girth and weight of individual fruit and life span were the important traits directly and indirectly influencing yield.

Considerable amount of genetic divergence was present in the thirty varieties selected. They were grouped into sixteen clusters including four single variety clusters. The divergence between different clusters was not always due to divergence in the same set of characters, but a combination of different sets of characters. The genetic diversity was found to be following geographical distribution. Based on the informations unveiled from these analysis, nine parents were selected and selfed. The inbreds were crossed in all possible combinations and a diallel set without reciprocals obtained.

There was wide variation in the range of heterosis. Positive heterosis was manifested in thirteen out of eighteen vegetative, fruiting, nutritive and quality attributes studied. As regards total yield, maximum hybrid vigour observed was 1366.51 per cent (Purple round x Vella nothi). Vitamin C, Capsaicin and Oleoresin content displayed appreciable amount of hybrid vigour, while there was negligible positive heterosis with respect to Vitamin A

content. The reduction in Vitamin C content in certain hybrid combinations is ascribed to the higher Capsaicin content. The studies revealed that heterosis breeding has pivotal role for effecting genetic improvement in this crop.

The best general combiners were identified. The variety Purple round was the best general combiner for many of the important economic attributes namely, number of primary branches, spread and life span. It was also the second best general combiner for number of leaves, number of fruits and total yield. As far as total yield is concerned the variety Vella notchi was the best general combiner. The same parent was the second best general combiner for weight, girth, size and Vitamin C content of fruit. Pant C-1, the leaf curl resistant variety was the best general combiner for number of fruits, Capsaicin and Oleoresin content. In most of the characters studied, the parents with high g.c.a. effects gave rise to best performing F_1s. But the best performing F_1s were not always the most heterotic F_1s.

Gene action relating to different characteristics was studied. Both graphical and numerical approaches were attempted to. The inheritance of characters revealed that over dominance was present in eleven out of eighteen characters studied. Epistasis was pronounced in eleven characters and it was mostly of complementary nature.

The studies unravelled that heterosis breeding has a paramount potential in augmenting genetic improvement in Capsicum annuum. The possibilities of exploring avenues in commercial production of hybrids with high yield potential coupled with nutritive and quality attributes are immense. The present study has identified two promising hybrids. Purple round x Vella notchi, both good general combiners for total yield have produced the hybrid with an yield of 1443.7 g of fresh fruits per plant. Besides, the hybrid is endowed with desirable economic attributes like more number of fruits (334), less number of seeds (26.7), long life span (230.2 days), higher Vitamin C (307.6 mg %), and Capsaicin (0.89%) contents. The hybrid being thick rinded is ideally suited as a fresh vegetable.

The second promising hybrid combination is Pant C-1 x Purple cluster, which produced an yield of 162.3 g and 142.8 number of fruits with a life span of 194.3 days. This hybrid has erect fruits similar to its parents and the added advantages include 8162.9 I.U. of Vitamin A and 139.7 mg % Vitamin C, 0.426% Capsaicin and 14.9% Oleoresin content. The other promising hybrids along with the aforementioned two hybrids open new vistas in identifying further elite types by single plant selection employing pedigree method of breeding.