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Studies of Genotype-Environment Interaction in Rice (Oryza Sativa L.)

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STUDIES OF GENOTYPE-ENVIRONMENT INTERACTION IN RICE (*Oryza sativa* L.)

A THESIS
SUBMITTED TO THE UNIVERSITY OF RAJSHAHI
TOWARDS THE FULFILMENT OF THE REQUIREMENTS
FOR THE DEGREE OF
MASTER OF PHILOSOPHY

BY
MOHD. MOSLEMUDDIN, M.Sc.

NOVEMBER, 1979

DEPARTMENT OF BOTANY
UNIVERSITY OF RAJSHAHI
BANGLADESH

DECLARATION

I hereby declare that the entire work now submitted as a thesis towards the fulfilment for the degree of Master of Philosophy at the University of Rajshahi is the results of my own investigation. I further certify that the work embodied in this thesis has not been concurrently submitted as candidature for any degree.

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Author

STUDIES OF GENOTYPE - ENVIRONMENT INTERACTION IN RICE (*Oryza sativa* L.)

(ABSTRACT)

Genotype-environment interaction of some agronomical characters including yield of eight inbred lines and some segregating generations of rice (*Oryza sativa* L.) was studied. The inbred lines consisted of three local and five exotic varieties such as Naizersail, Badshabhog, Kataribhog, Chinese, IR-8, IR-532, IR-20 and IR-5 and F_2 generations of five crosses made between tall and dwarf varieties were Chinese X Kataribhog, IR-8 X Chinese, IR-20 X Kataribhog, Chinese X Naizersail and IR-8 X Kataribhog.

The eight inbred lines were grown under eight different nutritional treatments of presence and absence of N, P and K fertilizers in pots during 1977 for season I and during 1978 for season II. Each experiment had three replications consisting two pots per variety and per dose of nutritional treatment under each replication and they were randomly arranged under direct sunlight. Five F_2 families and their five parents were also grown in 1978 under the same eight nutritional treatments having six replications for each treatment.

Due to the unavailability of data on yield and yield components for the three local varieties during season II, the data were grouped into the following four categories for analysis.

A. Yield and yield components of eight parental lines for season I.

B. Yield and yield components and some morphological and developmental characters of five parental lines for seasons I and II.

C. Morphological and developmental characters of eight parental lines for seasons I and II.

D. Yield and yield components of five F_2's and their five parents.

The data were collected on length of panicle, primary branches/panicle, spikelet number/panicle, kernel number/panicle, 100 kernel weight, yield/plant, tiller number, fresh shoot weight, dry shoot weight, fresh root weight, dry root weight and plant height. The data were then analysed following the techniques equivalent to those developed by Yates and Cochran (1938), Mather and Jones (1958), Finlay and Wilkinson (1963), Eberhart and Russell (1966), Bucio Alanis (1966), Bucio Alanis and Hill (1966), Perkins and Jinks(1968a), Bucio Alanis et al. (1969) and Breese (1969).

Genotype-environment interactions were found to operate in both parental lines and F_2 families. Greater portion of G X E interaction effects was accounted by the linear function of the environmental mean, although a significant part of the G X E effects was non-linear in nature. Both the linear and non-linear components of G X E effects were under the control of different gene systems. A great genetic diversity was observed in genotypes investigated.

As regards the effects of individual nutrition, N had the largest single effect on most of the characters. N, P and NP significantly increased the yield performances for all the varieties and the F_2's. Among the F_2's IR-8 X Mataribhog gave the highest yield performances. K had no effect on yield. High and low genotypic as well as environmental variations were found in the characters investigated.

The genotypes had varied responses to different environments. F_2 families were more responsive to the environments than those of their parental lines. The standard error of the responses were heterogenous indicating varied stability among the genotypes. F_2 families differed from their parents with respect to the stability within an environment but the stability values varied in different characters and crosses. Association of mean ($\bar{X}$), responses (b_i) and stability ($\bar{S}^2_d$) was present in some characters and absent in others. When they (b_i as well as $\bar{S}^2_d$) were examined between characters, they were found to be associated in some combinations while in other combinations no association was noted.

Significant dominant and additive effects were indicated in controlling the mean expression of these characters studied. Both dominant and additive components of variation interacted with the environment but they were of different function of the environmental means and were under different gene systems. Potence ratios were high in poor environments and low in good environments in some characters and in others the reverse was true.

Mohd. Moslemuddin

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CONTENTS

		Page
INTRODUCTION	...	1
REVIEW OF LITERATURE	...	6
MATERIALS AND METHODS	...	14
A. MATERIALS	...	14
B. METHODS	...	15
RESULTS	...	19
A. GXE INTERACTION OF YIELD AND YIELD COMPONENTS OF EIGHT-PARENTAL LINES OF RICE FOR SEASON. I.	...	19
(a) Means and Relative Importance to Different Nutrients	...	20
(b) Variability	...	26
(c) Regression	...	28
(d) Correlation	...	41
B. GXE INTERACTION OF YIELD AND YIELD COMPONENTS AND SOME MORPHOLOGICAL AND DEVELOPMENTAL CHARACTERS OF FIVE PARENTAL LINES OF RICE FOR SEASON I AND II.		57
(a) Means and Relative Importance to Different Nutrients	...	58
(b) Variability	...	67
(c) Regression	...	69
(d) Correlation	...	85
C. GXE INTERACTION OF SOME MORPHOLOGICAL AND DEVELOPMENTAL CHARACTERS OF EIGHT PARENTAL LINES OF RICE FOR SEASON I AND II.		107
(a) Means and Relative Importance to Different Nutrients	...	108
(b) Variability	...	112
(c) Regression	...	113
(d) Correlation	...	122

Page

D. GXE INTERACTION OF YIELD AND YIELD COMPONENTS OF $5F_2$S AND THEIR 5-PARENTS OF RICE. ... 136

(a) Means and Relative Importance to Different Nutrients ... 137

(b) Variability ... 141

(c) Regression ... 142

(d) Correlation ... 154

(e) Genetic Parameters ... 156

(i) Partition of Variation 156

(ii) Potence Ratio ... 168

DISCUSSION ... 189

SUMMARY ... 198

REFERENCES ... 200

INTRODUCTION

Rice is the principal food for more than half of the total human population of the world. About nine-tenths of the world's rice is produced and consumed in South and Southeast Asia, which contains over 90 percent of the total rice growing area excluding the mainland of China (Parthasarathy, 1972). Though this part of the world includes the major rice growing countries, some of the countries like Bangladesh and India face acute food shortage each year.

Based on geographic adaptation and morphological characters, the cultivated rice of the world can be broadly divided into three varietal groups; indica, japonica and javanica (Chandraratna, 1964; Chang, 1964; Chang and Bardenas, 1965 and Richharia, 1960). The japonica group includes varieties from Japan, Korea and Northern China. The indicas includes varieties from India, Southern China, Taiwan, Ceylon, Java and other regions. The Javanicas include a small number of varieties from Indonesia.

It was realized in the tropical Asia only in 1950 that the use of fertilizer has a direct role on rice yield. Research projects were started on variety-fertilizer response on indicas, on indica-japonica hybrids and on variety-fertilizer interaction in indicas and others during the period 1950-59 with the incentives of IRC. Baba (1954) pointed out that the varieties highly responsive of fertilizer invariably had short straw with short panicles and profuse tillering. The grain-to-straw ratio declined in low responsive varieties, but was relatively constant in highly responsive varieties. Of course several reports indicated negative results in the variety-fertilizer interaction (IRC, 1957, 1960). Two important features were pointed out on the fertilizer

response in the indicas : one was that Indicas responded least to nitrogen applied two months before harvest, whereas Japonicas responded significantly to nitrogen applied at any stage of their growth; the second feature was that there was a good chance of indentifying highly responsive varieties in crosses among indicas (Parthasarathy, 1972).

Genetic information on the inheritance of quantitative characters required to prepare effective and meaningful breeding programmes on rice was hardly known before the 1960's. Recently a number of works on the inheritance of quantitative characters of rice have, however, been reported by several workers (Chandraratna and Sakai, 1960; Mohamed and Hanna, 1964, 1965; Chang et al., 1965; Chang, 1967 a,b; Chang and Liu, 1967; Wu, 1968 a,b; Chang et al., 1969; Li, 1970; Li and Chang, 1970; Rahman and Eunus, 1973; Khaleque and Eunus, 1975; Khaleque et al., 1976 and others). Studies on the quantitative characters of rice become complicated when more than one environments are involved, as the change in environment is usually associated with the change in gene expression. For the improvement of the crop a breeder must have knowledge about the variability of the crop over a number of environments.

Genotype-environment interaction is the difference in response of two or more genotypes to a given change in the environment. In other words, the relative performances of different genotypes under different environments vary indicating the existence of genotype-environment interaction. The occurrence of genotype-environment interactions have long provided a major challenge to obtain a fuller understanding of the genetic control of variability. They have posed serious problems of interpretation of the evolutionary trends and have hampered the

rationalisation of policy and procedure for breeding improved variety of economic crops. Attempts to specify, estimate and correct their effects have recently met with some success. Two main approaches have been used. One is purely statistical analysis originally proposed by Yates and Cochran (1938) and used by Finlay and Wilkinson (1963) and Eberhart and Russell (1966) to detect and measure the magnitude of genotype-environmental interactions in barley and maize respectively. They did not try to show any relationship between the component of their analysis with the parameters of biometrical-genetical model. The second approach is based on fitting models which specify the contributions of genetic, environment and genotype-environmental interactions to generation means and variances. It also determines the contribution of additive, dominance and non-allelic gene action to the total genetics and interaction components. However, the most important conclusion which emerged from the analysis of data is the same for both kinds of analyses, namely, the magnitude of genotype-environment interactions is a linear function of the environmental effects (Mather and Jones, 1958; Jones and Mather, 1958; Jinks and Stevens, 1959; Bucio Alanis, 1966; Bucio Alanis and Hill, 1966).

The analysis of Yates and Cochran (1938) is applicable to any number of strains of varieties grown in any number of environments. The second analysis in its present form (Bucio Alanis, 1966; Bucio Alanis and Hill, 1966) is appropriate only to a pair of inbred lines and the generations that can be derived from an initial cross between them. This analysis, however, leads to more informative conclusions and can be used to predict across generations as well as across environments.

Perkins and Jinks (1968a) have bridged the gap between two alternative analyses. Expectation of the items in the statistical analysis of Yates and Cochran has been given in terms of standard models of genes and environmental action and genotype-environmental interaction and the analysis of Mucio Alanis was extended to cover many inbred lines and crosses among them.

The relationship of parameters used in the methods of Yates and Cochran (1938) and Finlay and Wilkinson (1963) and of Perkins and Jinks (1968a) are shown below :-

Parameter	Yates and Cochran (1938) Finlay and Wilkinson(1963) Statistics	Perkins and Jinks (1968) Statistics	Relationship
Slope	b	β	$b - 1 = \beta$
Genetic value	$\bar{Y}$	d	$\bar{Y} - d = \mu$
Grand mean	$\bar{\bar{Y}}$	μ	$\bar{\bar{Y}} = \mu$
Environment	X	E	$X - \mu = E$

Inspite of the presence of genotype-environment interaction, a breeder is trying to produce a variety with good general adaptation to the whole range of environmental and agronomic conditions of importance or to breed varieties adapted to specefic environments within which a selection programme is operating.

Genotype-environment interaction is now recognised as an important source of phenotypic variation. As it is under the control of gene, the breeders are able to select suitable genotypes in advanced generations by growing them under different environmental conditions. Knowledge about the type of genotype-environment interactions involved in populations help the plant breeders to breed and to select better virieties.

OBJECTIVE

The object of the present investigation is to study the genotype-environment interaction involving yield and yield components and some morphological and developmental characters of rice (*Oryza sativa* L.). It includes

A. GXE interaction of yield and yield components of eight parental lines of rice for season I.

B. GXE interaction of yield and yield components and some morphological and developmental characters of five parental lines of rice for seasons I and II.

C. GXE interaction of some morphological and developmental characters of eight parental lines of rice for seasons I and II.

D. GXE interaction of yield and yield components of 5 F_2S and their 5 parents.

All were investigated under eight artificially produced environments due to the presence and absence of N, P and K fertilizers and their combinations.

REVIEW OF LITERATURE

There are some papers dealing with the problems of genotype-environment interactions in various crop plants but very little is known about it in rice except the studies on variety X fertilizer interactions.

Johannsen (1909) for the first time put forward the idea of relationship between heredity and environments. According to him, the personal endowments of an individual are not solely due to genes but environments also play a significant part in determining the life situation. An investigation with beans (Phaseolus vulgaris) by Johannsen showed that seed weight in dwarf beans was the product of both heritable and non-heritable effects and the phenotypic variation in any pure line is due to environments.

Keeble and Pellow (1910) showed that height in peas was affected due to seasonal fluctuations. He also referred that caution should be taken during the collection of data from plants growing in different seasons for observing the seasonal fluctuations.

East (1915) reported that the continuous variation in the segregating generations for a quantitative character was due to both genetic and environmental effects.

Fisher (1918) for the first time developed a statistical method for partitioning variance of a quantitative character in segregating populations into its genetic and environmental components.

Hayes (1922) studied on the production of protein in Maize and suggested that low correlation could be expected whenever the expression of a character was strongly influenced by the surroundings in which the plant developed.

Smith (1944) described that the quantitative characters were g governed by a large number genes which were similar, relatively small, non-dominant and cumulative in action.

Based on the mathematical models of Fisher et al.,(1932) techniques have been developed to take into account the effects due to genotype-environment interactions (Mather, 1949, Mather and Jones, 1958; Jinks and Stevens, 1959). It involved the partitioning of the variation of quantitative data according to genetic and environmental effects and their interaction of inbred lines and their crosses in Nicotiana rustica (Bucio Alanis, 1966; Bucio Alanis and Hill, 1966; Perkins and Jinks,1968b). Here the degree of interaction has been expressed as a linear function of the effect of environment.

Lebsock and Kalton (1954), Kalton et al.,(1952) estimated environmental variance within several clonal populations. Upon analysis, these estimates exhibited a significant difference for characters controlled by genes indicating the presence of genotype X environment interactions. In the latter's studies, the environmental variance comprised two components, namely a true environmental effect and genotype X environment interaction.

Rajas and sprague (1952) studied the interaction of general and specific combining ability with locations and years for yield in Corn and found that the latter interactions were greater than the corresponding estimates involving general combining ability.

Fejer (1958) stated that the variation was not only by environmental effect but also due to genotype X environment interactions.

Matzinger et al., (1959) demonstrated the presence of large interactions of general combining ability with environment for yield in

corn, Liang (1967) for yield and other characters in Sorghum and Parods and Joshi (1970) for yield and yield components in wheat.

Finlay and Wilkinson (1963) have developed statistical techniques to compare the yield performance of a set of cereal varieties grown at several centres for several seasons. The regression of individual yield on the mean yield of all varieties for each site and season when tested for varieties and sites had a high degree of linearity and have been used as measures of adaptibility of the varieties. Similar techniques yielding similar results were reported by Yates and Cochran (1938).

Pfahler (1965) performed an experiment to demonstrate the environmental variability and genetic diversity within populations of oat and rye. He found that the performances of the varieties varied with the environments indicating the presence of genotype-environment interactions. He also noted that the variation of the populations was due to a true environmental effect and a genotype-environmental interactions.

Armstrong and Chrustie (1965) showed that the estimates of environmental variance were obtained for vegetative propagules of Orchardgrass clones. Data from vigour ratings, heading date and bloom date indicated that neither cutting regimes, nitrogen level, nor genotype affected the estimates. The results indicated that genotype X environmental interactions could be ignored in the estimation of the environmental variance.

Collins et al.(1965) showed the relationship between second ear development and genotype X environment interactions in Corn Belt Zeamays. The yield of 36 single crosses were compared statistically at 4 planting rates (8,000, 12,000, 16,000 and 20,000 plants per acre) at Ames, Ankeny and Iowa in 1961 and 1962. A comparison of the slopes the quadratic

regression lines of yield of plant populations and genotype X environmental interactions of the 3 types of crosses studied indicated that the 2 ear type corn yielded more consistently than 1 ear types when the population levels were changed.

Ree et al.(1967) studied variety X environmental interactions in rice in central and Southern Korea and found significant interaction only in variety X year in Central Korea.

Morishima et al.(1967) made an analysis of genetic variation in plant type of rice and seasonal change in genetic plant type. Genotype X season variations were studied in agronomic characters and plant type using F_3 lines from the crosses of Peta X 1-geotze, which were grown in wet and dry crop seasons. The results of variance analysis showed that variance due to genotype X season interactions was significantly large, indicating that the response to growing seasons was genetically controlled. Variation in the magnitude of seasonal differences in various characters were estimated by using the response index $R = \frac{\bar{X}_{wet} - \bar{X}_{dry}}{\bar{X}_{wet} + \bar{X}_{dry}}$. It was concluded that selection for seasonal adaptibility and high yielding capacity may be made simultaneously by using certain genetic criteria.

Ananda (1968) mentioned the relationship between variety and environment in Wheat. Variance analysis of data from trials involving 12 varieties at 4 locations for 3 years, showed variety X locality X year and variety X locality interactions to be significant, indicating that the performance of varieties varied with the environments. The interaction variances were found to decrease with the increase in the number of localities.

Kawano and Takahashi (1968) studied interrelationship between plant characters in rice and concluded that the genotype X environment interactions acted as a limiting factor for negative correlations between characters.

Baker (1969) carried on an experiment on yields of six cultivars of hard red spring wheat grown at each of nine locations in five different years to evaluate genotype X environment interactions. He concluded that all the genotype X environment interactions except genotype X year were significant and important.

Perkins (1970) worked with the final height data of a diallel set of crosses among eight inbred lines of Nicotiana rustica. The F_1S of Nicotiana rustica had an average higher performance and a higher sensitivity to environmental change than their parents. The crosses mainly responsible for the high values were those which were known to have an epistatic contributions to their generation means.

Westerman and Lawrence (1970) worked on Arabidopsis thalliana to measure the genotype X environment interactions. They mentioned that the evolutionary role of genotype X environment interactions in the population genetics of a species may take one or other of two mutually exclusive forms; the expression of a metrical character may be buffered against the environment or may vary in an adaptive manner with the environment. Westerman (1971) again worked on the same and concluded that both linear and nonlinear response of environment were controlled by additive and non-additive variation. The environmental variation was also studied by Fripp (1972), Hardwick and Wood (1972), Perkins (1974) and Jinks and Connolly (1973).

Fripp and Caten (1973) worked on Schizophyllum commune to find out the phenotype-environmental interactions. They mentioned that the relationship between the gentical system determining mean-expression and sensitivity to change in environment has been examined for dikaryotic growth rate in the Schizophyllum commune by examining the correlation between these aspects of phenotype in a population in which both were segregating simultaneously. For a collection of environments of diverse composition, a positive association was found between mean expression and linear sensitivity. The correlation was low, however, and approximately 90% of the variation in these two aspects was independent. In a more uniform set of environments, the association disappeared, demonstrating firstly that different genetical systems act in different environments; and secondly that atleast in certain circumstances mean expression and linear sensitivity were determined by separate gene systems. The association between mean expression and non-linear sensitivity also depended on the particular set of environments considered. It was concluded that the relationship between mean expression and sensitivity was markedly influenced by the environments involved, and that each combination of genotypes, environments and characters should be treated as a separate case.

Flower and Roche (1975) observed a large environmental effect when he worked on some agronomic and quality data of spring and winter wheat which was very useful for breding programms.

Khaleque (1975) worked on genotype-environment interactions for eighteen quantitative characters in a 5 x 5 diallel progenies of rice over two seasons. Joarder and Munus (1977) also made a study of genotype-environment interaction shown by heading and harvesting time

of Brassica compestris L. All of them showed that genotype-environment interactions were operative in both parental and F_2 generations and that a significant portion of these interactions was accounted for by the linear function of the environmental means. A part of the interactions were independent of this linear component. Both the linear and non-linear components were under the control of different gene systems and subjected to deminance. Interaction between the additive component and the environment was greater than that of the dominant component under different environments. The potence ratio was greater in poor environment and less in good environment in both the crops.

In 1975 Zuberi and Gale worked on the effect of soil nutrients on the expression of eleven metrical traits of Vavaver dubium and observed significant effect of all nutrients and Ca had the greatest single effect. Both linear and non-linear relationship between genotype-environment interactions and environmental mean were found for all traits.

Byth et al.(1976) worked on yield characters of forty nine wheat cultivars grown in each of sixty three international environments to study the genotype-environment interaction. Two-way pattern analysis using numerical classification defined separately groups of cultivars and groups of environments based on similarities in yield performance. The pattern analysis also provided useful means of studying the yield performance of cultivars over large set of environments, summerizing the data effectively in terms of similarities of mean yield or pattern of response. Mungomery et al.(1974) showed similar results for seed yield and protein percentage in soybeans.

Lin et al.(1977) presented a model combining features of Griffing's diallel cross analysis with regression analysis for

genotype-environment interactions using carp data of Moav et al.(1975). An analysis of variance based on this model provided information on the combining abilities of genetic effects and the interactions of these effects with environments from which inferences can readily be made on heterosis and heterosis-environment interactions.

Kayastha and Heyne (1978) worked with five resistant susceptible population of winter wheat (Triticum aestivum L.) and the susceptible cultivar 'Eagle' were grown in Kansas in 13 environments to evaluate their performance in different environmental conditions and to examine the usefulness of regression approach for environments. All the populations evaluated in the infected and un-infested environments exhibited a wide range of stability parameter estimates and the individual mean yield was important for interpreting the regression co-efficient and deviation from regression. Genotype X environment interactions was detected significantly in those genotypes and environments. Frey (1964) in Oats (Avena sativa L.) and St. Pierree et al.(1967) in barley also reported similar kind of results.

Francis et al.(1978) showed interactions of genotypes of bush beans (Phaseolus vulgaris L.) with planting system and croping season and evaluated it on the CIAT Station at 1000m elevation in Colombia . Significant correlations of bean yields were obtained for these cultivars grown in monocluture and in association with maize. Season X cultivar interactions in either system could complicate selection and rapid elimination of large numbers of progeny in a breeding programme. Baker (1974) explored cultivar X System interactions in Sorghum and found similar ranking of yields of four cultivars in monoculture. Finlay (1974) worked with twelve Soybean varieties and reported similar results.

MATERIALS AND METHODS

A. MATERIALS

The materials used consisted of eight rice varieties (three local and five exotic) and F_2 generations of five crosses made between five tall and dwarf varieties. The varieties and their characters were as follows :

1. Naizersail (local):- Plant tall, length and breadth of flag leaf moderate, leaf below flag leaf very long and narrow, leaves droop at maturity, susceptible to lodging and disease, highly photosensitive and yield moderate.
2. Badshabhog (local) :- Plant tall, long and narrow flag leaf and leaf below flag leaf, susceptible to lodging and disease, photosensitive and yield moderate.
3. Kataribhog (local) :- Plant tall, flag leaf moderately long and narrow, leaf below flag leaf long and narrow, leaves droop at maturity, susceptible to lodging but resistant to disease, photosensitive and yield moderate.
4. Chinese (exotic) :- Plant short, flag leaf short and broad, leaf below flag leaf short and narrow, resistant to lodging but susceptible to some diseases, photoneutral, early maturing and moderately high yielder.
5. IR-8 (exotic) :- Plant short, short-broad flag leaf and leaf below flag leaf, resistant to lodging and diseases, photoneutral, late flowering, high yielder.

6. IR-532 (exotic) :- Plant short, moderate long-broad flag-leaf, long-narrow leaf below flag leaf, resistant to lodging and diseases, moderately high yielder and photoneutral.

7. IR-20 (exotic) :- Plant short, short-broad flag leaf and leaf below flag leaf, resistant to lodging and disease, high yielder and photoneutral.

8. IR-5 (exotic) :- Plant moderately short, short broad flag leaf, long-narrow leaf below flag leaf, resistant to lodging, moderately high yielder, late maturing and photoneutral.

F_2 lines raised from the F_2 seeds were of the following crosses :

1. Chinese X Kataribhog
2. IR-8 X Chinese
3. IR-20 X Kataribhog
4. Chinese X Naizersail
5. IR-8 X Kataribhog

B. METHODS

The seeds of all the eight parental lines of rice were germinated in the well manured earthen pots (one pot per line) on 17th July 1977 for season I and 12th March 1978 for season II. At the age of 30 days they were transplanted in 30 cm. earthen pots (one pot per plant) containing 8 different nutritional treatment of N, P, K and their combinations including the zero dose. For each season, a total number of 384 earthen pots were filled up with moderately manured soil. The pots were randonly arranged in three replications. There were 128 pots per replications having two pots per population per dose of treatment.

In another set of experiments the seeds of 10 populations (5 F_2s and their 5 parents) were germinated in well manured earthen pots (one pot per population) on 19th July, 1978. At the age of 30 days seedlings were transplanted in 30 cm. earthen pots (one plant per pot) containing the same 8 treatments as used in the experiment with parental lines. The pots were arranged in six replications each of which included 160 pots. There were two pots per population per nutritional treatment and a total of 960 pots were in the experiment.

The eight treatments were O, N, P, K, NP, NK, PK and NPK. Urea, triple-super-phosphate (T.S.P.) and muriate of potash were used for N, P and K respectively. The pots containing different treatments, were randomly arranged within a replication and they were placed in open air and under direct sunlight in the Botanical Research Garden, University of Rajshahi, Bangladesh. Usual weedings and irrigations were done whenever it was necessary.

The doses of fertilizers applied were 5 gms of Urea for N, 5 gms of triple-super-phosphate (T.S.P.) for P and 2½ gms of muriate of potash for K. The first dose of fertilizers applied included 2 gms of Urea and full amount of triple-super-phosphate and of muriate of potash. They were mixed thoroughly with the soil of pots before transplantation. The second dose was of 2 gms Urea and final dose of 1 gm Urea only were applied at the time of tiller initiation and of flowering respectively.

Data were collected on individual plant basis and analyses were made on the mean value of two plants per treatment per population.

Data were taken on yield and yield components and on some morphological and developmental characters of rice. The characters

were as follows :

Yield and yield components

1. Length of panicle : Length of panicle was measured in cm from the first node of primary branches to the tip of the panicle.
2. Number of primary branches/panicle : Total number of primary branches per panicle were counted.
3. Number of spikelets/panicle : It includes the total number of kernels including the false ones (not filled up).
4. Number of kernels/panicle : Filled up grains per panicle were counted.
5. 100 kernel weight : Weight of 100 kernels in gms were taken after complete sun drying.
6. Yield/Plant : Weight of total fully developed sundried kernels of the plant in gm.
7. Number of tillers : Total number of tillers bearing panicles were counted.

Morphological and developmental characters

1. Fresh shoot weight (FSW) : Fresh weight of each plant without grains was taken in gm just after harvest.
2. Dry shoot weight (DSW) : After harvesting, plants were dried in the sun for days together, then after keeping them in an oven at 100°C for 24 hours their weights were taken in gm.
3. Fresh root weight (FRW) : After harvest the root of each plant was cleaned from mud by washing with water, surface water was removed by pressing with blotting paper. Then the weight of root was taken in gm.

4. Dry root weight (DRW) : The roots after proper washing were dried in the sun for several days and then after keeping them in an oven at 100°C for 24 hours their weights were then taken in gm.

5. Plant height (PH) : Plant height was measured in cm from the base of the plant to the tip of the main tiller.

The data for yield and yield components of the three local varieties were not available in season II. The data obtained were, therefore, grouped into the following categories as for analyses :

A. Yield and yield components of eight parental lines for season I.

B. Yield and yield components and some morphological and developmental characters of five parental lines for seasons I and II.

C. Morphological and developmental characters of eight parental lines for seasons I and II.

D. Yield and yield components of 5 F_2S and their 5 parents.

In order to study the genotype-environment interaction at phenotypic and genotypic levels the data were analysed following the statistical techniques equivalent to those developed and used by Finlay and Wilkinson (1963) in barley; Eberhart and Russell (1966) in maize; Bucio Alanis (1966), Bucio Alanis and Hill (1966), Perkins and Jinks(1968a), Bucio Alanis et al. (1969) in Nicotiana rustica; Breese (1969) in grasses and Yates and Cochran (1938) in a group of experiments. Phenotypic, genotypic and environmental variability were calculated by following standard procedures. The components of variation, genetic and environmental effects including their interactions were estimated following the methods developed by Mather and Jones (1958). Details of the statistical procedures were given along with the description of results wherever it was considered necessary.

RESULTS

A. G X E INTERACTION OF YIELD AND YIELD COMPONENTS OF EIGHT-PARENTAL LINES OF RICE FOR SEASON I .

(a) Means and Relative Importance to Different Nutrients

Mean performances of all the seven characters over three replications and eight genotypes show that most of the characters were affected by different nutrients which acted as environments (table 1). The environmental means indicates that the populations in general gave better yield performances in treatments having nitrogen(N) and the performances significantly decreased in other environments (table 1). The highest yield was observed in NPK and the lowest and more or less equal performances were found in K and O treatments. The number of tillers was found to be more in N, NP, NK and NPK and low in K and O treatments. This indicated that under good environments the difference between populations become more pronounced than in poor environments.

Population means over replications and treatments for all the characters are also shown in table 2. Population means indicates that Badshabhog gave the highest panicle length, spikelet number/panicle and kernel number/panicle but had low yield performances. Kataribhog also gave an overall long panicle length. Chinese and IR-20 gave the highest number of primary branches/panicle and the best yield performances but IR-20 gave much more spikelet number/panicle than that of Chinese. The highest number of tillers was found in Naizersail and IR-532.

The results of analysis of variance of all the seven characters are shown in table 3. The item genotype (G) was highly significant in all the cases against the experimental error indicating a real difference existed among the genotypes taken. There was also a real effects of different treatments on yield/plant and tiller number as the item environment (E) is highly significant in these characters. But the

environment (N) is non-significant in case of panicle length, primary branches/panicle, spikelet number/panicle, kernel number/panicle and 100 kernel weight. The analysis of variance further show that the genotypes interacted significantly with all the environmental effects as the item GXN was highly significant in all the characters except primary branches/panicle and 100 kernel weight where it was non-significant. This indicate that all the genotypes for all the characters except primary branches/panicle and 100 kernel weight responded differently under different environments.

As the analysis of variance show that the genotypes responded differently under different treatments, the next-step was to evalute the individual effects of the nutrients for each genotype. For this, the environmental sum of squares was then partitioned into items measuring the effects of N, P, K and all their possible interactions. The magnitude of the main effects of N for a given character is the mean performances of plants receiving N, less the mean performance of those not receiving N. Similarly the main effects of P and K is the mean performance of plants receiving P and K, less the mean performance of those not receiving P and K respectively. The NXP interaction is the mean performance of plants receiving N and P, less the mean of those receiving N but not P and those receiving P and not N, plus the mean of those receiving neither N nor P. The NXK interaction is the mean performance of plants receiving P, NK, NPK and Nil,less the mean of those receiving N, K, NP and PK. The PXK interaction is the mean performance of those plants receiving N, PK, Nil and NPK, less the mean of those receiving P, K, NP and NK. The NXPXK interaction is the mean performance of those plants getting N, P, K and NPK, less the mean of those receiving NP, NK, PK and Nil nutrients. The effects of

N, P, K and their interactions on the individual genotype are shown in table 4.

Panicle Length : With respect to panicle length N was found to have positive significant effect on Badshabhog, IR-532, IR-20 and Kataribhog and negative significant effects on Naizersail, IR-8 and IR-5 whereas it had no effect on Chinese. The effect of P was positive and significant on IR-532, IR-20 and Kataribhog but it was negatively significant on the remaining genotypes except Chinese where its effect was non-significant. The effect of K was significantly positive on Badshabhog and IR-8, and significantly negative on Naizersail, Chinese and IR-20. On the remaining genotypes the effect of K was negative and was non-significant. Among the interaction effects, the NK had significantly positive effect on Naizersail, Chinese, IR-532 and IR-20, whereas, the other four varieties had significant but negative effect. The effect of NP was the highest and positive on IR-8 and positive significant effect was also found on Naizersail and Chinese. Badshabhog, IR-5 and Kataribhog had significantly negative effects of NP. PK had positive significant effect on Badshabhog and Chinese but significantly negative effect on Naizersail, IR-8, IR-532 and Kataribhog. Only IR-8 and IR-532 had significant and positive effects of NPK but the negative effects were noted on the remaining genotypes (table 4).

Primary Branches/panicle : N had significantly positive effect on the primary branches/panicle of Naizersail, Chinese, IR-532 and IR-20 whereas the effect was significant but negative in the case of IR-5 and Kataribhog. N Significant effect of N was noted on other two genotypes. The effects of P was significantly positive on Chinese, IR-8, IR-532 and IR-20 but negative on IR-5 and Kataribhog. All the varieties except IR-532 and IR-5 had significant effect due to K, though the effect was somewhere

negative. The interactions NP, NK and PK had significant effect on most of the genotypes. Significant effect of NPK was noted on Naizersail, Badshabhog, IR-20 and IR-5 (table 4).

Spikelet Number/panicle : Positive and significant effect of N was observed on the spikelet number/panicle in Badshabhog, Chinese and IR-20 but the effect was negatively significant in IR-8, IR-532 and Kataribhog. Most of the genotypes had significantly negative effect due to P except Chinese, IR-532 and IR-5 whereas K had significant positive effect. Among the interactions PK produced significant effect in all the genotypes, some of them having negative effect. NP exhibited positively significant effect on Chinese, IR-532, IR-20 and Katribhog but significantly negative on Badshabhog only;NP had no effect on IR-5. NK had significantly positive effect only in IR-20 but the effect was significantly negative in all other seven genotypes, except Kataribhog where it was non-significant. Naizersail and IR-20 showed significantly negative effect and Chinese and IR-532 showed significantly positive effect due to interaction NPK.

Kernel Number/panicle : N produced positive significant effect on the kernel number of Chinese, IR-20 and IR-5 while the other five genotypes were negatively affected indicating that N increased the kernel number in some genotypes and significantly decreased the kernel number in some genotypes. Most of the genotypes exhibited negative effect due to P; positive effect was observed in Chinese, IR-8 and Katribhog. K increased the kernel number of Naizersail, Badshabhog, IR-532 and IR-20 and decreased it in case of Chinese, IR-8, IR-5 and Kataribhog. The effects of NP was significantly positive incase of Chinese, IR-8 and Kataribhog but it was negative in case of Naizersail,

IR-532, IR-20 and IR-5. The effects of NK was significant in all the cases except Kataribhog but the effect was positive on Badshabhog, IR-8 and IR-20 only. Majority of the genotypes exhibited negative effect due to PK and NPK.

100 Kernel Weight : All the eight genotypes showed negative response due to the effect of N, which indicated decreasing effect of N on the 100 kernel weight. P had positive effect on Naizersail, Badshabhog, IR-532 and Kataribhog and negative effect on the rest four genotypes but the effect was significant in case of Naizersail, IR-8 and IR-532 only. Naizersail, Badshabhog, IR-532, IR-20 and Kataribhog exhibited positive effect due to K. All the genotypes exhibited positive effect due to NP combination but the effect was significant incase of Naizersail, Chinese, IR-532, IR-20 and Kataribhog. NK had significant effect on all the genotypes except Naizersail but the effect was positive in case of Badshabhog, IR-8, IR-532, IR-20 and IR-5. PK produced negative effect in most of the cases. NPK had positive effect in Badshabhog, Chinese, IR-8, IR-5 and Kataribhog.

Yield/Plant : N and P produced significantly positive effect in all the genotypes indicating that N and P separately increased the yield per plant. K significantly decreased the yield of all the genotypes except Badshabhog. All the genotypes exhibited positive effect due to NP. NK also had positive effect on all the genotypes except IR-8. The effect of PK was positive incase of Naizersail, Chinese, IR-532, IR-20 IR-5 and Katribhog. NPK had positive effect on the yield of all genotypes except Naizersail and IR-8.

Tiller number : N and P separately increased the tiller number of all the genotypes. K had positive effect on Badshabhog, IR-8 and

IR-532 only and the rests exhibited negative effect. NP and NK also increased the tiller number of all the genotypes except Kataribhog where NP had no significant effect. Positive effect of PK was found in all the cases except Badshabhog and IR-20. N:K also significantly increased the tiller number in all except Badshabhog.

(b) Variability

The phenotypic variance was repartitioned into genotypic, environmental and G X E variation from the component analysis of variance assuming a mixed model with a fixed number of populations (g) and a random sample of environments (e) with (r) replications. The expectation of mean squares are as follows :

Source	M.S.	Expectation of M.S.
Population (G)	M_1	$\delta^2_E + r\delta^2_{GE} + re\delta^2_G$
Dose (E)	M_2	$\delta^2_E + rg\delta^2_E$
G X E	M_3	$\delta^2_E + r\delta^2_{GE}$
Error	M_4	δ^2_E

Where δ^2_E, δ^2_G and δ^2_{GE} are environmental, genotypic and G X E variances respectively. The genotypic, environmental and G X E variances (δ^2_G, δ^2_E and δ^2_{GE}) were calculated as follows :

$$\delta^2_G = (M_1 - M_3)/(r \times e)$$

$$\delta^2_{GE} = (M_3 - M_4)/r$$

$$\delta^2_E = M_4$$

Estimates of δ^2_G, δ^2_{GE} and δ^2_E along with co-efficients of variability are shown in table 5.

Greater portion of the total phenotypic variation was of genetic in nature in case of primary branches/panicle, spikelet number/panicle and 100 Kernel weight, whereas, the influence of δ^2_E was greater than δ^2_G in cases of panicle length, kernel number, yield/plant and tiller number. The influence of δ^2_{GE} was negative in primary branches/panicle and 100 kernel weight. Highest co-efficient of variability for δ^2_G was found in case of primary branches/panicle, spikelet number/panicle and 100 kernel weight. The magnitude of co-efficient of variability for δ^2_E was however, higher in cases of panicle length, kernel number/panicle, yield/plant and tiller number. Low co-efficient of variability for δ^2_{GE} was found in all the cases.

(c) Regression

In the analysis of variance (table 3) all the main items were significant and the genotypes (G) interacted significantly with different treatments. As the interaction item is significant in most of the cases, no immediate generalization can be made on the relative performances of these genotypes over a restricted range of environmental contrast; indeed, the analysis argues that valid comparison can only be made in each environment separately.

Since the analysis of variance can give no further useful account of G X E interactions, it may be considered that a dynamic relationship existed between genotypes and environmental effects as proposed by Finlay and Wilkinson (1963). The data were then subjected to regression analysis equivatent to those developed by Yates and Cochran (1938), Finlay and Wilkinson (1963), and Perkins and Jinks(1968). The eight different treatments of combinations of N, P and K were treated as different environments which were measured quantitatively by the means of all the eight genotypes.

The mean sum of squares measuring the interactions of the genotypes with environment were partitioned into an item measuring differences between the slopes of the eight regressions and the residual items which measured the scatter of the points about the regression line (table 6). It is clear from the table 6 that major part of the genotype-environment variance was due to the difference between the slopes of the linear regressions except primary branches/panicle and spikelet number/panicle where the regression mean squares were non-significant. The diviation mean squares were significantly greater than that of error in most of the cases except primary branches/panicle

and kernel number/panicle. They indicated that deviation from linearity can not be explained in terms of field error. However, linear mean square was significantly greater than deviation mean square in most of the cases.

The rate of change of interactions within each genotype did not vary with environment if the heterogenity item alone was significant. Each genotype had, therefore, its own characteristic linear response to environmental change. When the residual item alone is significant it indicates no relationship between g's and e's. In the present case however, both the items when tested against experimental error, were significant in case of panicle length, 100 kernel weight, yield/plant and tiller number. On the other hand the two items were non-significant in case of primary branches/panicle. Either deviation or regression items were significant in case of spikelet number/panicle and kernel number/panicle respectively. The heterogenity item was again tested against residual item (table 6) to investigate the significant proportion of the genotype-environment interaction variance accounted by it. Only the primary branches/panicle showed significant linear variation which was of independent of the non-linear variation of the genotype-environment interaction but the value was significant at 5% level. The other characters showed non-significant values for heterogeneity.

Regression techniques for studying the G X E interactions are among the most widely used methods for investigating the response patterns of the genotypes. For each genotype the linear regression (b_i) of individual values on the environmental means (E) were computed and the correlation co-efficients (r) between them were also calculated and they are shown in table 7. The linear regression co-efficients in

table 7 correspond to the b_i values of Finlay and Wilkinson (1963); and to the ($1 + \beta_i$) values of Eberhart and Russell (1966); after subtracting 1.0, they correspond with β_i values of Perkins and Jinks (1968a). For convenience of comparison of regression values, the β_i values are also included in table 7. Both high and low correlation co-efficients (r) were found which indicated linear and non-linear variations of these genotypes.

The regression co-efficients are in effect measure of responses to increaments in an improving environments. As these increaments were measured by the mean of all the genotypes, the average response for one set of genotypes under consideration must have a regression co-efficient of 1.0. Regression co-efficients > 1.0 and < 1.0 indicated above and below average response respectively by a variety. As revealed by joint regression, the distribution of all the eight b_i values were heterogenous and for this all the genotypes had different responses to different environments.

For panicle length, Naizersail had an above average response ($b_i = 4.49 \pm 1.29$) but the other varieties showed non-significant below average response. Low correlation co-efficients of all these varieties, except Naizersail, also showed that the most of the non-linear variations were associated with these genotypes. Chinese and IR-532 showed below average responses and had negative non-significant b_i values (-0.12 ± 0.66) and -0.25 ± 0.54 respectively) and negative low correlation co-efficients which also indicated the non-linear variations.

Only Badshabhog and Chinese showed significant linear response to the environments in case of primary branches/panicle. Chinese showed

the highest b_i value. IR-8 and IR-20 also showed above average responses to the environments, the responses, however, were non-significant. The lowest b_i values observed in IR-5(0.01) and Kataribhog (0.02) respectively indicated practically no response to the environments. The other two varieties, Naizersail and IR-532 showed below average response. Badshabhog and Chinese showed the high correlation co-efficient values.

In the case of spikelet number/panicle IR-532 showed the highest linear response and had a b_i value 2.61 ± 0.76. It also had a high correlation co-efficient value indicating the linear response accounted for most of the variations over environments for this genotype. Naizersail, IR-8 and Kataribhog showed above average non-significant response to the environments. Badshabhog and IR-20 showed below and above average negative responses respectively and had low correlation co-efficient value. The other two varieties showed below average responses to the environments.

IR-8 and Kataribhog showed the highest and above average significant linear responses for kernel number/panicle having b_i values 2.78 ± 0.89 and 1.31 ± 0.67 respectively. Though Chinese and Badshabhog had above average responses (b_i = 1.23 ± 1.58 and 1.21 ± 1.25 respectively) but the responses were non-significant to the environments. The lowest b_i value was found in IR-5 (b_i = 0.07 ± 0.76). The other three varieties showed below average responses to the environments. Most of the varieties showed low co-relation co-efficient values.

With respect to 100 kernel weight, IR-532 and IR-20 showed above average significant responses to the environments. Responses of Naizersail, IR-8 and IR-5 were above average but they were non-significant.

The remaining three varieties showed below average responses. The correlation co-efficients were low in most of the cases.

In relation to yield/plant all the varieties except IR-8 showed significant linear responses to the environments. Among them Chinese, IR-532 and IR-20 showed above average responses whereas Kataribhog, Naizersail, Badshabhog and IR-8 showed below average responses to the environments. High correlation co-efficient values indicated the linear variation accounted for most of the variation over the environments for genotype. Only IR-8 showed non-significant below average response and low correlation co-efficient value.

All the varieties showed significant linear responses to the environments in case of tiller number. Among them Naizersail, IR-532 and IR-20 showed above average and the other five varieties showed below average responses. All the genotypes had high correlation co-efficient values and indicated the presence of linear variation in them.

Actual regression lines of performance of each genotype against the corresponding environmental means are shown in Figs. 1-7. To avoid confusion, individual points were not plotted in the figures. Crossing of regression lines was very marked in most of the characters indicating that G X E interactions were very marked in these characters. For panicle length Chinese and IR-532, for spikelet number Badshabhog and IR-20 responded negatively to good environments. Very marked differences were found under good environments in case of tiller number i.e. good environments increased the tiller number and the increasing effect varied in different genotypes.

The stability parameter $\bar{s}_d^2$ calculated by subtracting error m.s. from remainder m.s. (Eberhart and Russell, 1966) which measures the unpredictable irregularities in the response to the environments are shown in table 7. The standard error(S_{b_i}) calculated separately for each linear regression from deviation are also included in table 7. The standard error (S_{b_i}) proves to the heterogenous as X^2 in the Bartlett's test (shown at the bottom of each character in table 7) indicated that the observed deviation from their expected one was significant in all cases except 100 kernel weight and yield/plant. Thus it indicated that the genotypes had their own intrinsic variation around their regression slopes and was characteristic of a particular population; and was under genetic control. As revealed from joint regression and standard error (S_{b_i}), the $\bar{s}_d^2$ has highly heterogenous in most of the characters. Among the seven characters panicle length, primary branches/panicle and 100 kernel weight showed considerable stability as shown by their low $\bar{s}_d^2$ values irrespective to their signs. All other characters except tiller number showed low stability as shown by their high $\bar{s}_d^2$ values.

Explanation to the Figs. 1-7.

Fig. 1. Regression of individual population mean on environmental mean for eight parental lines in panicle length.

Fig. 2. Regression of individual population mean on environmental mean for eight parental lines in primary branches/panicle.

Fig. 3. Regression of individual population mean on environmental mean for eight parental lines in spikelet number/panicle.

Fig. 4. Regression of individual population mean on environmental mean for eight parental lines in kernel number/panicle.

Fig. 5. Regression of individual population mean on environmental mean for eight parental lines in 100 kernel weight.

Fig. 6. Regression of individual population mean on environmental mean for eight parental lines in yield/plant.

Fig. 7. Regression of individual population mean on environmental mean for eight parental lines in tiller number.

The genotypes in the graphs (represented by their serial numbers) are as follows : 1 = Naizersail, 2 = Badshabhog, 3 = Chinese, 4 = IR-8, 5 = IR-532, 6 = IR-20, 7 = IR-5 and 8 = Kataribhog.

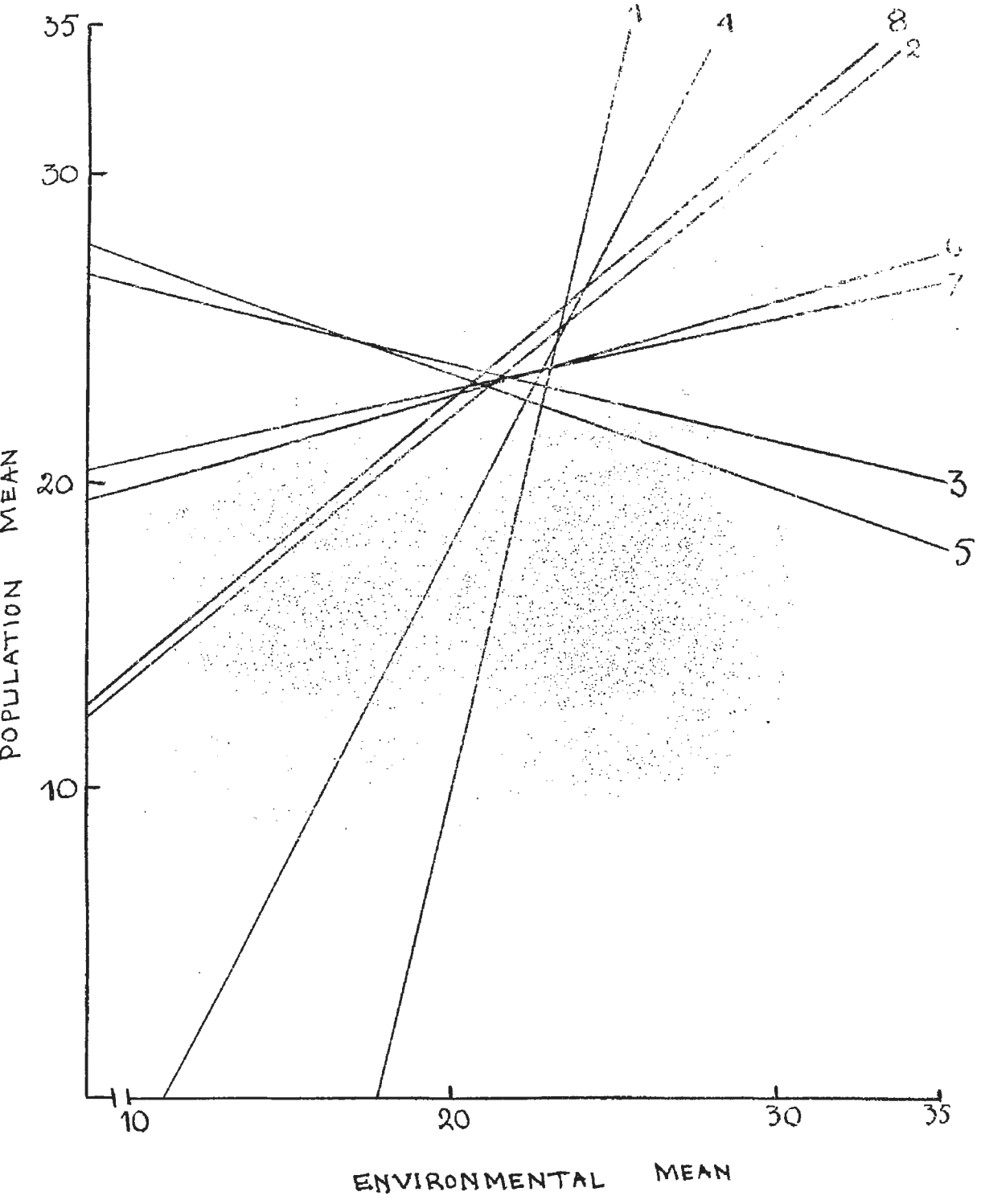
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FIG. 1

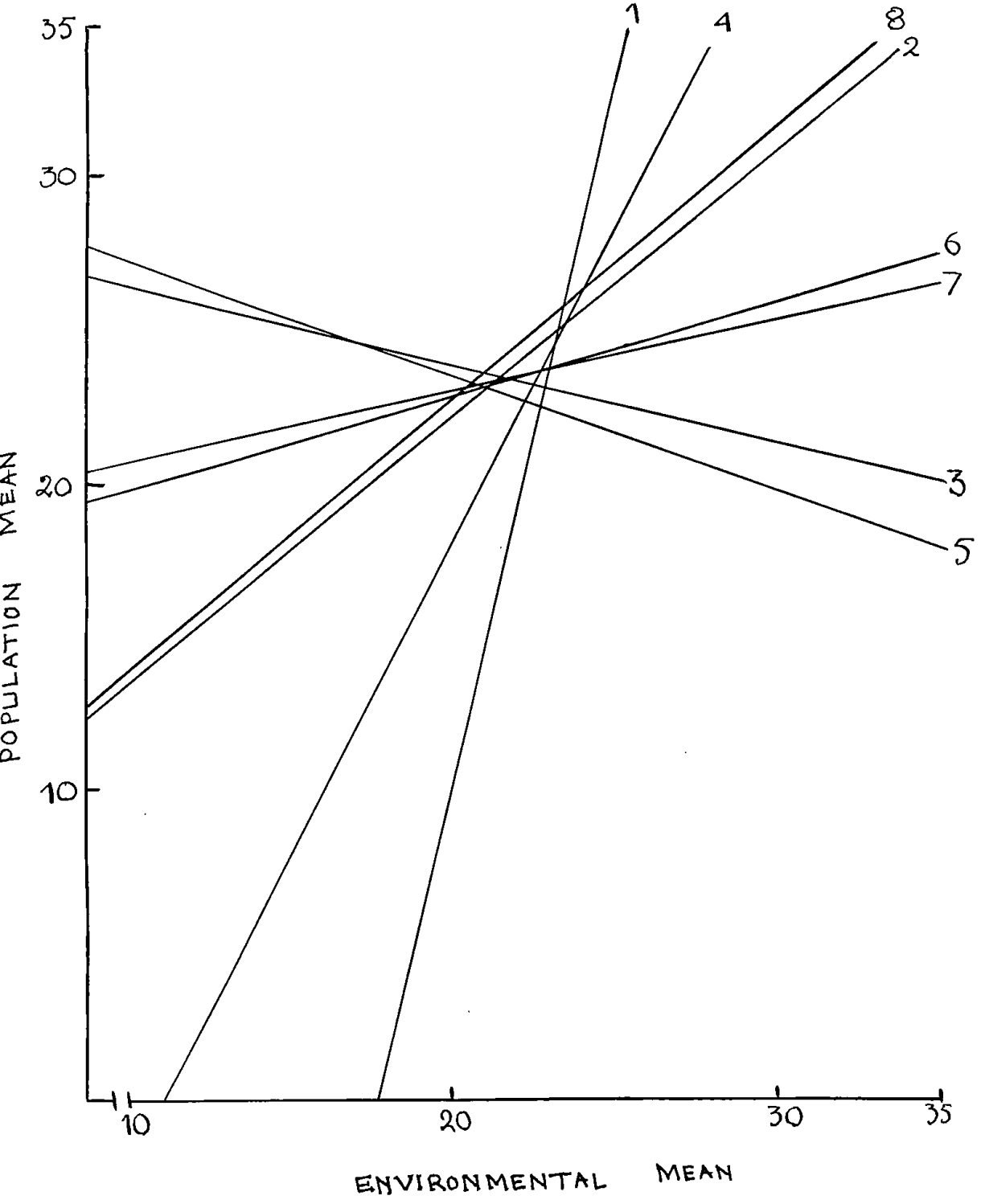
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FIG. 1

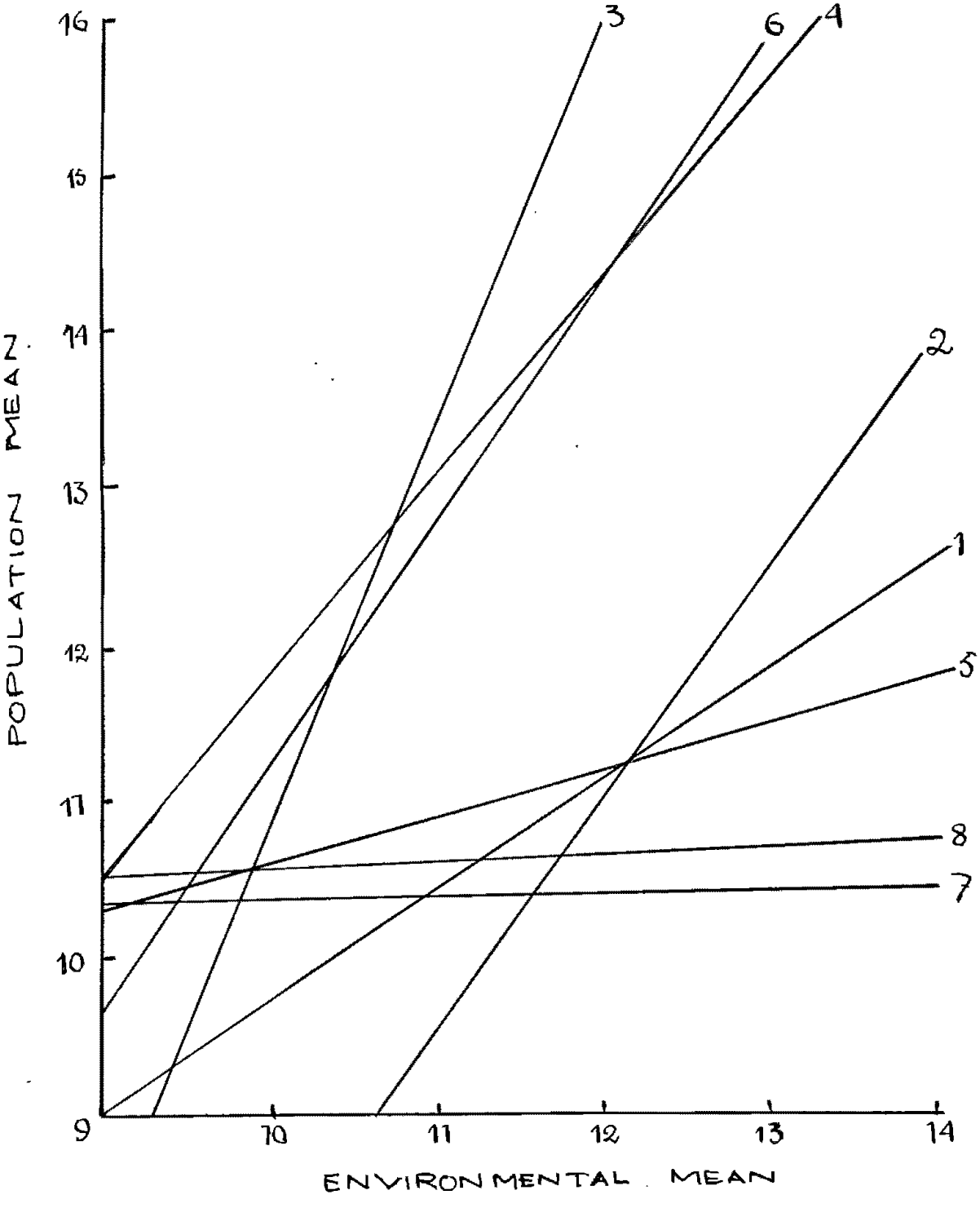
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FIG. 2

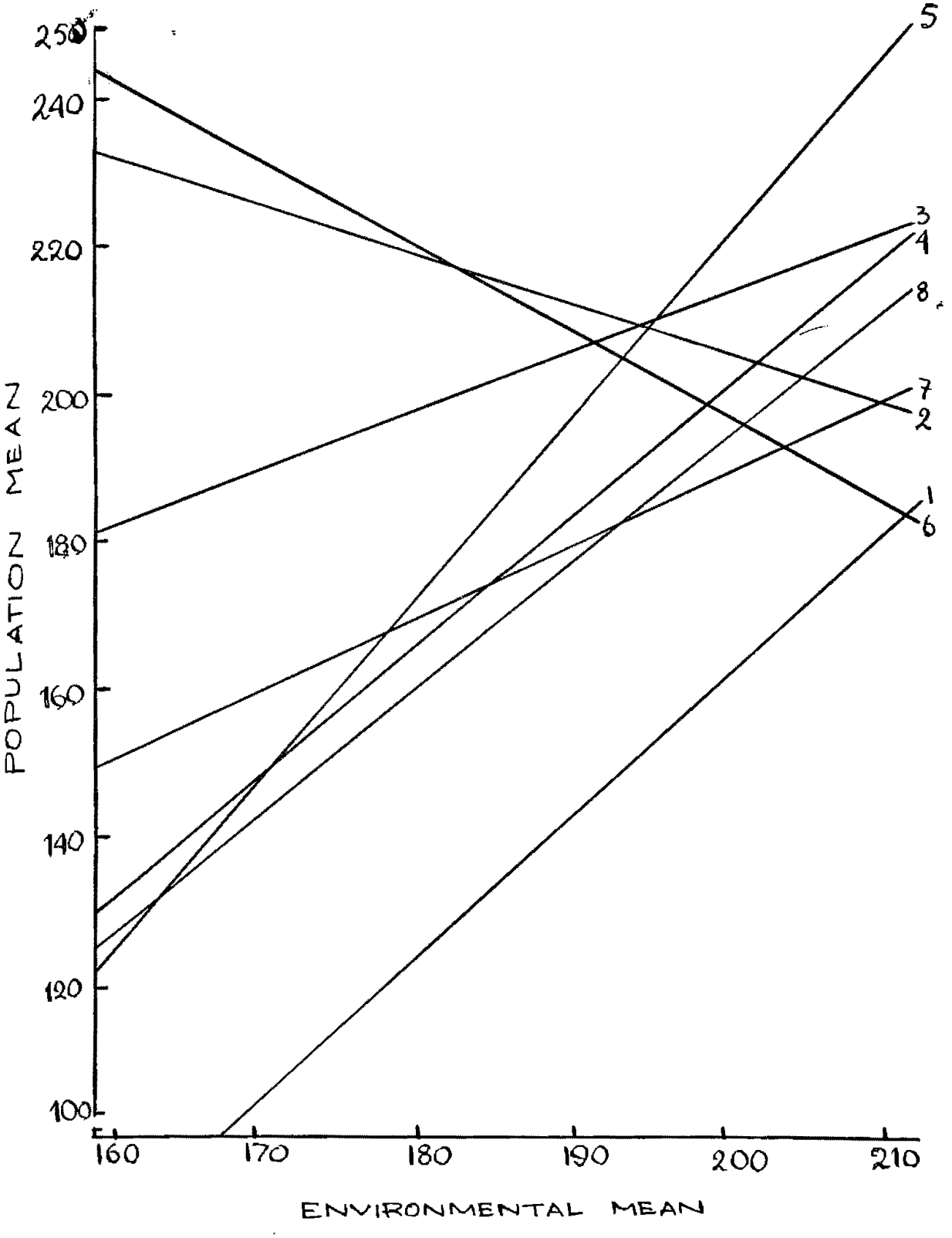
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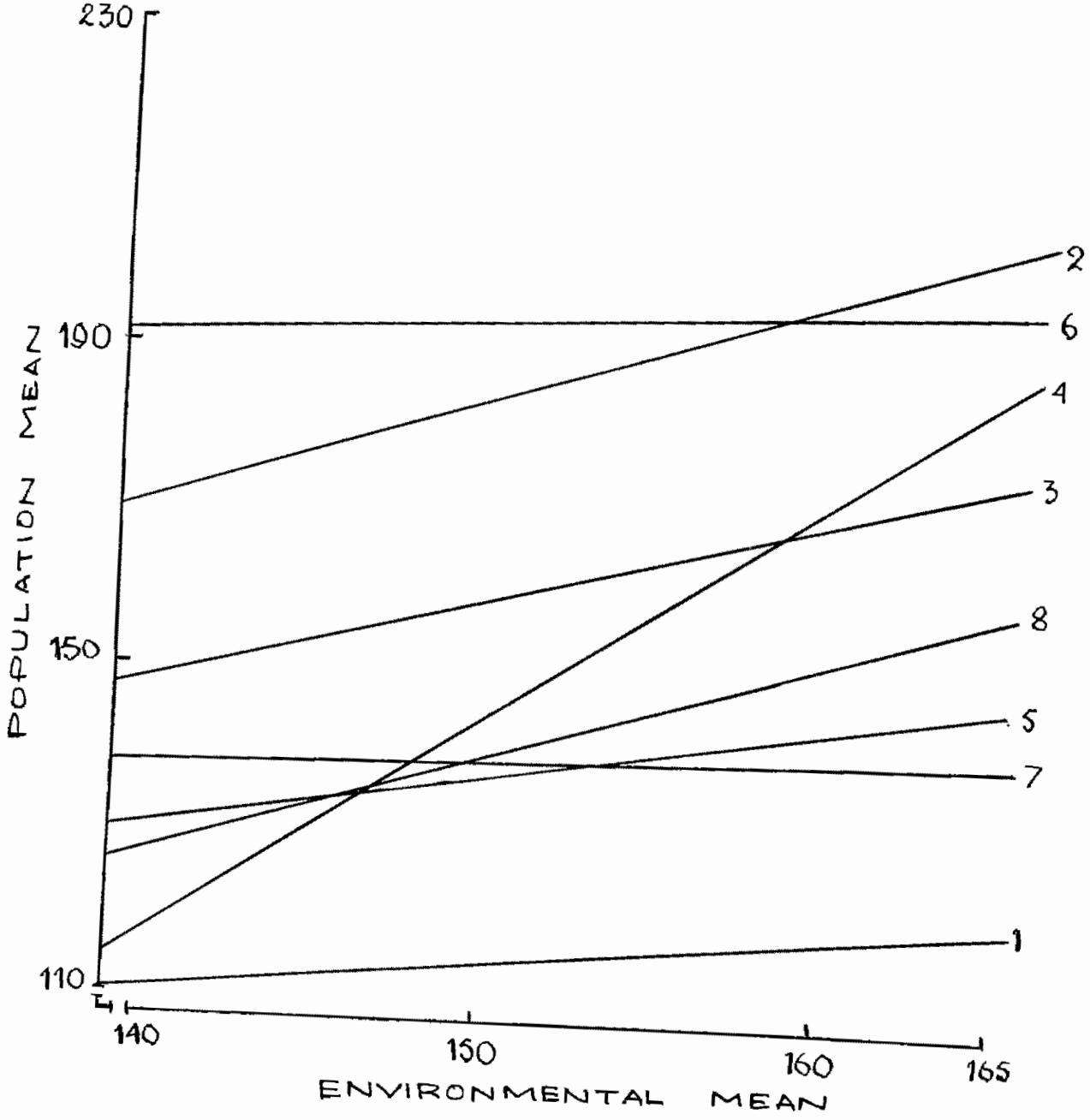
FIG. 3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ENVIRONMENTAL MEAN

FIG. 4

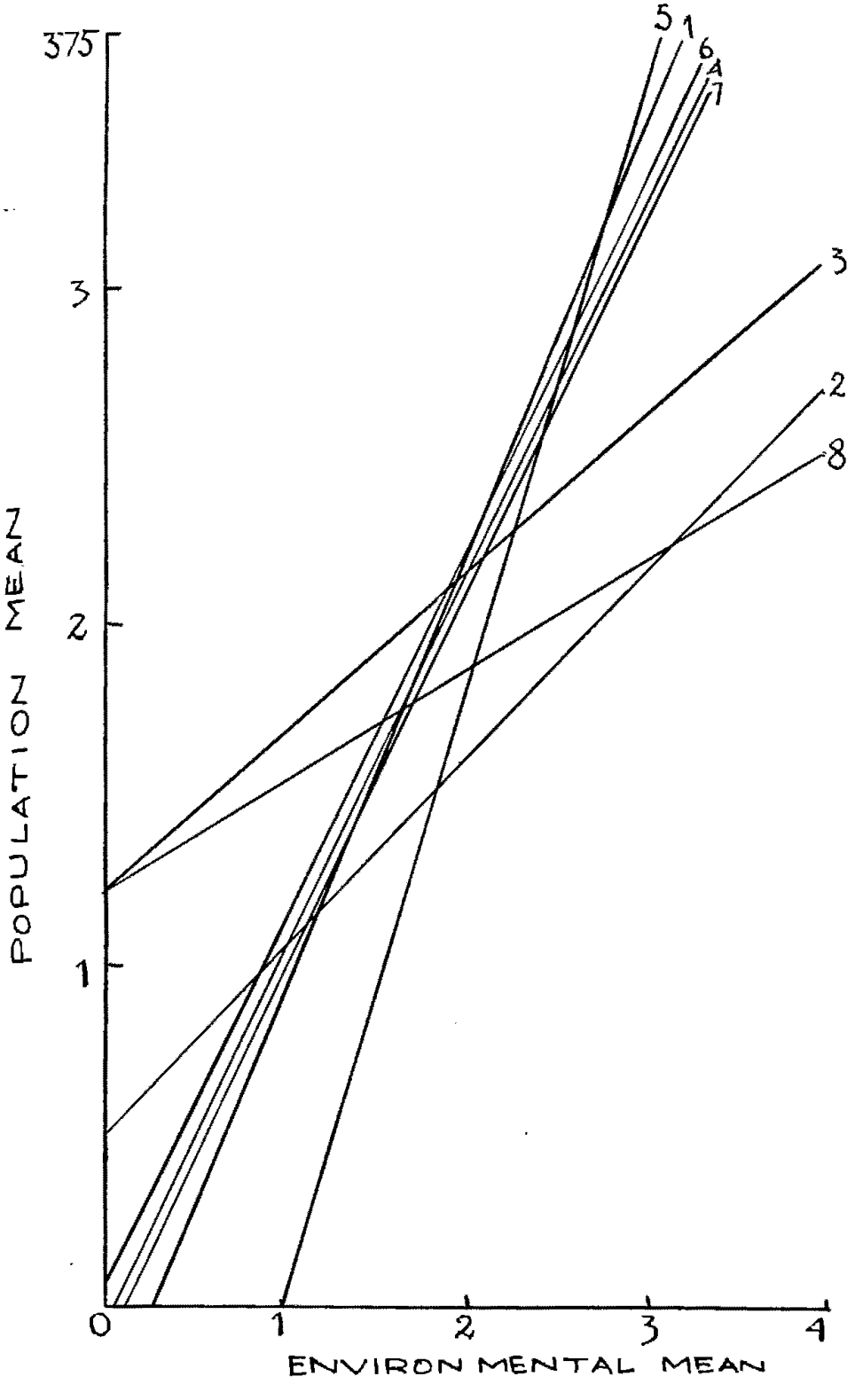

FIG. 5

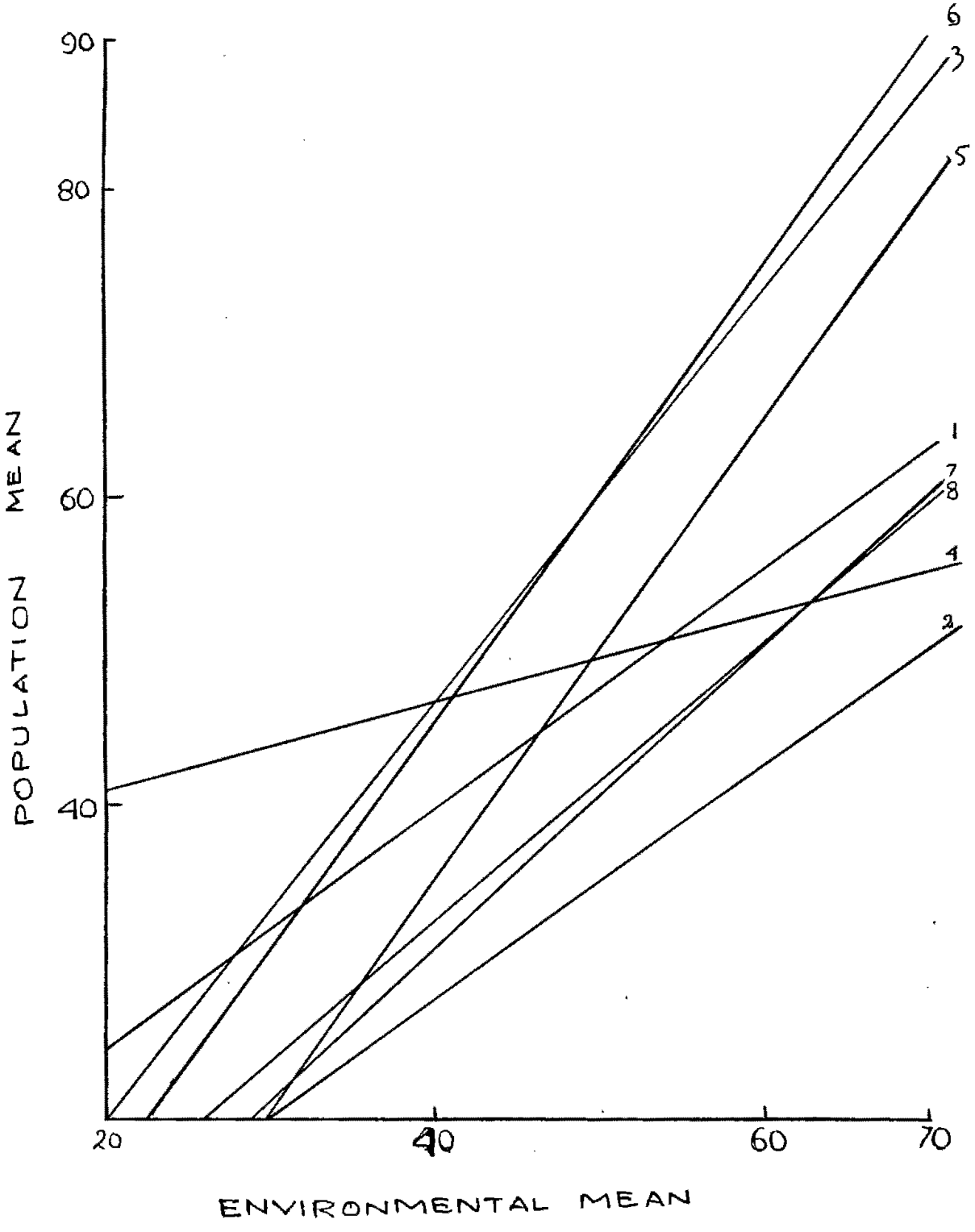
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FIG. 6

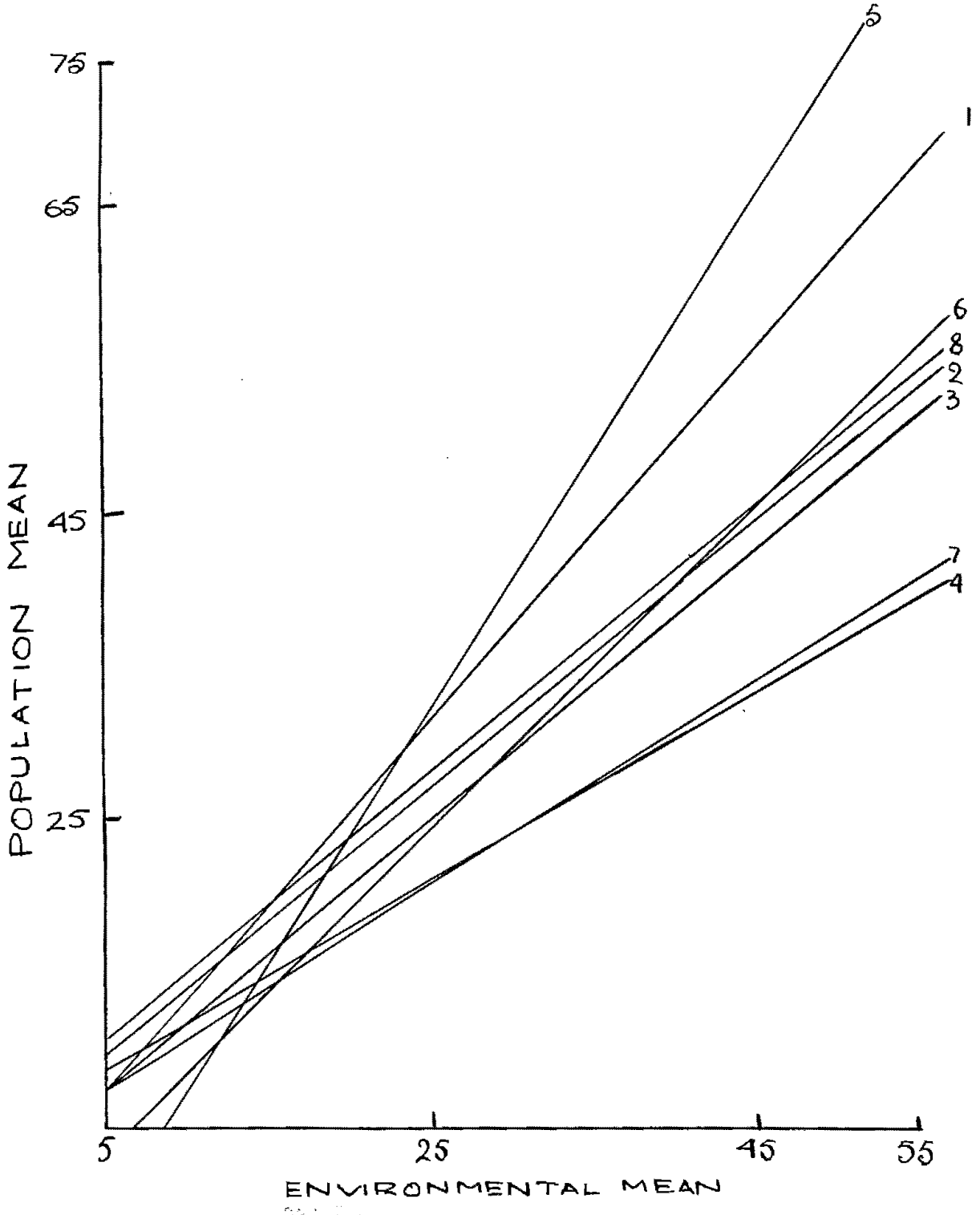
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FIG. 7

(d) Correlation

The relationship that exists between two or more independent variables of a population is called correlation. Correlation co-efficient(r) was calculated by usual product moment correlation method. Correlation co-efficients 'within' as well as 'between' characters were measured and are shown in tables 8 and 9 respectivwly.

Correlation co-efficient between mean ($\bar{X}$) and response (b_i), between mean ($\bar{X}$) and stability ($\bar{S}^2_d$) and between response (b_i) and stability ($\bar{S}^2_d$) within a character were calculated and are shown in table 8. Mean performances ($\bar{X}$) were significant and positively correlated with response (b_i) in yield/plant and tiller number indicating that the genotypes with higher mean performances were responsive to the environmental changes. Further the mean performances ($\bar{X}$) were significant and positively correlated with stability ($\bar{S}^2_d$) in kernel number/panicle and tiller number indicating a close relationship existed between mean performances and stability. Other characters showed non-significant correlation co-efficient between mean ($\bar{X}$) and response (b_i) and between mean ($\bar{X}$) and stability ($\bar{S}^2_d$) and suggested that the two aspects of phenotype were independent to each other. The correlation co-efficients were non-significant between response (b_i) and stability ($\bar{S}^2_d$) in all the characters indicated that the response (b_i) and stability ($\bar{S}^2_d$) were independent to each other, an indicative of different gene control for b_i and $\bar{S}^2_d$.

Correlation co-efficients between responses (b_i) and between stabilities ($\bar{S}^2_d$) among the characters were studied and are shown in table 9. In majority of the cases the correlation co-efficients between responses (b_i) among the characters were non-significant

indicating that the variation in responses of a character with changing environment was not correlated with that of another character. Only there was a relationship between primary branches/panicle and spikelet number/panicle as the correlation co-efficient in these cases were significant but the relationship was negative. With respect to correlations between stabilities ($\bar{s}^2_d$) among the characters tiller number showed significant correlations with panicle length and yield/plant, whereas kernel number/panicle showed significant correlation with spikelet number/panicle. The other characters showed no correlations with any of the characters.

Table 1. Environmental means over replications and genotypes.

Characters	Treatments							
	0	N	P	K	NP	NK	PK	NPK
Panicle length	23.87	24.00	23.57	24.13	24.44	23.98	23.55	23.52
Primary branches/ panicle	11.35	11.33	11.50	11.36	11.29	11.85	11.42	11.71
Spikelet number/ panicle	178.96	176.44	176.92	190.35	179.90	181.73	176.71	179.71
Kernel number/ panicle	162.96	148.31	154.65	161.94	150.50	151.50	147.85	149.85
100 kernel weight	2.08	1.98	2.12	2.10	2.03	2.02	2.02	2.12
Yield/plant	54.71	61.49	58.31	39.40	70.96	58.23	41.60	80.85
Tiller number	23.39	29.33	23.21	16.92	32.92	27.98	18.33	40.77

Table 2. Population means over replications and environments.

Genotypes	Panicle length	pri.br./ panicle	Spikelet number/ panicle	Kernel number/ panicle	100 kernel weight	Yield/ plant	Tiller number
Naizersail	23.27	10.48	125.94	116.15	2.25	55.88	32.09
Badshabhog	25.06	9.69	220.86	186.02	1.65	43.05	27.00
Chinese	23.68	13.56	199.87	161.29	2.19	74.04	25.33
IR-8	23.90	13.12	187.04	146.04	2.30	51.87	21.50
IR-532	22.67	10.98	173.37	139.21	1.82	65.49	32.91
IR-20	23.54	12.89	221.41	194.25	2.21	75.60	24.79
IR-5	23.48	10.43	171.50	141.99	2.18	49.62	21.09
Kataribhog	25.47	10.65	160.71	142.61	1.90	50.00	28.15

Table 3. Results of Analysis of Variance of different characters.

Item	D.F.	Panicle Length M.S.	Panicle Length V.R.	Primary branches/panicle M.S.	Primary branches/panicle V.R.
Genotype (G)	7	21.12	10.26***	52.45	47.49***
Environments(N)	7	2.23	2.08	0.98	
G X N	49	3.14	1.53***	0.77	
Replication	2	2.75	1.34	0.04	
Error	126	2.06		1.104	
		Spikelet number/panicle		Kernel number/panicle	
Genotype(G)	7	24907.91	37.97***	16027.64	20.26***
Environments(N)	7	514.71		839.36	1.06
G X N	49	887.34	1.35***	867.73	1.10***
Replication	2	44.91		423.13	
Error	126	655.99		791.09	
		100 kernel weight		Yield/plant	
Genotype(G)	7	1.30	37.24***	3507.18	17.95***
Environment(N)	7	0.051	1.47	4553.20	23.30***
G X N	49	0.028		315.56	1.62***
Replication	2	0.05	1.45	72.21	
Error	126	0.034		195.39	
		Tiller number			
Genotype(G)	7	458.08	19.28***		
Environment(N)	7	1487.41	62.62***		
G X N	49	53.84	2.27***		
Replication	2	25.46	1.07		
Error	126	23.76			

Table 4. Results of effects of nutrients on eight genotypes.

	N	P	K	NP	NK	PK	NPK
				Panicle length			
1.	-1.97***	-6.11***	-7.05***	3.23***	7.03***	-4.25***	-2.75***
2.	5.37***	-5.51***	4.17***	-3.69***	-2.57***	1.51**	0.25
3.	0	-0.06	-2.20***	1.26*	1.40**	2.26***	-1.46**
4.	-4.39***	-2.67***	3.13***	8.93***	-2.07***	-4.99***	1.53**
5.	0.99***	1.93***	-0.81	0.53	1.67***	-0.99*	1.21*
6.	5.40***	2.92***	-1.54**	0.80	2.74***	-0.54	-0.26
7.	-2.00***	-1.94***	-0.80	-1.94***	-1.20*	0.46	-1.54**
8.	3.17***	4.23***	-0.65	-2.17***	-2.35***	-2.89***	-1.97***
				Primary branches/panicle			
1.	0.82*	0.50	1.50***	0.18	-0.18	-1.00*	1.82***
2.	0.49	-0.51	2.17***	-1.51***	0.49	0.17	1.17***
3.	2.82***	1.16**	1.84***	-1.16**	2.16***	-1.50***	-0.50
4.	-0.66	1.00**	1.68***	1.32***	2.00***	-1.66***	-0.66
5.	1.83***	1.17**	-0.51	1.83***	0.83*	0.17	0.15
6.	3.16***	1.16**	0.84*	-1.50***	0.82*	2.18***	-3.16***
7.	-2.17***	-2.83***	0.17	-0.51	1.17***	1.15**	0.83*
8.	-1.84***	-1.50***	-0.84*	-1.82***	0.84*	-1.50***	0.18

Contd.....

Table 4 (contd.)

	N	P	K	NP	NK	PK	NPK
				Spikelet number/panicle			
1.	16.18	-55.16**	1.16	7.50	49.50**	-76.84**	-21.50*
2.	44.18**	-50.84**	46.16**	-70.84**	-9.84	46.50**	-12.18
3.	21.66*	49.68**	-47.66**	35.00**	-19.66*	-65.00**	103.00**
4.	-67.66**	26.34*	44.35**	-5.66	-37.00**	-75.00**	-3.00
5.	-66.99**	-25.67*	36.99**	61.65**	-22.33*	-21.00*	23.67**
6.	65.33**	-12.67	12.67	42.67**	145.33**	60.65**	-48.01**
7.	-9.33	-65.33**	24.67**	0.01	-53.99**	39.33**	12.67
8.	-44.67**	23.67*	12.01	66.67**	-5.67	-45.33**	-5.65
				Kernel number/panicle			
1.	-0.17	-45.17**	3.51	-13.17	-41.17**	-64.85**	-20.17*
2.	41.82**	-91.16**	24.16*	13.16	93.84**	-42.50**	-7.50
3.	-84.99**	76.99**	-84.99**	59.01**	-28.33**	-11.67	87.67**
4.	-128.32**	5.66	-13.66	66.32**	27.00**	-29.66*	-13.00
5.	-48.32**	-31.00**	20.34*	-2.32	-21.66*	23.66*	-6.34
6.	39.33**	-58.01**	21.22*	-4.67	115.94**	53.33**	-44.01**
7.	1.67	-51.01**	-0.33	-7.01	-51.01**	30.99*	25.67*
8.	-39.17**	19.17	-13.83	71.83**	-11.49	-36.51**	-6.49

(Contd.....)

Table 4 (contd.)

	N	P	K	NP	NK	PK	NPK
				100 kernel weight			
1.	-0.10	0.38***	0.62***	0.52***	0.12	-0.20**	-0.10
2.	-0.05	0.05	0.01	0.07	0.31***	0.29***	0.11
3.	-1.96***	-0.05	-0.41***	0.25***	-0.31***	-0.63***	0.63***
4.	-0.49***	-0.19**	-0.15*	-0.17**	0.39***	0.29***	0.55***
5.	-0.41***	0.49***	0.45***	0.41***	0.33***	-0.45***	-0.17**
6.	-0.26***	0.12	0.28***	0.16*	0.52***	0.02	-0.14*
7.	-0.13*	-0.03	-0.49***	0.07	0.53***	0.03	0.33***
8.	-0.11	0.09	0.23***	0.17**	-0.21**	-0.01	0.15*
				Yield/plant			
1.	88.99***	12.33*	-41.67***	-10.99***	9.65	23.67***	-25.01***
2.	81.34***	5.00	2.98	20.66***	34.00***	-6.34	10.00*
3.	52.99***	101.67***	-43.67***	78.33***	67.67***	14.99***	37.01***
4.	22.40***	30.74***	-13.62**	0.06	-0.94	-50.60***	-2.60
5.	114.24***	74.10***	-13.22**	61.10***	54.42***	21.24***	4.24
6.	120.49***	43.49***	-30.51***	33.17***	64.49***	0.17	33.17***
7.	87.01***	15.33***	-45.67***	14.67**	13.67**	39.99***	6.01
8.	52.67***	20.65***	-17.67***	13.33**	66.33***	50.99***	53.67***

Contd.....

Table 4 (Contd.)

	N	P	K	NP	NK	PK	NPK
				Tiller number			
1.	70.00***	9.66***	-27.34***	7.66***	20.66***	19.00***	16.32***
2.	46.33***	17.33***	5.01**	23.34***	8.67***	-2.33	-0.35
3.	33.67***	27.35***	-0.33	24.33***	22.01***	10.33***	7.99***
4.	29.33***	8.33***	8.33***	7.67***	9.67***	20.67***	16.01**
5.	78.00***	33.34***	1.34	33.34***	28.00***	19.34***	13.32**
6.	54.99***	21.67***	-3.33	20.33***	13.33***	-4.67**	8.67***
7.	34.67***	6.99***	-8.99***	1.67	16.33***	0.65	5.33**
8.	46.16***	16.16***	-13.50***	-0.16	25.51***	23.50***	21.18***

*, ** and *** at 5%, 1% and 0.1% level.

1 = Kaizersail, 2 = Badshabhog, 3 = Chinese

4 = IR-8, 5 = IR-532, 6 = IR-20,

7 = IR-5 and 8 = Kataribhog.

Table 5. Estimates of δ^2_G, δ^2_{GE} and δ^2_E and the co-efficient of variability for the seven characters.

	Panicle length	Pri.br./ panicle	Spikelet number/ panicle	Kernel number/ panicle	100 kernel weight	Yield/ plant	Tiller number
δ^2_G	0.74	2.15	1000.86	631.66	0.052	132.98	16.84
δ^2_{GE}	0.36	-0.11	77.12	25.55	-0.002	40.06	10.03
δ^2_E	2.06	1.104	655.99	791.09	0.034	195.39	23.76
$cv\delta^2_G$	3.09	18.73	555.76	411.64	2.52	228.53	63.28
$cv\delta^2_{GE}$	1.51	-0.96	42.82	16.65	-0.097	68.84	37.69
$cv\delta^2_E$	8.63	8.83	364.26	515.54	1.65	335.78	89.29

Table 6. Results of joint Regression Analysis.

Item	D.F.	M.S.	$V.R_1$	$V.R_2$
Panicle length				
Linear Regression	7	6.31	1.97	3.06**
Deviation	42	3.21		1.56***
Error	126	2.06		
Primary branches/panicle				
Linear Regression	7	1.47	2.26*	1.33
Deviation	42	0.65		
Error	126	1.104		
Spikelet number/panicle				
Linear Regression	7	1259.02	1.53	1.92
Deviation	42	825.39		1.26***
Error	126	655.99		
Kernel number/panicle				
Linear Regression	7	1563.14	2.08	1.98*
Deviation	42	751.83		
Error	126	791.09		
100 kernel weight				
Linear Regression	7	0.101		2.97**
Deviation	42	0.220		6.47***
Error	126	0.034		
Yield/plant				
Linear Regression	7	406.04	1.35	2.08*
Deviation	42	300.48		1.54***
Error	126	195.39		

Contd.....

Table 6 (contd.)

Item	D.F.	M.S.	V.R$_1$	V.R$_2$
Tiller number				
Linear Regression	7	82.97	1.69	3.49***
Deviation	42	48.99		2.06***
Error	126	23.75		

$$V.R_1 = \frac{\text{M.S.}}{\text{Deviation M.S.}} \qquad V.R_2 = \frac{\text{M.S.}}{\text{Error M.S.}}$$

Table 7. Regression co-efficients b_i, S_{b_i}, β_i, stability $\bar{S}^2_d$ and correlation co-efficient (r) for the eight genotypes grown under eight different environments.

Genotypes	b_i	S_{b_i}	β_i	$\bar{S}^2_d$	r
			Panicle length		
Naizersail	4.49	1.29	4.00	-0.87	0.82
Badshabhog	0.74	1.64	-0.26	-0.058	0.18
Chinese	-0.12	0.66	-1.12	-1.73	-0.08
IR-8	1.97	1.87	0.97	0.54	0.39
IR-532	-0.25	0.54	-1.25	-1.84	-0.18
IR-20	0.19	1.17	-0.81	-1.05	0.07
IR-5	0.14	0.67	-0.86	-1.72	0.08
Kataribhog	0.81	1.15	-0.19	-1.08	0.28
Bartlett's $X^2_{(d.f.=7)}$ testing homogenity of S_{b_i} = 17.81*					
			Primary branches/panicle		
Naizersail	0.71	0.65	-0.29	-0.99	0.41
Badshabhog	1.42	0.59	0.42	-1.01	0.70
Chinese	2.73	0.58	1.73	-1.01	0.89
IR-8	1.32	0.83	0.32	-0.91	0.54
IR-532	0.31	0.81	-0.69	-0.92	0.15
IR-20	1.58	1.34	0.58	-0.60	0.43
IR-5	0.01	1.10	-0.99	-0.76	0.002
Kataribhog	0.02	0.97	-0.98	-0.84	0.009
Bartlett's $X^2_{(d.f.=7)}$ testing homogenity of S_{b_i} = 41.29***					

Contd.....

Table 7 (Contd.)

	b_1	S_{b_1}	β_1	$\bar{s}_d^2$	r
			Spikelet number/panicle		
Naizersail	1.99	1.02	0.99	-506.27	0.63
Badshabhog	-0.67	1.40	-1.67	-373.21	-0.19
Chinese	0.80	1.72	-0.20	-228.13	0.19
IR-8	1.81	1.23	0.81	-491.95	0.51
IR-532	2.61	0.76	1.61	-573.25	0.82
IR-20	-1.24	2.14	-2.24	5.13	-0.23
IR-5	0.97	1.11	-0.03	-478.70	0.34
Kataribhog	1.74	0.91	0.74	-535.55	0.61
Bartletts $X^2_{(d.f.=7)}$ testing homogenity of S_{b_1} = 43.80***					
			Kernel number/panicle		
Naizersail	0.42	0.83	-0.58	-620.56	0.20
Badshabhog	1.21	1.25	0.21	-403.89	0.38
Chinese	1.23	1.58	0.23	-176.27	0.30
IR-8	2.78	0.89	1.78	-564.15	0.72
IR-532	0.69	0.57	-0.31	-711.16	0.45
IR-20	0.29	1.41	-0.71	-302.48	0.08
IR-5	0.07	0.76	-0.93	-646.65	0.04
Kataribhog	1.31	0.67	0.31	-679.44	0.62
Bartlett's $X^2_{(d.f.=7)}$ testing homogenity of S_{b_1} = 29.12***					

Contd.....

Table 7 (Contd.)

	b_i	S_{b_i}	β_i	σ^2_i	r
			100 kernel weight		
Naizersail	1.32	0.79	0.32	-0.022	0.56
Badshabhog	0.57	0.44	-0.43	-0.031	0.45
Chinese	0.47	1.10	-0.53	-0.01	0.17
IR-8	1.11	0.84	0.11	-0.02	0.47
IR-532	1.85	0.78	0.85	-0.022	0.68
IR-20	1.16	0.53	0.16	-0.029	0.66
IR-5	1.08	0.69	0.08	-0.025	0.53
Kataribhog	0.34	0.39	-0.66	-0.032	0.30

Bartlett's $X^2_{(d.f.=7)}$ testing homogenity of S_{b_i} = 11.13^{NS}

			Yield/plant		
Naizersail	0.79	0.27	-0.21	-100.98	0.77
Badshabhog	0.78	0.17	-0.22	-157.58	0.89
Chinese	1.36	0.35	0.36	-35.30	0.85
IR-8	0.24	0.24	-0.76	-120.79	0.39
IR-532	1.51	0.16	0.51	-159.47	0.97
IR-20	1.47	0.11	0.47	-179.58	0.98
IR-5	0.94	0.20	-0.06	-141.26	0.89
Kataribhog	0.91	0.28	-0.09	-93.70	0.80

Bartlett's $X^2_{(d.f.=7)}$ testing homogenity of S_{b_i} = 11.998^{NS}

Contd.....

Table 7 (Contd.)

	b_i	S_{b_i}	β_i	σ^2_d	r
			Tiller number		
Kaizersail	1.24	0.27	0.24	7.62	0.88
Badshabhog	0.88	0.14	-0.12	-15.18	0.93
Chinese	0.89	0.14	-0.11	-15.20	0.93
IR-8	0.63	0.15	-0.37	-14.09	0.86
IR-532	1.67	0.11	0.67	-18.60	0.99
IR-20	1.06	0.12	0.06	-16.89	0.96
IR-5	0.64	0.09	-0.36	-19.78	0.94
Kataribhog	0.90	0.25	-0.10	3.87	0.83

Bartlett's $X^2_{(d.f. = 7)}$ testing homogenity of S_{b_i} = 44.03***

Table 8. Results of correlation co-efficients within characters.

	Correlations		
	Between mean ($\bar{X}$) and b_1	Between mean ($\bar{X}$) and $\bar{S}_d^2$	Between b_1 and $\bar{S}_d^2$
Panicle length	-0.04	0.60	0.65
Primary branches/panicle	0.69	0.19	-0.24
Spikelet number/panicle	-0.67	0.69	-0.59
Kernel number/panicle	-0.001	0.74*	0.047
100 kernel weight	0.154	0.34	0.074
yield/plant	0.76*	0.13	-0.099
Tiller number	0.89**	0.93***	0.22

*, ** and *** at 5%, 1% and 0.1% level D.F. = 6

Table 9. Results of correlation co-efficients between responses b_1 (upper right) and between stabilities $\bar{S}_d^2$ (lower left) among characters.

	Panicle length	Pri.br./ panicle	Spikelet number/ panicle	Kernel number/ panicle	100 kernel weight	yield/ plant	Tiller number
Panicle length		-0.133	0.606	0.121	0.149	-0.61	0.021
Primary branches/ panicle	-0.254		-0.892**	0.292	-0.328	0.148	-0.18
Spikelet number/ panicle	-0.075	0.488		0.421	0.693	-0.382	0.609
Kernel number/ panicle	0.033	-0.004	0.868**		-0.283	-0.641	-0.388
100 kernel weight	-0.232	-0.29	0.031	0.258	-	0.209	0.634
Yield/ plant	-0.225	-0.536	-0.12	0.253	0.466		0.603
Tiller number	0.987***	-0.477	-0.667	-0.634	-0.263	0.78*	

B. G X E INTERACTION OF YIELD AND YIELD COMPONENTS AND SOME MORPHOLOGICAL AND DEVELOPMENTAL CHARACTERS OF FIVE PARENTAL LINES OF NIGS FOR SEASONS I AND II.

(a) Means and Relative Importance to Different Nutrients

Means of twelve characters over replications and genotypes for two years are shown in table 10. The table shows that almost all the characters were affected by seasons and different nutritional treatments. The environmental means (table 10) also show that populations in general gave better performances in N combination treatments. All the characters except panicle length, primary branches/panicle and 100 kernel weight were greatly affected by the nutritional treatments.

Population means over replications, nutritional treatments and seasons for all the characters are shown in table 11. IR-8 and IR-20 gave the highest panicle length and primary branches/panicle. The highest numbers of spikelet and kernel/panicle was found in IR-20 while Chinese, IR-532 and IR-20 gave the best yield performances. In case of tiller number IR-532 gave the highest number of tillers. Fresh shoot weight was the highest in IR-532 but that of dry shoot was high in IR-5. Fresh and dry root weight was high in IR-8 but the highest plant height was observed in IR-5.

Results of analysis of variance for all the characters are shown in table 12. The results showed that the items genotype (G) and season (Y) were highly significant in all the characters indicating that a real difference existed among the genotypes studied and that the genotype were greatly affected by seasons. The results also show that a real effects of treatments were found in yield/plant, tiller number, fresh shoot weight, dry shoot weight, fresh and dry root weight as the nutrition (N) item was highly significant in these characters. The other characters exhibited no effect of nutrition. The analysis also shows that the populations interacted significantly with all the

environmental effects (climatic and edaphic) in most of the characters. The item G X Y was significant in all the cases except in 100 kernel weight where it was non-significant. The item G X N was non-significant in primary branches/panicle and plant height whereas the item N X Y was non-significant in all the cases except yield/plant, tiller number and fresh and dry shoot weight. The third order interaction i.e. G X Y X N was non-significant in five characters viz. primary branches/panicle, spikelet number/panicle, kernel number/panicle, 100 kernel weight and dry shoot weight. As the replication item was significant in fresh shoot weight and dry root weight, all the items in these two characters when tested by replication m.s. showed non-significant.

As the analysis of variance shows that the genotypes responded differently under different nutritional treatments and seasons, the next step was to evaluate the individual effect of the nutrients and seasons for each genotype separately. The results of effects of nutrients on all the characters of each genotype are shown in table 13.

Panicle Length : For panicle length N had positive significant effect on IR-20 and significantly negative effect on IR-8 and IR-5 in Y_1 only. N had no effect on Chinese and non-significant effect on IR-532 in Y_1 but in Y_2 the effect of N was positively significant in most of the varieties except IR-20 where it was negative and non-significant. The effect of P was positive and significant on IR-532 and IR-20 but significantly negative on IR-8 and IR-5 in Y_1 but its effect was positive and significant on Chinese, IR-20 and IR-5 and negatively significant on IR-532 during Y_2. K had significant effect on Chinese, IR-8 and IR-20 in Y_1 but positive effect was found only

on IR-8, whereas, in Y_2 positive significant effect was found on IR-8 and IR-20 but negative significant effect was on Chinese and IR-5. Among the interactions NP had the highest positive significant effect on IR-8 in Y_1. The other significant effect due to NP was found on Chinese in both the seasons and on IR-5 during Y_1. NK had significant effect on all the varieties and the effect was negative on IR-8 and IR-5 in Y_1, significant effect was found in all the varieties except IR-20 during Y_2; the effect was negative in case of IR-532 only. PK had positive significant effect on Chinese in both the seasons, negative significant effect on IR-8 in Y_1, on IR-532 and IR-5 in Y_2. NPK had positive effect on Chinese in Y_1, on IR-8 in both the seasons on IR-532 in Y_1 and on IR-20 and IR-5 in Y_2.

Primary Branches/Panicle : The effects of N, P, K and NK were positively significant and that of NP and PK were negatively significant on Chinese during Y_1 but positive and significant effect was found for P, NP, NK and NPK during Y_2 whereas N showed negatively significant effect. The effects of P, K, NP and NPK were positively significant on IR-8 and PK had negatively significant effect during Y_1 whereas the effects of P and NK were positively and those of N and NP were negatively significant during Y_2. In case of IR-532, N, P, NP and NK had positive significant effect in Y_1 but during Y_2 N, NP, PK and NPK had significant negative effects. The effects of N, P, K and PK significantly increased the primary branch number and NP and NPK significantly decreased the primary branch number during Y_1 whereas during Y_2 significant positive effect was noted due to P only and N, NP, NK and NPK produced significantly negative effect. The effects of NK, PK and NPK were significantly

positive and those of N and P were significantly negative during Y_1 but N, NP, NK and PK significantly increased and P, K and NPK significantly decreased the primary branch number in IR-5 during Y_2 (table 13).

Spikelet Number/panicle : N, P, NP and NPK significantly increased the spikelet number/panicle and N, NK and PK significantly decreased the spikelet number during Y_1 whereas the effect of N, P, PK and NPK were positively significant and that of K was negatively significant on Chinese during Y_2. In case of IR-8 the effects of all the nutrients except P and K were negative during Y_2. All the nutritional effects were significant on IR-532 during Y_1 of which P, K, NP and NPK had positive effects and the rests had negative effects but during Y_2 significant positive effect was found due to N, P, NP and significant negative effect was due to PK only. During Y_1, N, NP, NK and PK significantly increased the spikelet number in IR-20; the heighest effect was due to NK whereas the effect of NPK was negatively significant. During Y_2 all the nutrients except K decreased the spikelet number. In case of IR-5 positive effects were found due to K, NP, PK and NPK and the rests had negative effects during Y_1 while positive effects of N, K, NK, PK and NPK and negative effects of P, NK, P and K were observed during Y_2 (table 13).

Kernel Number/panicle : N significantly decreased the kernel number of Chinese during Y_1, of IR-8 and IR-532 during both Y_1 and Y_2, whereas it significantly increased the kernel number of IR-20 during Y_1, of Chinese and IR-5 during Y_2. P had positive effects on Chinese and IR-8 in both the seasons, on IR-20 and IR-5 during Y_2 but its

effect was significantly negative on IR-20 and IR-5 in Y_1 and on IR-532 in both the seasons. The effect of K were significantly positive on IR-532 and IR-20 whereas on Chinese its effect was significantly negative during Y_1. Positive significant effect of K was observed on Chinese, IR-8 and IR-20 during Y_2. NP had positive effects on Chinese and IR-8 and negative effect on IR-532, IR-20 and IR-5 during Y_1 while all the varieties except IR-20 and IR-5 responded positively during Y_2. All the varieties responded significantly to NK but the responses were negative in case of Chinese, IR- 532 and IR-5 during Y_1 whereas NK had positive effect on IR-8, IR-20 and IR-5 and negative effect on Chinese and IR-532 during Y_2. PK significantly increased the kernel number in Chinese during Y_2, in IR-532 and IR-20 during Y_1 and in IR-5 in both the seasons but it significantly decreased the kernel number of IR-532 during Y_2 and of IR-8 in both the seasons. NPK had positive effects on Chinese in both the seasons, on IR-8 and IR-532 during Y_2 and on IR-5 during Y_1, but its effects were negative on IR-8 and IR-532 during Y_1 and on IR-20 in both the seasons.

100 Kernel Weight : In case of 100 kernel weight the effects of all the nutrients except NP and NPK during Y_1 were negative in both the seasons on Chinese. In case of IR-8 all the nutritional treatments were significant in both the seasons except K and PK during Y_2 but positive significant effects of NK, PK and NPK was observed during Y_1 and of NK, NPK during Y_2. IR-532 responded significantly to all the nutritional treatments in both the seasons except N and NP during Y_2 of which positive significant effect was found due to P, K, NP and NK during Y_1 and due to P, K and NPK during Y_2. Positive and significant effect on IR-20 was observed on account of K, NP and NK during Y_1 and due to K, NK and PK during Y_2. On IR-5 positive and significant effect

was found due to NK and NPK during Y_1 and due to NP, NK and NPK during Y_2 but N and K showed negative effect on IR-5 during both the seasons.

Yield/Plant : N significantly increased the yield of all the five varieties during Y_1 and Chinese and IR-5 during Y_2 but it significantly decreased the yield/plant of IR-8 and IR-532 during Y_2. P had significant positive effect on all the varieties during Y_1 and IR-8 during Y_2 whereas it significantly decreased the yield/plant of chinese during Y_2. K decreased the yield performances of all the varieties in both the seasons as its effect was negative in most of the cases except IR-8 and IR-5 during Y_2. Positive effects due to NP were observed for all the varieties during Y_1 but its effects were negative on all the cases except Chinese and IR-8 during Y_2. NK had significant positive effect on all the varieties except IR-8 where its effect was negative during Y_1, whereas the effects were non-significant on all the varieties during Y_2. Positive significant effect of PK was found in case of Chinese, IR-532 and IR-5 during Y_1 and Chinese during Y_2. PK decreased the yield of IR-8 in both the seasons and that of IR-532, IR-20 and IR-5 during Y_2. Positive significant effect of NPK was observed on Chinese and IR-20 during Y_1 only.

Tiller number : Application of N alone significantly increased the tiller number of all the varieties during both the seasons. P also had significant positive effects on all the varieties in both the seasons except Chinese and IR-5 during Y_2. All the varieties responded negatively due to the effects of K except IR-8 and IR-532 during Y_1 and IR-5 during Y_2. NP had significant positive effects on Chinese during Y_1, on IR-8, IR-532 and IR-20 in both the seasons but the effect was negative on Chinese and IR-5 during Y_2. NK had positive effects on all the varieties except IR-5 in both the seasons. The effects of PK were

positive and significant on Chinese and IR-532 during both the seasons, IR-8 during Y_1 whereas the effects were negative in case of IR-20 in both the seasons and IR-8 and IR-5 during Y_2. Significant effects of NPK were observed on all the varieties except IR-8 during Y_2 but the effects were negative in case of IR-532, IR-20 and IR-5 during Y_2.

Fresh shoot weight (FSW) : N significantly increased the fresh shoot weight of all the varieties during both the seasons. P had positive effects on all the varieties in both the seasons except IR-5 in Y_2. The positive effects of P were however, non-significant in case of Chinese and IR-532 during Y_2 only. Significant effects of K were found for all the varieties except Chinese during Y_1 and IR-5 during Y_2 of which positive significant effect was found only for IR-532 during both the seasons, on IR-532, IR-20 and IR-5 during Y_1 whereas during Y_2 its effect was negative on Chinese, IR-532, IR-20 and IR-5. Positive effects due to NK were observed on all the varieties in both the seasons except Chinese in Y_2. PK had significant positive effect on Chinese during both the seasons, on IR-532 in Y_1 and on IR-20 in Y_2 but its effect was negatively significant on IR-20 in Y_1 and on IR-8 and IR-5 during Y_2. Positive significant effects due to NPK were observed on Chinese, IR-8, IR-532 and IR-20 during Y_1 and on IR-5 during both the seasons whereas its effects were negative on IR-8, IR-532 and IR-20 during Y_2.

Dry Shoot Weight (DSW) : All the varieties had significantly positive effect in both the seasons due to N and P. The effect of K was negative in all the cases except Chinese during Y_1. NP combination had positive effect on all the varieties except IR-20 during Y_2 and IR-5 in both the seasons. NK had positive effect on all the varieties except Chinese during Y_2. The effect of PK was positive on Chinese

during Y_2 and on IR-20 during Y_1 on IR-8 and IR-5 during Y_1 and on IR-532 in both the seasons. NPK had the positive effect on all the varieties in both the seasons exception being IR-20 during Y_2.

Fresh Root Weight (FRW) : In this case N had positive and significant effect on all the varieties studied. All the varieties, except Chinese during Y_2 and IR-20 during Y_1, showed significant positive effect due to P. The effect of K was positive on all the varieties during Y_2 but during Y_1 positive effect was found on IR-5 only. The combination of NP had positive effect on most of the cases. NK also increased the fresh root weight except Chinese during Y_2 and IR-532 during Y_1. In most of the cases PK and NPK significantly decreased the fresh root weight.

Dry Root Weight (DRW) : The effects of all the nutrients were significantly increased the dry root weight for Chinese during Y_1 but decreased during Y_2. For IR-8 the effects of N, P, NP and NPK were positive in both the seasons. Negative effect was observed due to K in both the seasons. On IR-532 N, P, NK and NPK had positive effect but K significantly decreased the dry root weight during Y_1, whereas during Y_2 all the nutritional treatments except NPK significantly increased the dry root weight. All the nutrients except N and NP decreased the dry root weight of IR-20 during Y_1 but during Y_2, dry root weight was increased by all the nutrients. On IR-5 significant positive effect was found due to P, K, NP, NK and NPK during Y_1 and due to K, NP, NK and NPK during Y_2 but negative effect was produced by N and PK in both the seasons.

Plant Height (PH) : N had significant positive effect on Chinese and IR-5 during Y_2, on IR-8 during Y_1 and on IR-532 in both the seasons. Most of the varieties had positive effect due to P. R had negative effect in most of the cases. Significant positive effect of NP was noted on Chinese during Y_2 and on IR-8 during Y_1. NK had significant positive effect on Chinese and IR-532 during Y_1, on IR-8 in both the seasons and on IR-5 during Y_2. Most of the varieties responded negatively to the effects of PK and NPK.

(b) Variability

The phenotypic variance was repartitioned into genotypic (δ^2_G), environmental (δ^2_E), N X G (δ^2_{NG}), G X Y (δ^2_{GY}) and G X N X Y (δ^2_{GNY}) variation from the component analysis of variance assuming a mixed model with a fixed number of populations (G), random sample of environments (N) with (r) replications and seasons (Y). The expectation of mean squares are as follows :-

Source	M.S.	Expectation of M.S.
Population(G)	M_1	$\delta^2_E + r\delta^2_{NYG} + rY\delta^2_{GN} + rN\delta^2_{GY} + rNY\delta^2_G$
N X G	M_2	$\delta^2_E + r\delta^2_{NYG} + rY\delta^2_{GN}$
G X Y	M_3	$\delta^2_E + r\delta^2_{NYG} + rN\delta^2_{GY}$
G X N X Y	M_4	$\delta^2_E + r\delta^2_{NYG}$
Error	M_5	δ^2_E

The genotype, environmental and the interactions variances were calculated as follows :-

$$\delta^2_G = (M_1 - M_2) - (M_3 - M_4)/rNY$$

$$\delta^2_{NG} = (M_2 - M_4)/rY$$

$$\delta^2_{GY} = (M_3 - M_4)/rN$$

$$\delta^2_{GNY} = (M_4 - M_5)/r$$

$$\delta^2_E = M_5$$

Estimates of δ^2_G, δ^2_{NG}, δ^2_{GY}, δ^2_{GNY} and δ^2_E and their co-efficient of variability for the twelve characters are shown in table 14. Greater

portion of the total phenotypic variation was of genetic in nature in case of tiller number and plant height whereas the influence of δ^2_E was greater in all the cases except tiller number and plant height. The influence of δ^2_{NG} was negative in case of panicle length, yield/plant, fresh root weight and plant height. Fresh root weight and dry root weight showed negative δ^2_G value. The δ^2_{GY} was greater than δ^2_G in case of panicle length, yield/plant, fresh shoot weight, dry shoot weight, fresh root weight and dry root weight. The influence of δ^2_{GNY} was very low in most of the cases compared to any of the interactions and was negative in the case of primary branches/panicle, spikelet number/panicle, kernel number/panicle, 100 kernel weight and dry shoot weight. The co-efficient of variability was very high in case of spikelet number/panicle, kernel number/panicle, tiller number, fresh shoot weight and dry shoot weight.

(c) Regression

As the interaction item was significant in the analysis of variance in most of the cases, the data were subjected to regression analysis. For this the eight treatments of N, P, K were treated as different environments over two seasons. There were thus a total of sixteen environments which were measured quantitatively by the means of all the five genotypes.

The sum of mean squares of interactions were repartitioned (joint regression analysis) and are shown in table 15. The heterogenity regression item was significant in all the cases except 100 kernel weight, yield/plant, fresh shoot weight and fresh root weight indicating the genotype-environment interaction was due to the difference between slopes of the linear regressions. The deviation mean square was significantly greater than that of error M.S. for all cases except 100 kernel weight and the linear mean square was significantly greater than deviation M.S. in most of the characters.

Both the items when tested against experimental error were significant except in the case of 100 kernel weight only. Linear regression item was non-significant in case of yield/plant, fresh shoot weight and fresh root weight. The regression item when tested by residual item alone was significant in case of dry root weight and primary branches/panicle. In other characters it was non-significant.

Regression co-efficients b_i, β_i, standard error (S_{bi}), Stability ($\bar{S}^2_d$) and correlation co-efficient (r) between environmental mean of each genotype were calculated and are shown in table 16. Both high and low correlation co-efficients (r) were found which indicated linear

and non-linear variations of these genotypes. As revealed by joint regression, the distribution of all the five b_i values were heterogenous and for this all the genotypes had different responses to different environments.

For panicle length IR-8, IR-20 and IR-5 showed above average responses but the other two varieties showed non-significant below average response. Low correlation co-efficient (r) values of all the varieties indicated that non-linear variations were associated with the genotypes.

Four varieties such as Chinese, IR-8, IR-532 and IR-20 showed significant responses to environments incase of primary branches/panicle but IR-532 showed below average response. IR-5 practically had no response to environments (b_i = 0.01); it also had low correlation co-efficient value indicating the presence of non-linear variations. All other varieties had high correlation co-efficient (r) indicating that the linear response accounted for most of the variations over environments in these genotypes.

In case of spikelet number/panicle all the five genotypes showed significant linear responses to the environments but responses above average were observed in Chinese and IR-20. All the genotypes except IR-8 had high correlation co-efficients (r) values.

All the five genotypes showed significant linear responses in case of kernel number/panicle. Above average responses were observed in case of Chinese and IR-20. The other three varieties had a more or less same responses to the environments. All the varieties except Chinese and IR-532 had low correlations which indicated the presence of non-linear variation.

All the five genotypes responded significantly in case of 100 kernel weight. Above average responses were found in IR-20 and IR-5 Most of the genotypes had low correlation co-efficient (r) values indicating the presence of non-linear variation in these genotypes for the character.

In case of yield/plant significant linear responses were observed in all the varieties but Chinese, IR-532 and IR-20 had above average responses. Correlation co-efficient (r) values were very high in all the cases indicating the presence of linear variation in these genotypes.

All the varieties showed significant linear responses to the environments in case of tiller number. Among them IR-532 and IR-20 had above average responses and the rests had below average responses to the environments. All varieties showed high correlation co-efficient(r) values which indicated that linear responses accounted for most of the variation over environments for these genotypes.

In case of fresh shoot weight significant linear responses were observed in all the varieties but Chinese, IR-8 and IR-532 had above average responses while the rests had below average responses to the environments. High correlation co-efficient(r) values were observed in all the cases.

All the genotypes responded significantly to the environments in case of dry shoot weight and the responses of IR-8 and IR-5 were above average. All except IR-532 had high correlation co-efficient values.

In case of fresh root weight IR-8 showed the highest responses ($b = 2.17 \pm 0.25$) to the environments. The significant linear responses were observed in case of Chinese, IR-8 and IR-5 of which IR-5 had above average response and the other two had below average response. Low correlation co-efficient (r) values were found in three out of five genotypes.

For dry root weight all the five genotypes showed significant linear responses to the environments. The highest responses were observed in IR-8 (1.85 ± 0.25) and IR-532 (b = 1.05 ± 0.46). The other three genotypes had below average responses. All the varieties except IR-8 had low correlation co-efficient (r) values indicating the presence of non-linear variation in the genotypes.

In case of plant height significant linear responses were observed in all cases. The above average responses were met in Chinese, IR-20 and IR-5 while IR-8 and IR-532 showed below average responses. All genotypes showed high correlation co-efficient (r) values.

The standard error (S_{bi}) proved to be heterogenous as X^2 in Bartlett's test (shown at the botton of each character in table 16) was significant in most of the cases. This indicated that the extent of deviation from regression line was specefic to and characteristic of particular population which was under gene control. The $\bar{S}^2_d$, another measure of variation arround the regression slope, was highly heterogenous in these characters as revealed by joint regression and S_{bi} results. Most of the genotypes showed considerable stability as shown by their low $\bar{S}^2_d$ values in case of panicle length primary branches/panicle and 100 kernel weight. High $\bar{S}^2_d$ values indicated the instability of the genotypes. For tiller number and plant height the genotypes showed high $\bar{S}^2_d$ values.

The actual regression line of the performances of each genotype in the different environments against the corresponding environmental mean are shown in Figs. 8-19. To avoid confusion, individual points were not plotted in the figures. Crossing of regression line was very marked in most of the characters indicating that G X E interactions were marked in these characters.

Explanation to the Figs. 8-19.

Fig. 8. Regression of individual population mean on environmental mean for five parental lines in panicle length.

Fig. 9. Regression of individual population mean on environmental mean for five parental lines in primary branches/panicle.

Fig. 10. Regression of individual population mean on environmental mean for five parental lines in spikelet number/panicle.

Fig. 11. Regression of individual population mean on environmental mean for five parental lines in kernel number/panicle.

Fig. 12. Regression of individual population mean on environmental mean for five parental lines in 100 kernel weight.

Fig. 13. Regression of individual population mean on environmental mean for five parental lines in yield/plant.

Fig. 14. Regression of individual population mean on environmental mean for five parental lines in tiller number.

Fig. 15. Regression of individual population mean on environmental mean for five parental lines in fresh shoot weight.

Fig. 16. Regression of individual population mean on environmental mean for five parental lines in dry shoot weight.

Fig. 17. Regression of individual population mean on environmental mean for five parental lines in fresh root weight.

Fig. 18. Regression of individual population mean on environmental mean for five parental lines in dry root weight.

Fig. 19. Regression of individual population mean on environmental mean for five parental lines in plant height.

The serial numbers in the graphs are for 3 = Chinese, 4 = IR-8, 5 = IR-532, 6 = IR-20 and 7 = IR-5.

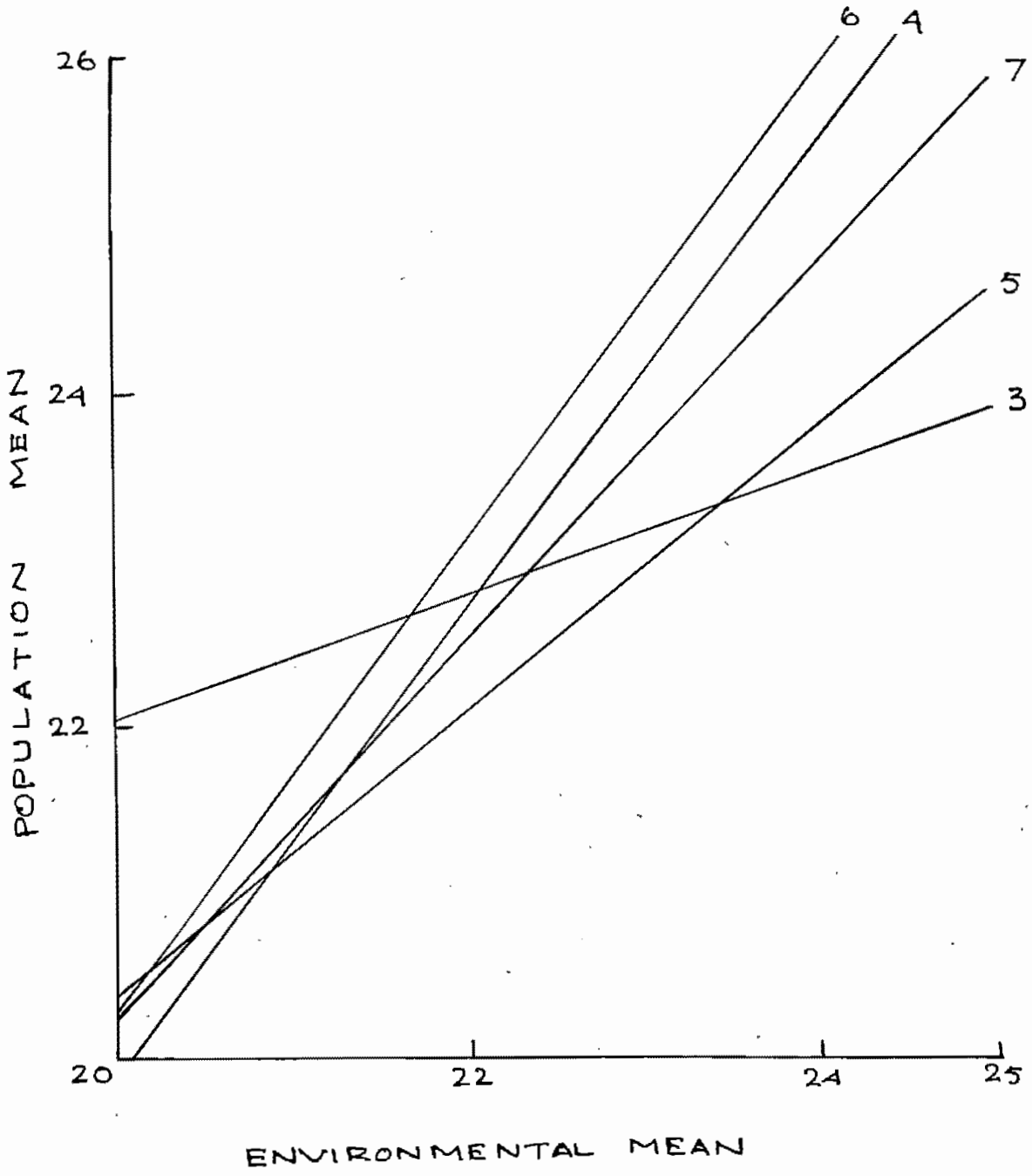

6
4
7
5
3
26
24
22
20
22
24
25
POPULATION MEAN
ENVIRONMENTAL MEAN

FIG. 8

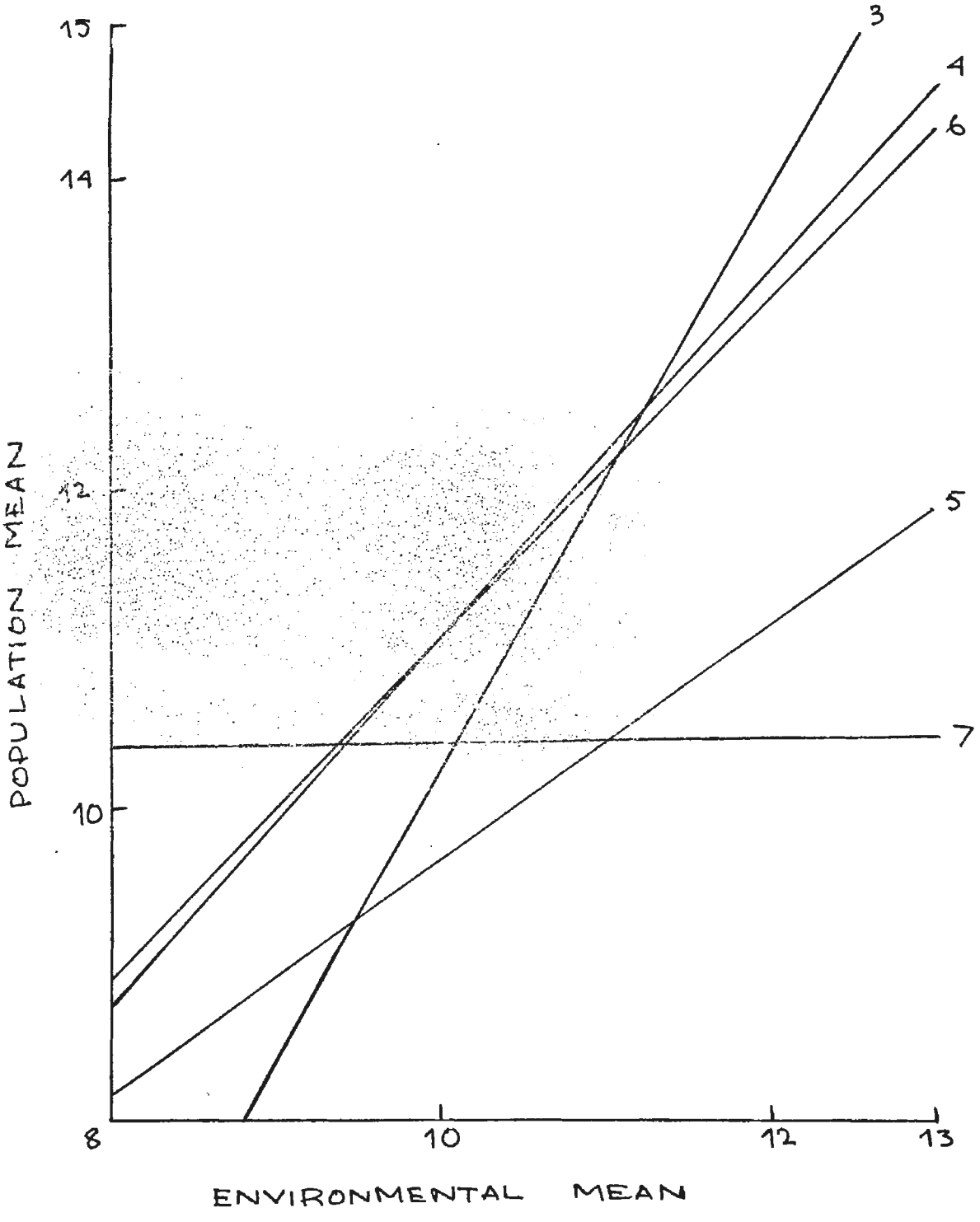

15
14
12
10
8
POPULATION MEAN
3
4
6
5
7
10
12
13
ENVIRONMENTAL MEAN

FIG. 9

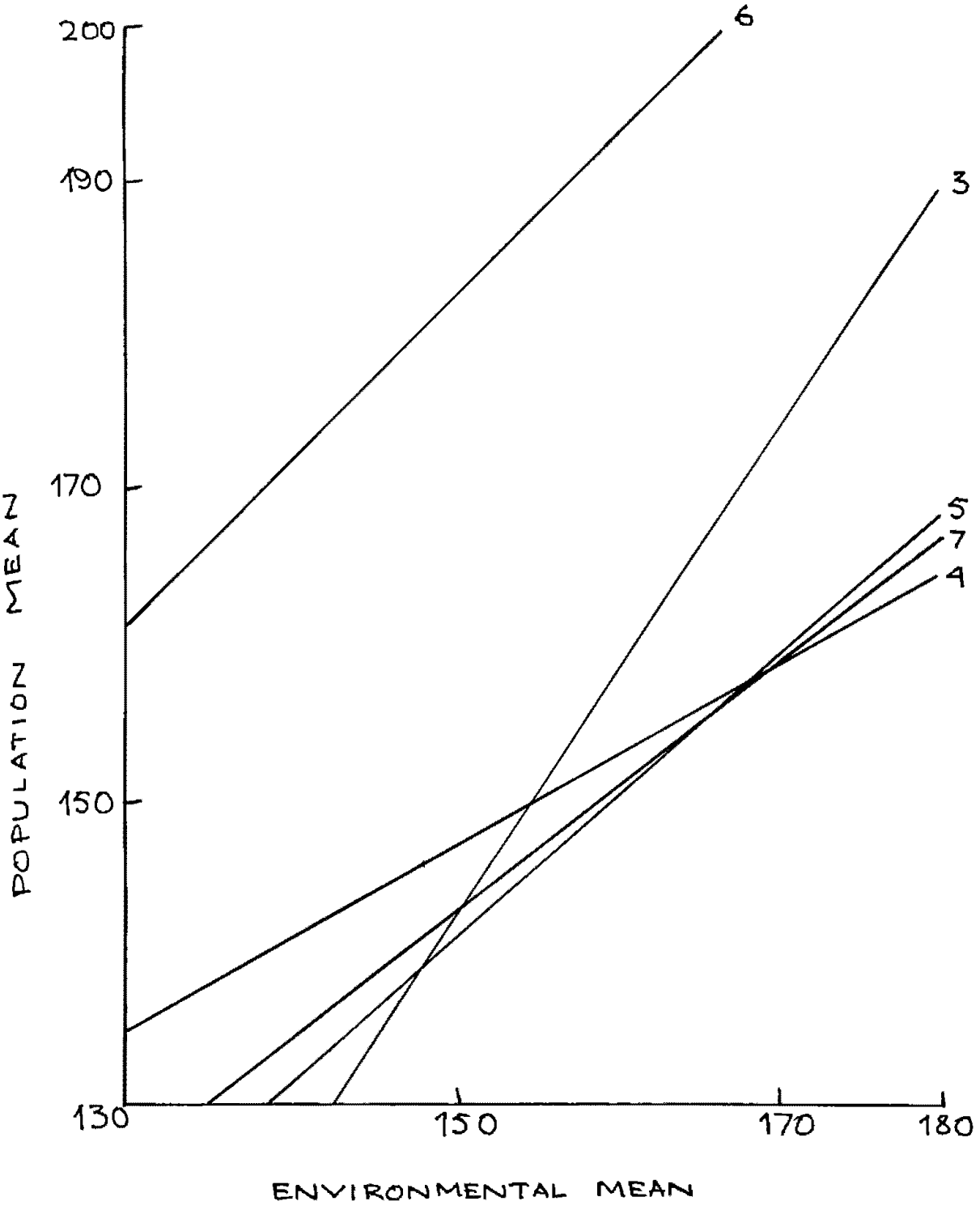

200
190
170
150
130
POPULATION MEAN
6
3
5
7
4
150
170
180
ENVIRONMENTAL MEAN

FIG. 10

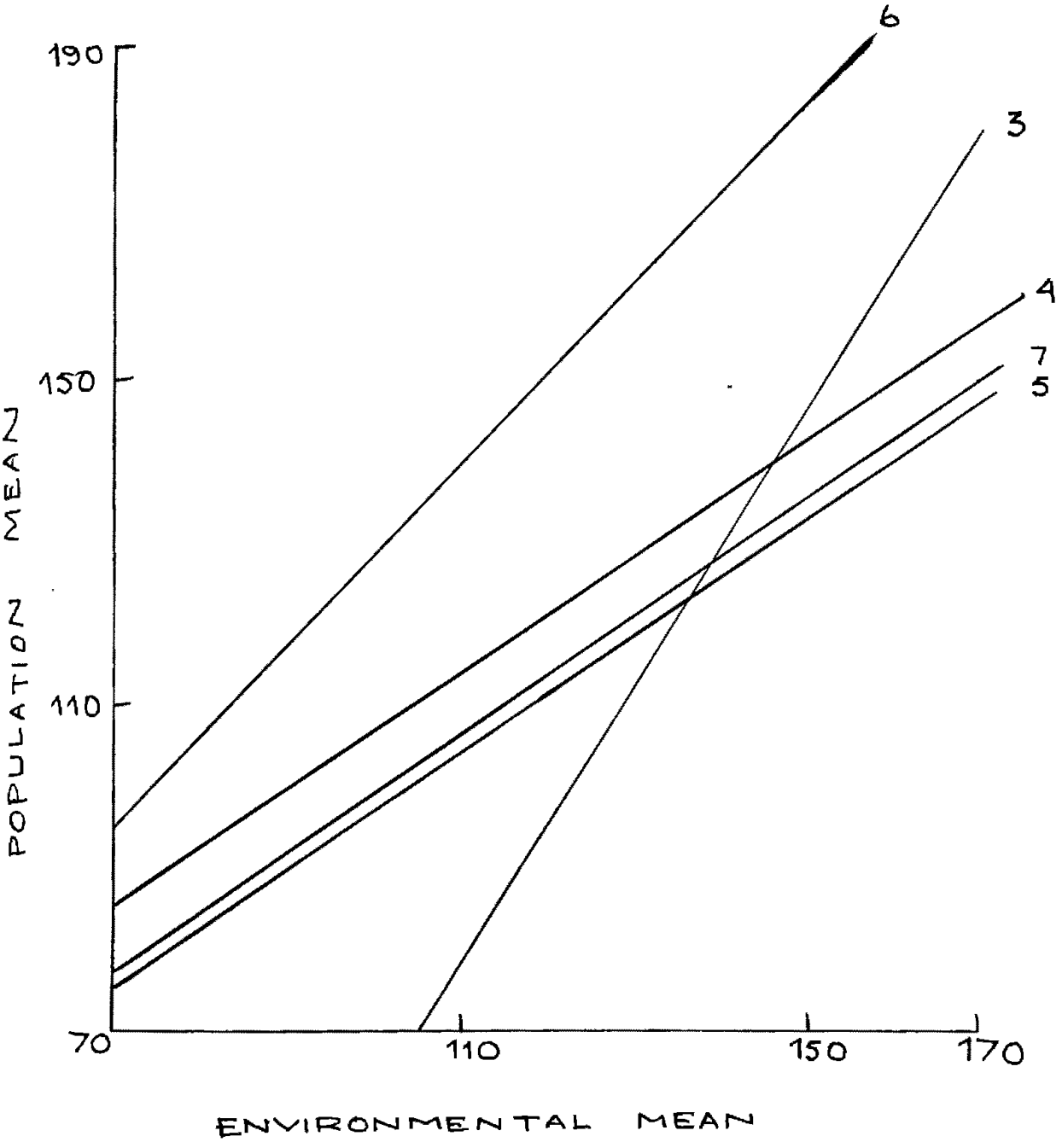

6
3
4
7
5
190
150
110
70
110
150
170
POPULATION MEAN
ENVIRONMENTAL MEAN

FIG. 11

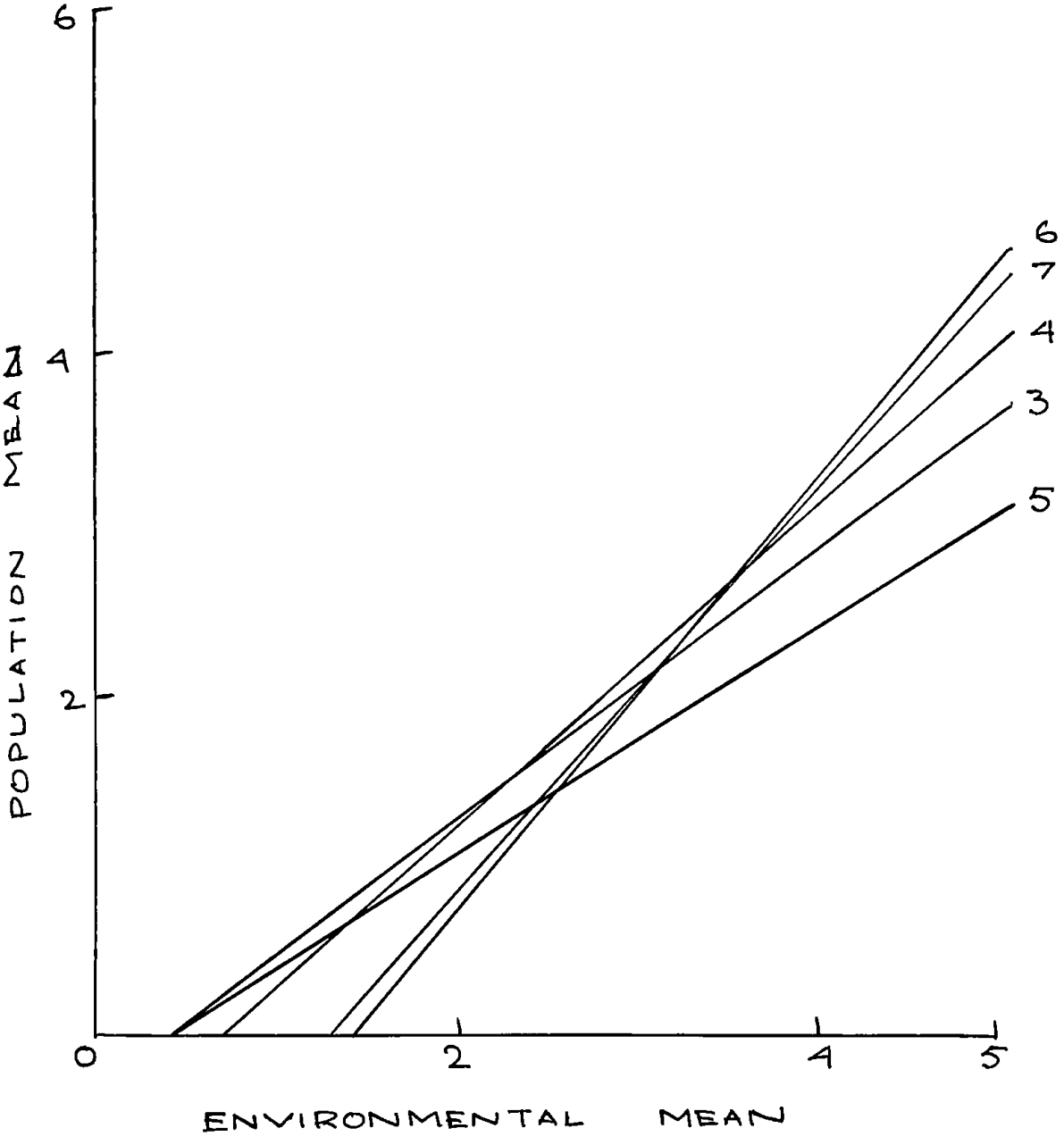


FIG. 12

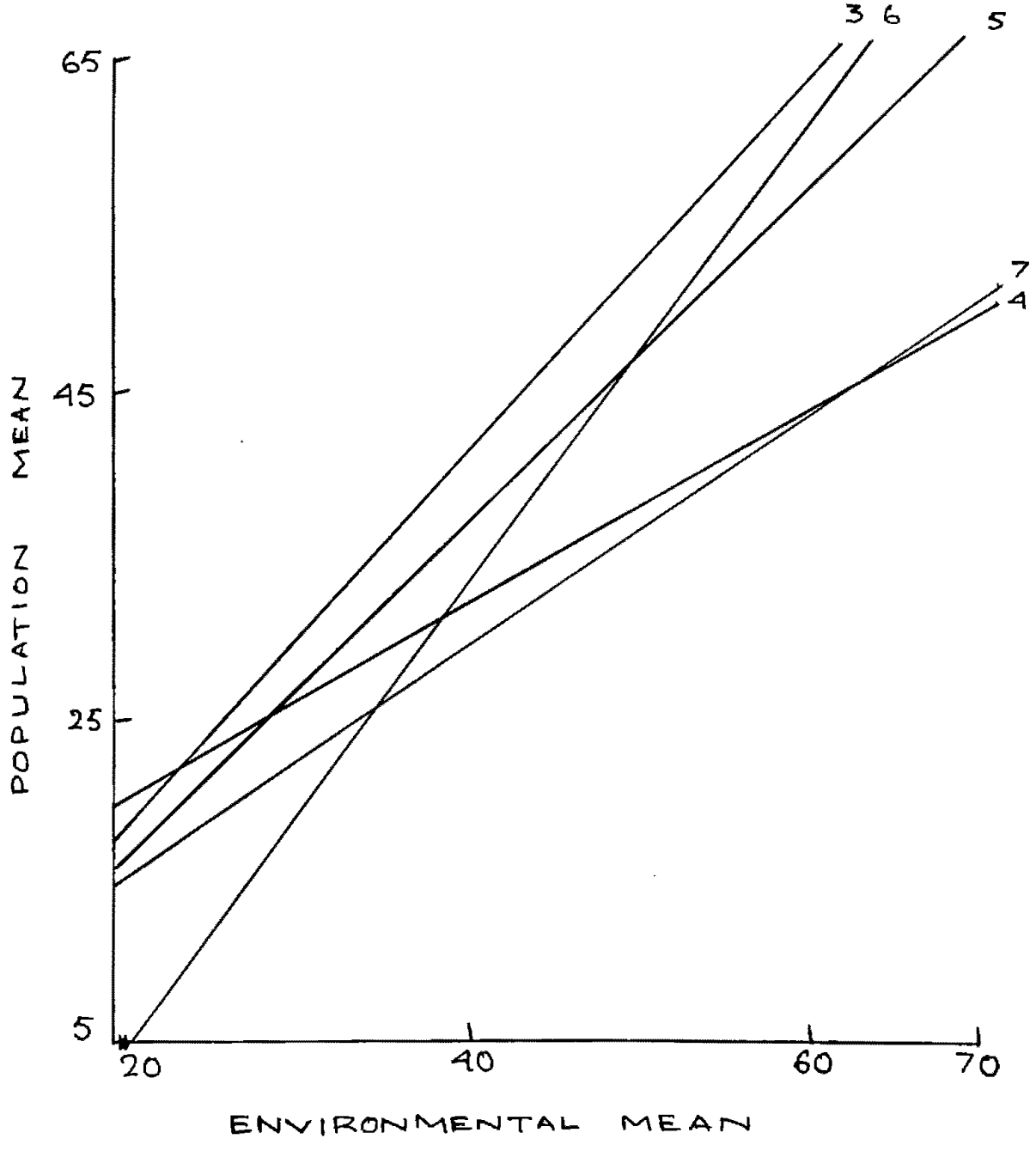

3
6
5
7
4
65
45
25
5
POPULATION MEAN
20
40
60
70
ENVIRONMENTAL MEAN

FIG. 13

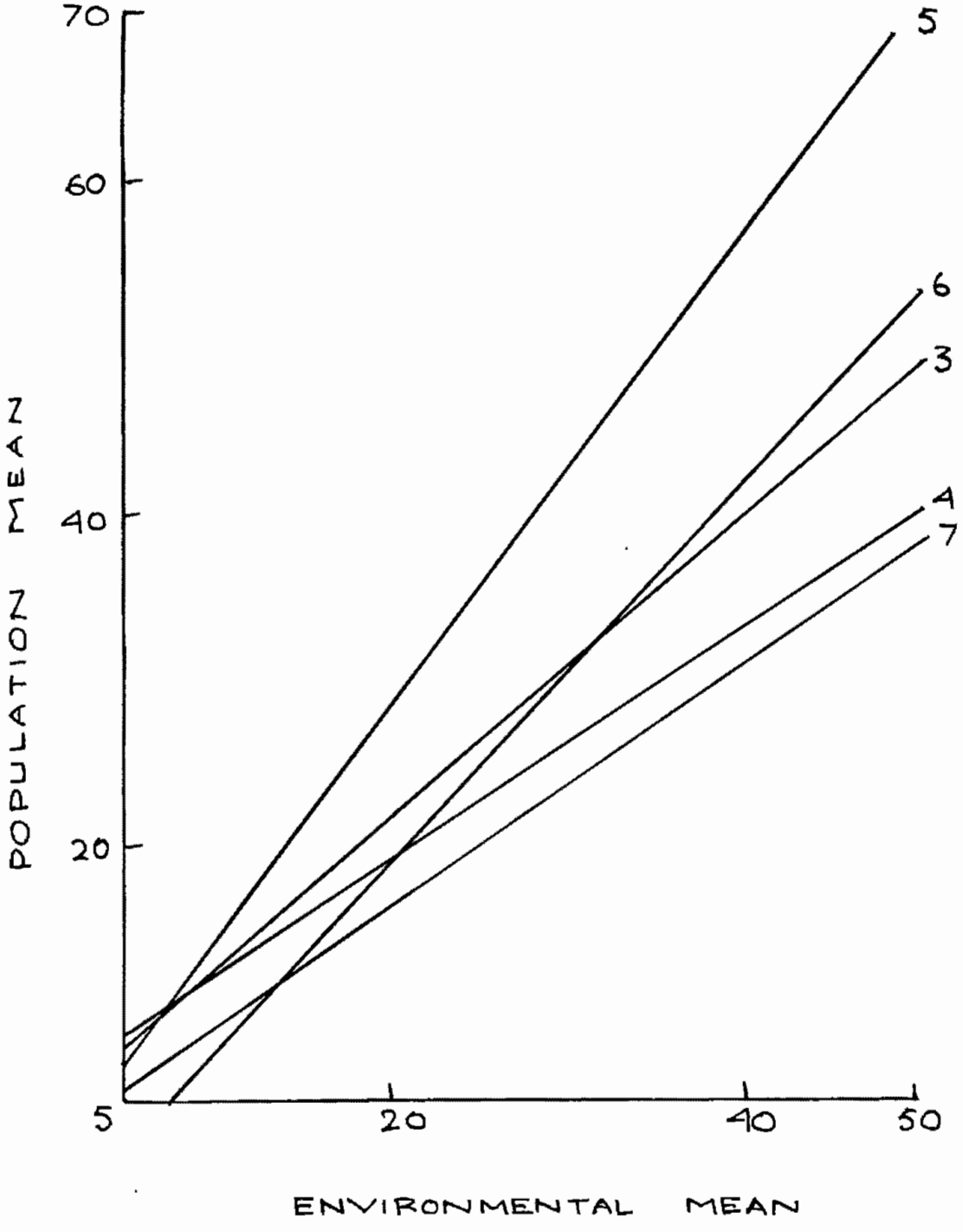

70
60
40
20
5
20
40
50
5
6
3
4
7
POPULATION MEAN
ENVIRONMENTAL MEAN

FIG. 14

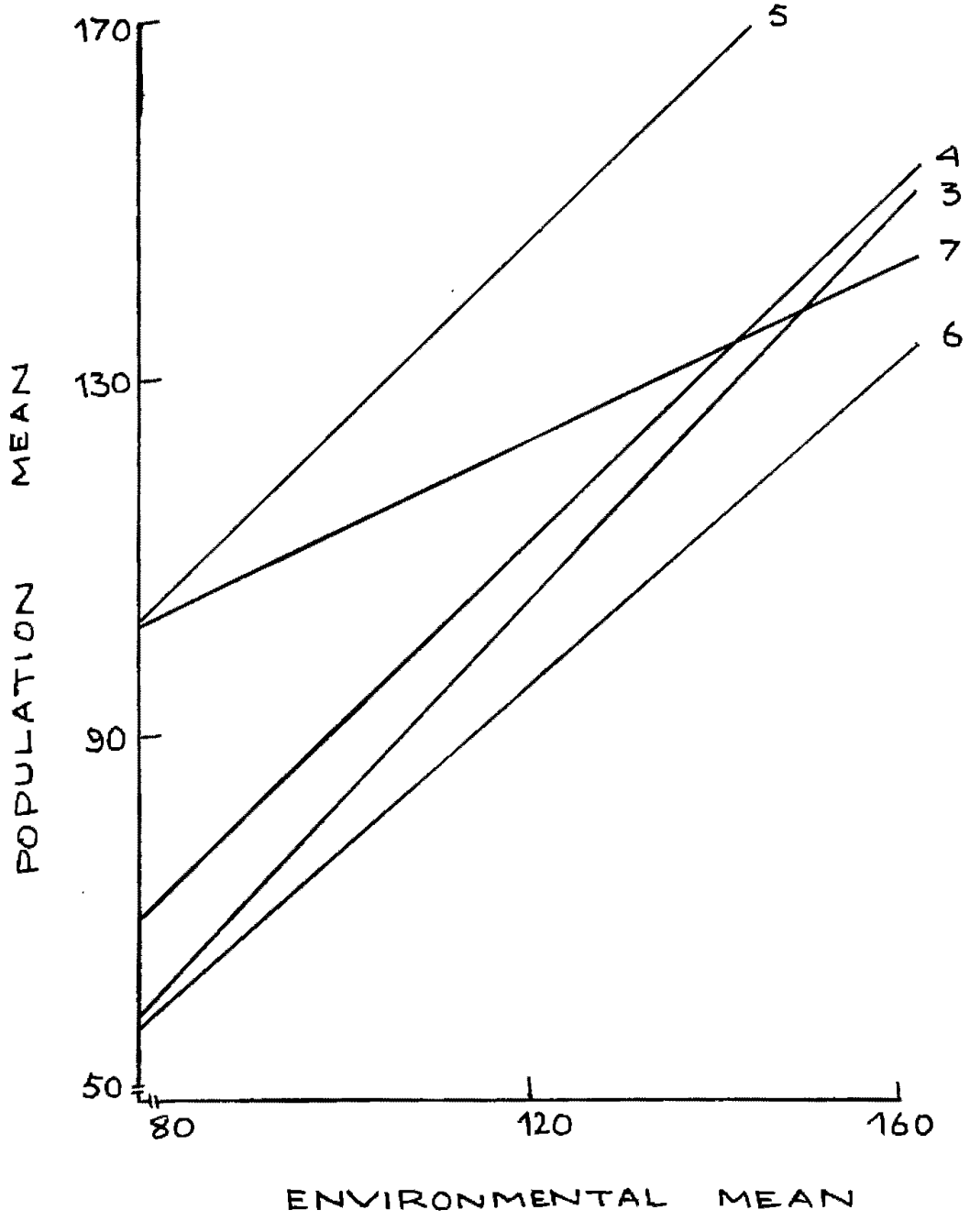

170
130
90
50
POPULATION MEAN
80
120
160
ENVIRONMENTAL MEAN
5
4
3
7
6

FIG. 15

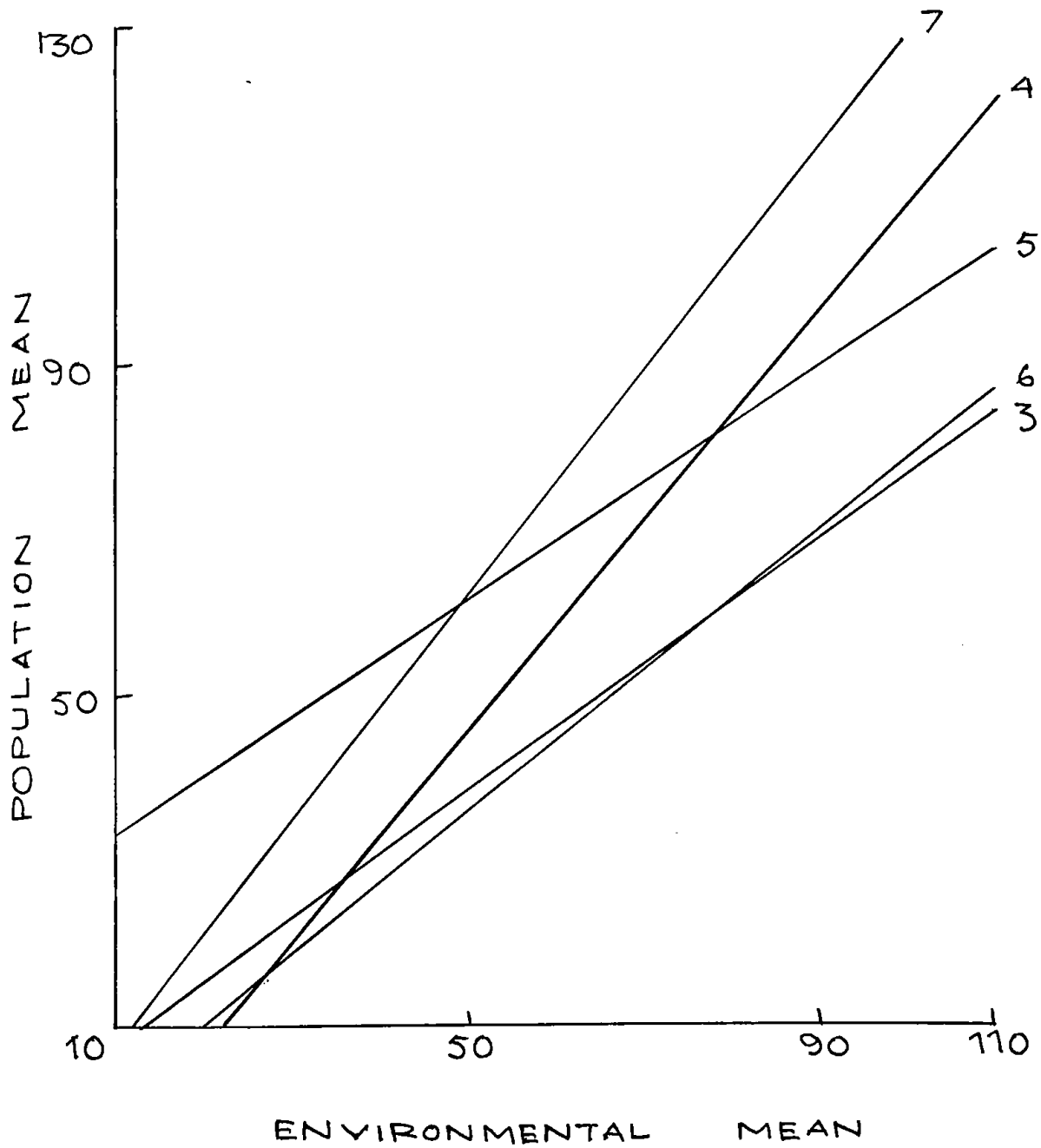

130
90
50
10
POPULATION MEAN
7
4
5
6
3
10
50
90
110
ENVIRONMENTAL MEAN

FIG. 16

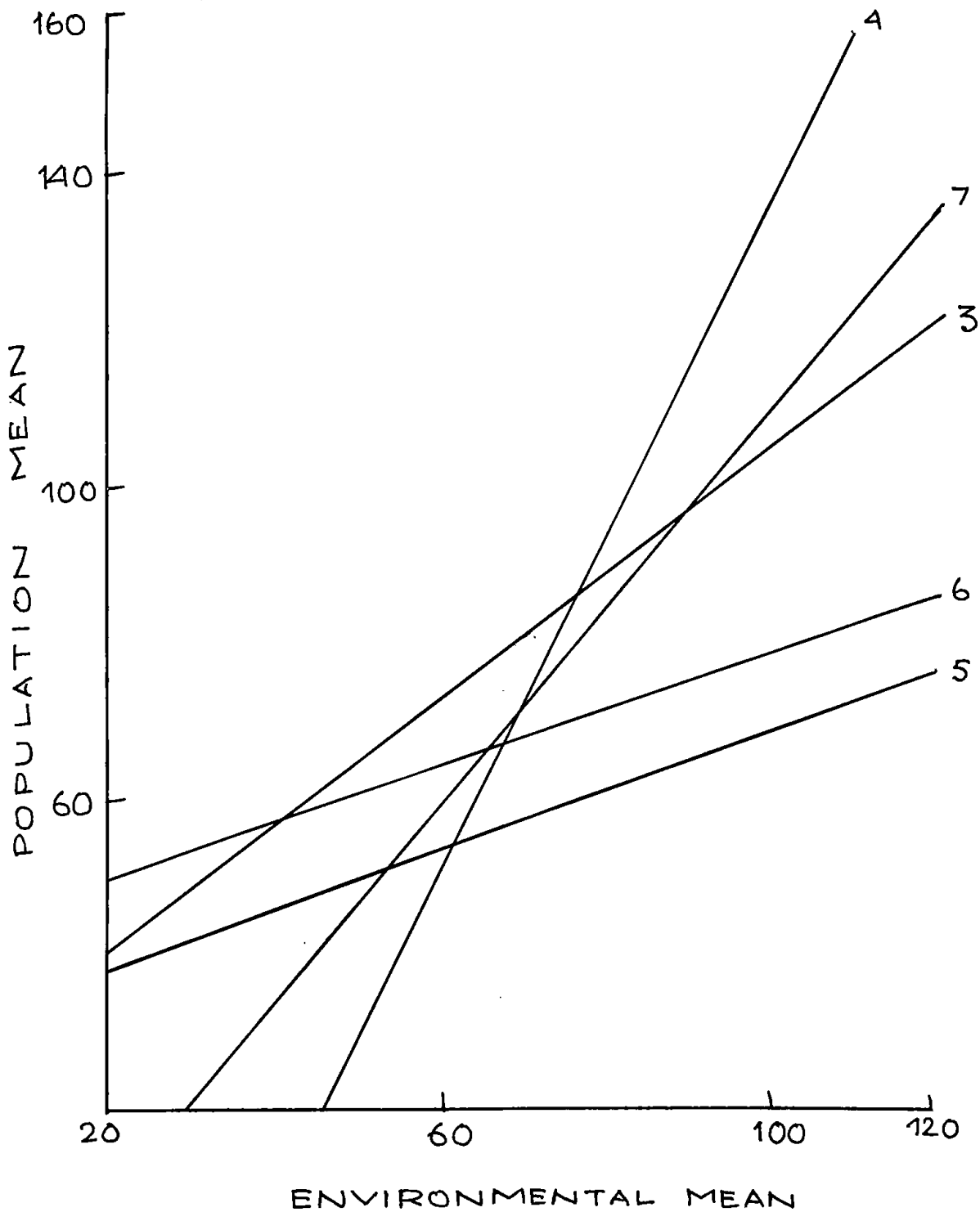

160
140
100
60
POPULATION MEAN
4
7
3
6
5
20
60
100
120
ENVIRONMENTAL MEAN

FIG. 17

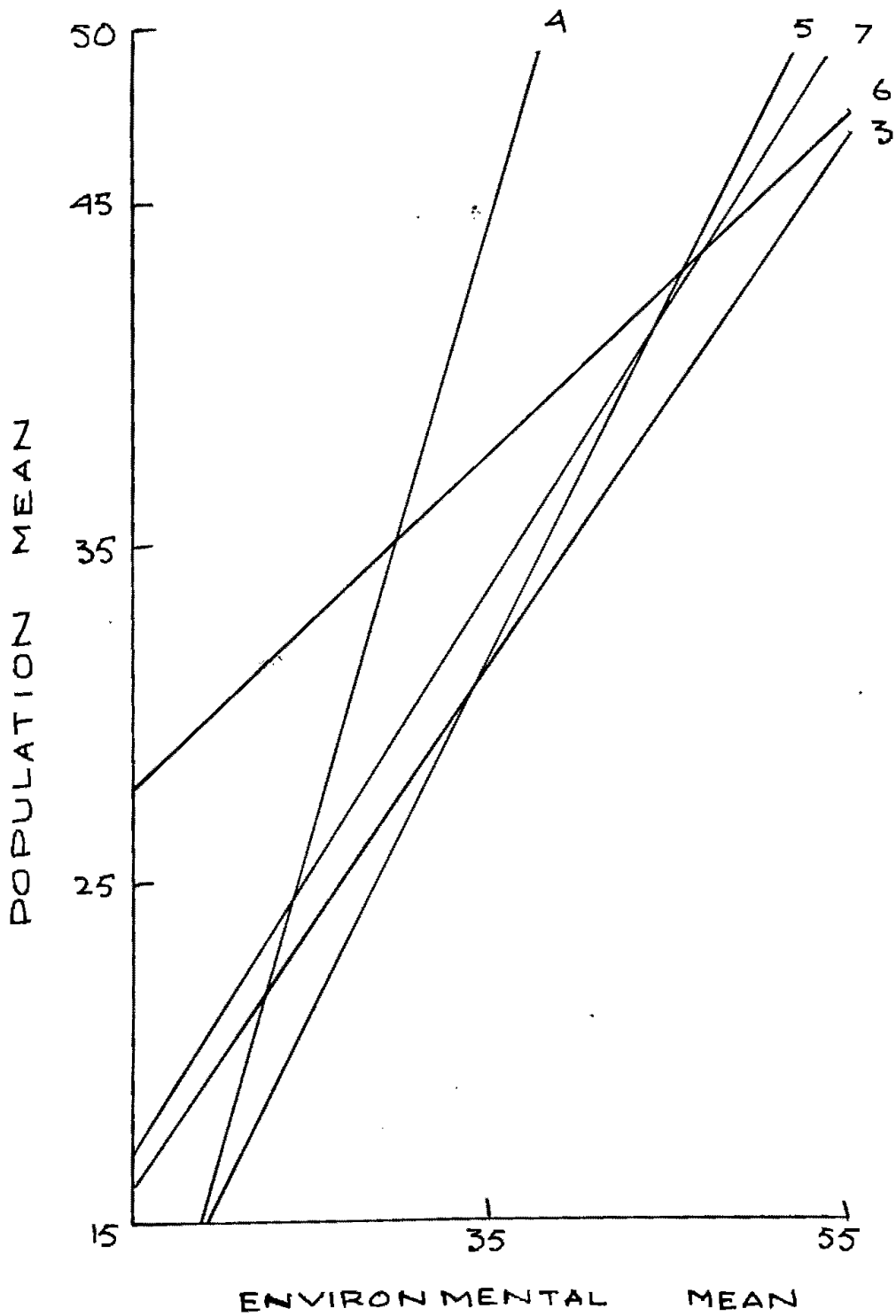

50
45
35
25
15
POPULATION MEAN
A
5
7
6
3
35
55
ENVIRONMENTAL MEAN

FIG. 18

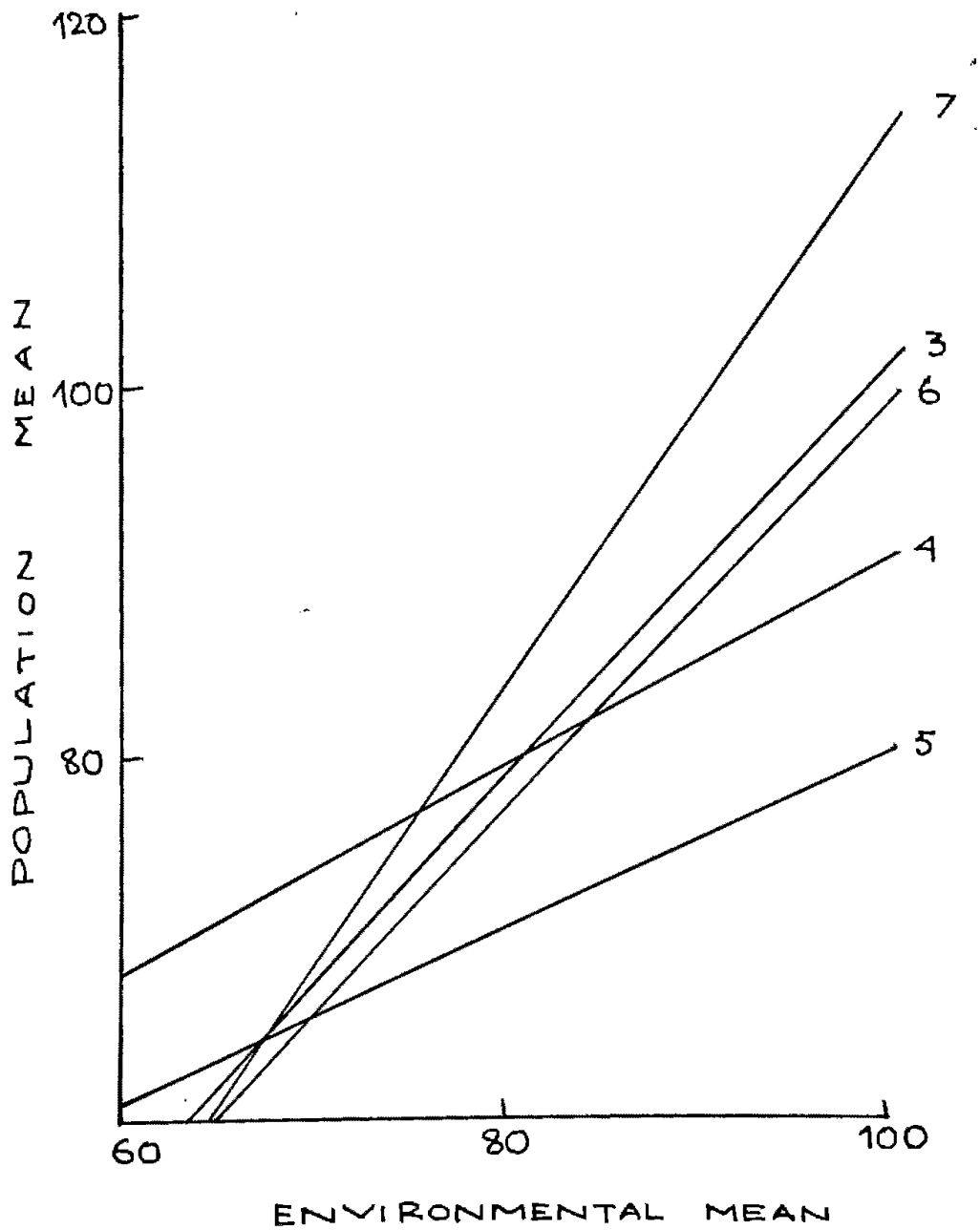

120
100
80
POPULATION MEAN
7
3
6
4
5
60
80
100
ENVIRONMENTAL MEAN

FIG. 19

(d) Correlation :

Correlation co-efficients (r) "within" as well as "between" characters were measured and are shown in table 17 and 18 respectively.

Within a character, the correlation co-efficient (r) between mean ($\bar{X}$) and responses (b_i), between mean ($\bar{X}$) and stability ($\bar{S}^2_d$) and between responses (b_i) and stability ($\bar{S}^2_d$) were calculated and are shown in table 17. Mean performances were positive and significantly correlated with response (b_i) in case of fresh root weight and plant height which indicated that the genotypes with higher mean performances were responsive to the environmental changes. The mean performances ($\bar{X}$) were significant and positively correlated with stability ($\bar{S}^2_d$) in fresh shoot weight only. Significant correlation between mean ($\bar{X}$) and $\bar{S}^2_d$ was in observed dry root weight but the correlation was negative. Most of the characters showed non-significant correlation co-efficient (r) between mean ($\bar{X}$) and response (b_i) and between mean ($\bar{X}$) and stability ($\bar{S}^2_d$) which suggested that the two aspects of phenotype were independent to each other. The correlation co-efficients (r) were non-significant between response (b_i) and stability ($\bar{S}^2_d$) in all the characters and the (r) values were negative in most of the cases. They indicated that the response (b_i) and stability ($\bar{S}^2_d$) were independent to each other, and indicative of different gene control of b_i and $\bar{S}^2_d$.

Correlation co-efficients (r) between responses (b_i) and between stabilities ($\bar{S}^2_d$) among the characters were measured and are shown in table 18. In most of the cases correlation co-efficients between responses (b_i) among the characters were non-significant which indicated

that the variation in response of a character with changing environments was not correlated with that of another character. There was a relationship between spikelet number/panicle with kernel number/ panicle as the correlation co-efficient(r) value was significant in this case. In the case of correlation between stabilities ($\bar{\sigma}^2_d$) among the characters (table 18), panicle length were positively and significantly correlated with spikelet number/panicle, kernel number/panicle and dry shoot weight but significantly and negatively correlated with tiller number and fresh root weight. Spikelet number/panicle was significantly and negatively correlated with tiller number dry shoot weight and fresh root weight and significantly but positively correlated with kernel number/panicle. Kernel number was significantly and negatively correlated with tiller number, dry shoot weight and dry root weight. Most of the characters showed non-significant correlation co-efficient(r) values between stabilities among character which suggested that the variation of $\bar{\sigma}^2_d$ values of one character was independent of that of another character i.e. fluctuation in the stability values with the changing environments of one character was not associated with that of the other.

Table 10. Environmental means over replications and genotypes

Seasons	Treatments							
	0	N	P	K	NP	NK	PK	NPK
Panicle length								
1977(Y_1)	23.78	23.09	23.42	23.65	23.79	23.32	23.02	23.59
1978 (Y_2)	23.62	23.95	24.36	23.30	24.54	24.24	23.37	24.92
Primary branches/ panicle								
1977(Y_1)	12.19	11.93	12.10	11.87	12.17	12.63	12.14	12.57
1978(Y_2)	11.13	10.60	10.90	10.54	10.60	11.13	11.23	10.80
Spikelet number/ panicle								
1977(Y_1)	187.00	181.27	186.20	197.40	185.00	184.07	181.67	190.53
1978(Y_2)	133.40	132.73	136.00	136.34	132.40	142.94	135.00	138.80
Kernel number/ panicle								
1977(Y_1)	169.20	153.00	159.93	163.40	149.87	146.40	155.80	154.93
1978(Y_2)	122.53	120.67	121.47	123.27	118.27	122.67	126.00	127.40
100 kernel weight								
1977(Y_1)	2.17	2.07	2.25	2.18	2.10	2.10	2.06	2.18
1978(Y_2)	2.02	1.98	2.05	2.03	1.95	1.95	1.94	2.05
Yield/plant								
1977(Y_1)	64.80	63.22	65.30	44.10	80.67	60.67	45.40	88.48
1978(Y_2)	25.80	26.79	27.74	24.76	26.89	27.90	26.83	25.57
Tiller number								
1977(Y_1)	21.30	26.53	22.03	17.03	30.93	25.87	17.07	40.23
1978(Y_2)	17.10	18.94	16.50	12.57	21.33	19.74	14.20	21.58
Fresh shoot weight								
1977(Y_1)	142.24	196.97	168.70	119.87	234.03	182.10	108.97	276.70
1978(Y_2)	79.64	108.87	95.70	55.97	118.40	115.97	67.73	118.97
Dry shoot weight								
1977(Y_1)	54.50	81.37	68.07	48.47	96.67	76.84	46.27	114.47
1978(Y_2)	38.77	55.63	49.23	26.03	56.63	56.40	31.40	61.00
Fresh root weight								
1977(Y_1)	85.80	95.90	96.67	81.50	121.83	102.00	75.50	122.53
1978(Y_2)	62.10	71.63	73.57	63.00	81.44	82.87	59.80	98.07
Dry root weight								
1977(Y_1)	35.54	39.77	37.84	36.11	44.81	36.97	29.74	49.61
1978(Y_2)	31.57	32.61	31.71	29.37	37.87	36.74	26.73	48.84
Plant Height								
1977(Y_1)	93.39	93.92	96.66	93.83	96.03	93.09	94.53	95.38
1978(Y_2)	78.77	81.31	82.77	80.68	83.14	84.87	81.97	81.14

Table 11. Population means over replications, treatments and seasons.

Characters	Chinese	IR-8	IR-532	IR-20	IR-5
Panicle length	23.20	24.17	23.00	24.62	23.73
Primary branches/ panicle	12.19	12.32	10.47	12.20	10.45
Spikelet number/ panicle	158.71	153.06	150.46	193.56	150.69
Kernel number/ panicle	131.15	136.75	126.65	174.32	129.52
100 kernel weight	2.14	2.24	1.78	2.10	2.08
Yield/plant	53.34	38.32	47.86	47.90	37.02
Tiller number	22.40	19.30	29.30	19.33	16.78
Fresh shoot weight	128.31	134.76	168.57	116.23	135.19
Dry shoot weight	47.25	60.02	69.84	45.90	77.53
Fresh root weight	94.05	105.03	63.69	73.82	92.69
Dry Root weight	32.24	45.91	32.03	38.59	34.31
Plant height	90.51	85.79	75.66	89.74	99.39

Table 12. Results of Analysis of Variance of different characters

Item	D.F.	Panicle length		Primary branches/panicle	
		M.S.	V.R.	M.S.	V.R.
Season (Y)	1	25.48	8.85**	106.67	76.19***
Nutrition (N)	7	4.92	1.71	1.68	1.20
N X Y	7	1.52		0.59	
Genotype (G)	4	20.44	7.10***	44.58	31.84***
G X Y	4	14.26	4.96***	12.73	9.09***
G X N	28	2.88	1.00***	1.27	
G X Y X N	28	3.37	1.17***	1.14	
Replication in years	4	3.60	1.25	1.34	
Error	156	2.88		1.40	

		Spikelet number/panicle		Kernel number/panicle	
Season (Y)	1	153976.57	212.65***	18729.33	24.60***
Nutrition (N)	7	490.70		527.44	
N X Y	7	368.65		438.51	
Genotype (G)	4	17388.86	24.02***	18729.33	24.60***
G X Y	4	4366.27	6.03***	3346.48	4.40**
G X N	28	1187.73	1.65***	1093.44	1.44***
G X Y X N	28	601.51		585.76	
Replication in years	4	138.92		315.06	
Error	156	724.10		761.43	

Contd.....

Table 12 (Contd.)

Item	D.F.	100 Kernel weight		Yield/plant	
		M.S.	V.R.	M.S.	V.R.
Season (Y)	1	1.31	27.29***	81585.96	530.47***
Nutrition (N)	7	0.09	1.88	1835.23	11.93***
N X Y	7	0.01		1729.20	11.25***
Genotype (G)	4	1.29	26.88***	2333.19	15.17***
G X Y	4	0.04		1794.12	11.67***
G X N	28	0.06	1.25***	204.93	1.33***
G X Y X N	28	0.01		243.95	1.59***
Replication in years	4	0.08	1.73	58.47	
Error	156	0.048		153.80	

		Tiller number		Fresh shoot weight	
Season (Y)	1	3273.04	192.26***	412468.97	337.69***
Nutrition (N)	7	868.46	51.02***	47767.17	39.11***
N X Y	7	188.35	11.07***	10402.27	8.52***
Genotype (G)	4	1130.76	66.42***	18135.27	14.85***
G X Y	4	75.89	4.46***	6792.02	5.56***
G X N	28	44.38	2.61***	1871.11	1.53***
G X Y X N	28	36.45	2.14***	1280.53	1.05***
Replication in years	4	6.20		365.26	
Error	156	17.03		1221.42	

Contd.....

Table 12. (Contd.)

Item	D.F.	Dry shoot weight M.S.	Dry shoot weight V.R.	Fresh root weight M.S.	Fresh root weight V.R.
Season (Y)	1	41870.44	183.99***	33571.19	54.62***
Nutrition (N)	7	9904.65	43.53***	6672.85	10.86***
N X Y	7	1370.02	6.02***	409.31	
Genotype (G)	4	9162.03	40.26***	13370.16	21.75***
G X Y	4	4791.96	21.06***	14580.11	23.72***
G X N	28	415.06	1.83***	641.48	1.05***
G X Y X N	28	174.97		749.01	1.22***
Replication in years	4	58.89		1998.71	3.25***
Error	156	227.56		614.66	

		Dry root weight		Plant height	
Season (Y)	1	1142.76	10.10***	9785.67	411.94***
Nutrition (N)	7	1197.48	10.58***	45.24	1.91
N X Y	7	59.17		29.72	1.25
Genotype (G)	4	1629.38	14.40***	3551.25	149.50***
G X Y	4	2329.25	20.59***	411.11	17.31***
G X N	28	214.39	1.90***	21.37	
G X Y X N	28	133.70	1.18***	30.66	1.29***
Replication in years	4	642.70	5.68***	19.33	
Error	156	113.15		23.76	

Table 13. Results of effects of nutrients on five genotypes

Panicle length

	Chinese		IR-8		IR-532		IR-20		IR-5	
	Y_1	Y_2	Y_1	Y_2	Y_1	Y_2	Y_1	Y_2	Y_1	Y_2
N	0	2.56**	-4.39***	1.29*	0.99	9.06***	5.40***	-0.07	-2.00***	2.20***
P	-0.06	5.18**	-2.67***	1.03	1.93*	-2.94**	2.92**	3.95***	-1.94*	2.20***
K	-2.20**	-4.96**	3.13**	3.51***	-0.81	-0.26	-1.54*	5.07***	-0.80	-6.40***
NP	1.26	5.20***	8.93***	-0.23	0.53	-0.86	0.80	-0.93	-1.94*	-0.74
NK	1.40	2.44**	-2.07**	1.77**	1.67*	-2.86**	2.74**	0.59	-1.20	7.92***
PK	2.26**	5.30***	-4.99***	0.23	-0.9	-3.26***	-0.54	-0.47	0.46	-4.72***
NPK	-1.46	2.58**	1.53	2.49***	1.21	-2.94**	-0.26	0.13	-1.54*	4.54*

Primary branches/panicle

N	2.82***	-0.84*	-0.66	-1.50***	1.83***	-0.99*	3.16***	-2.00***	-2.12***	2.00***
P	1.16*	0.84	1.00	2.50***	1.17*	-0.33	1.16*	1.00*	-2.83***	-3.34***
K	1.84***	0.50	1.68**	0.82	-0.51	1.67***	0.84*	0.34	0.17	-1.00*
NP	-1.16***	2.16***	1.32*	-2.50***	1.83***	-1.67***	-1.50***	-3.66***	-0.51	1.68**
NK	2.16***	1.82***	2.00***	1.82***	0.83*	0.33	0.82	-1.68**	1.17**	2.66***
PK	-1.50***	0.82	-1.66**	-0.18	0.17	-2.33***	2.18**	0.68	1.15**	4.00***
NPK	-0.50	1.50**	-0.66	0.18	0.15	-1.67**	-3.16**	-2.66**	0.83*	-3.66**

Contd.....

Table 13. (Contd.)

Spikelet number/panicle

	Chinese		IR-8		IR-532		IR-20		IR-5	
	Y_1	Y_2	Y_1	Y_2	Y_1	Y_2	Y_1	Y_2	Y_1	Y_2
N	21.66	102.34**	-67.66*	43.66*	-66.99**	39.67**	65.33**	-16.34	-9.33	21.66
P	45.68*	20.34	26.34	28.00*	25.67*	36.33**	-12.67	-24.34	-65.33**	-3.68
K	-47.66**	-49.66**	44.35*	68.00**	36.99**	-2.33	12.67	61.00**	24.67*	15.66
NP	35.00**	9.00	-5.66	6.00	61.65**	39.65**	42.67***	-78.32**	0.01	-5.00
NK	-19.66	-1.00	-37.00**	54.00**	-22.33*	-15.67	145.33**	-10.34	-53.99**	46.34**
PK	-65.00**	54.32**	-75.00**	-82.00**	-21.00	-43.01**	60.65**	-26.34*	39.33**	58.32**
NPK	103.00***	20.34	-3.00	34.68*	23.69*	-5.67	-48.01**	-49.68**	12.67	1.00

Kernel number/panicle

N	-84.99**	70.67**	-128.32**	-92.96**	-48.32**	-51.33**	39.33**	11.00	1.67	27.32**
P	76.99**	2.67	5.66	41.00**	-31.00**	-39.33**	-58.01**	7.00	-51.01**	8.68
K	-84.99**	45.33**	-13.66	51.66*	20.34	-20.67	21.33	89.00**	-0.33	7.34
NP	59.01**	14.67	66.32**	8.34	-2.32	46.67**	-4.67	-47.66**	-7.01	-18.66
NK	-28.33*	-17.33	27.00**	15.00	-21.66	-43.99**	115.99**	27.66*	-51.01**	48.00**
PK	-11.67	43.99**	-29.66*	-41.66*	23.66	-35.99**	53.33**	2.34	30.99**	68.00**
NPK	87.67**	2.67	-13.00	31.00**	-6.34	0.04	-44.01**	-4.32	25.67*	-12.66

Contd.....

Table 13 (Contd.)

100 kernel weight

	Chinese		IR-8		IR-532		IR-20		IR-5	
	Y_1	Y_2	Y_1	Y_2	Y_1	Y_2	Y_1	Y_2	Y_1	Y_2
N	-1.96*	0.19*	-0.49**	-0.45**	-0.41**	-0.10	-0.26**	0.10	-0.13	-0.33**
P	-0.05	-0.15*	-0.19*	-0.19*	0.49**	0.26**	0.12	0.08	-0.03	0.07
K	-0.41**	-0.11	-0.15*	0.01	0.45**	0.26**	0.28**	0.28**	-0.49**	-0.57**
NP	0.25**	0.43**	-0.17*	-0.19*	0.41**	-0.04	0.16*	0.12	0.07	0.27**
NK	-0.31**	-0.05	0.39**	0.21**	0.33**	-0.16*	0.52**	0.32**	0.53**	0.51**
PK	-0.63**	-2.01**	0.29**	-0.05	-0.45**	-0.20**	0.02	0.42**	0.03	-0.09
NPK	0.63**	0.55**	0.55**	0.15*	-0.17*	0.22**	-0.14	-0.22**	0.33**	0.51***

Yield/plant

N	52.99**	39.50**	22.40**	-16.34*	114.24**	-43.47*	120.49**	1.43	87.01**	32.43**
P	10.67*	-12.18**	30.74**	11.66**	74.10**	5.53	43.49**	6.09	15.33**	-5.57
K	-43.67**	-20.16**	-13.62**	5.00	-13.22**	-9.47*	-30.51**	-5.89	-45.67**	13.29**
NP	78.33**	1.50	0.06	5.34	61.10**	-7.79	33.17**	-7.77	14.67**	-18.97**
NK	67.67**	-5.84	-0.94	5.00	54.42**	8.53	64.49**	3.57	13.67**	0.85
PK	14.99**	11.16*	-50.60**	-11.00	21.24**	-6.47	0.17	-1.77	39.99**	-6.91
NPK	37.01**	-1.84	-2.60	2.00	4.24	-4.47	33.17**	0.09	6.01	-5.11

Contd.....

Table 13 (Contd.)

	Chinese		IR-8		IR-532		IR-20		IR-5	
	Y_1	Y_2	Y_1	Y_2	Y_1	Y_2	Y_1	Y_2	Y_1	Y_2
					Tiller number					
N	33.67***	36.00***	29.33***	22.17***	78.00***	15.73***	54.99***	23.00***	34.62***	9.18**
P	27.35***	2.66	8.33***	10.83***	33.34***	11.39***	21.67***	4.66*	6.99**	-3.18*
K	-0.33	-7.66**	8.33***	-10.17**	1.34	-9.59**	-3.33*	-9.00***	-8.99**	7.50**
NP	24.33***	-0.34	7.67**	12.15***	33.34**	8.73***	20.33***	3.34**	1.67	-7.84**
NK	22.01***	1.34	9.67**	9.83***	28.00***	31.07***	13.33***	4.32**	16.33***	-7.16**
PK	10.33**	7.32*	20.67***	-2.83	19.34**	11.41**	-4.67*	-1.34	0.65	-6.16**
NPK	7.99**	3.68*	16.01***	-1.51	13.32***	-3.93**	8.67***	-6.66**	5.33**	-5.50**
					Fresh shoot weight					
N	327.33***	141.67***	197.15***	173.00***	578.00***	206.17***	357.33***	102.32***	315.33***	191.67***
P	199.33***	21.33	115.83***	119.66**	162.66**	22.83	108.67***	42.34**	124.67***	-4.35
K	9.67	-58.99**	-156.83***	-39.66**	37.32**	-113.85***	-55.33***	-28.68*	-81.33***	21.33
NP	185.33***	-11.33	136.51***	70.34**	136.34**	-53.83**	117.01***	-11.00	30.33*	-70.67***
NK	121.67***	-2.33	5.17	73.02**	213.00***	166.17***	45.01**	1.34	139.69***	58.33***
PK	99.67***	35.33**	9.17	-57.00***	58.34**	2.83	-25.01*	29.00*	-16.33	-64.33***
NPK	155.67***	15.99	41.17***	-13.00	35.34**	-20.51	96.01***	-26.34*	121.33***	32.67**

Contd.....

Table 13 (Contd.)

	Chinese		IR-8		IR-532		IR-20		IR-5	
	Y_1	Y_2	Y_1	Y_2	Y_1	Y_2	Y_1	Y_2	Y_1	Y_2
					Dry shoot weight					
N	98.68**	64.00**	160.34**	62.00**	179.16**	120.00**	124.68**	48.68**	197.33**	117.50**
P	56.00**	27.66*	81.34**	37.00**	51.50**	46.34**	60.32**	21.34*	72.39**	55.16**
K	8.66	-42.00**	-14.34*	-26.34**	-10.50*	-31.66**	-15.68*	-16.32*	-40.99**	-10.84
NP	52.66**	7.66	75.64**	12.66*	32.50**	9.34	56.00**	-5.34	-9.01	-75.50**
NK	50.68**	-5.32	34.66**	38.00	26.50**	98.66**	6.00	3.00	77.67**	44.18**
PK	0	15.66**	3.66	-22.32**	31.48**	28.00**	-15.00**	0.34	12.67*	-39.16**
NPK	15.34**	11.66*	19.34**	3.34	23.84**	1.68	51.32**	-10.34	80.65**	37.18**
					Fresh root weight					
N	79.99**	40.50**	174.00**	109.84**	78.00**	152.00**	105.32**	32.49**	76.66**	35.34**
P	71.67**	-17.83*	90.66**	31.50**	20.68	83.66**	8.96	32.51**	76.66**	24.34**
K	-13.33	5.83	-87.68**	6.50	-22.66**	40.00**	-19.70*	5.83	50.00**	35.00**
NP	80.01**	-49.50**	95.66**	69.84**	-1.34	59.34**	13.64	2.51	20.00*	4.00
NK	58.33**	-22.18*	-16.00	98.16**	8.68	71.00**	0.30	45.83**	110.02**	13.34
PK	0.51	-76.84**	-39.34**	66.50**	6.00	4.66	-4.70	12.49	-73.34**	-55.66**
NPK	-15.01	-13.50	-14.34	31.52**	-8.66	-7.66	5.30	19.17*	60.00**	73.32**

Contd.....

Table 13 (Contd.)

	Chinese		IR-8		IR-532		IR-20		IR-5	
	Y_1	Y_2	Y_1	Y_2	Y_1	Y_2	Y_1	Y_2	Y_1	Y_2
					Dry root weight					
N	26.94**	24.01**	47.66**	60.86**	31.66**	91.66**	54.33**	28.32**	-1.00	-21.50
P	9.35*	-10.99**	32.34**	20.12**	10.00**	50.00**	-5.33	17.34**	21.66**	-2.16
K	8.99*	-0.33	-26.00**	-6.86	-15.00**	26.66**	-13.99**	0.66	18.32**	19.50**
NP	24.33**	-12.01**	42.00**	43.20**	-1.66	44.66**	15.65**	2.34	28.34**	21.18**
NK	19.33**	4.01	-10.34**	42.86**	6.66	32.00**	-6.33	23.66**	38.32**	8.84*
PK	0.33	-5.67	2.34	28.86**	-5.00	13.66**	-2.67	9.32*	-0.34	-25.82**
NPK	7.99*	-5.33	12.68**	6.52	6.66	-8.32*	-0.33	9.00*	54.34**	46.16**
					Plant height					
N	-14.23**	4.82**	3.50*	2.00	8.00**	9.50**	1.99	-4.34*	0.83	19.34**
P	15.11**	1.82	2.16	12.00**	4.33*	-3.16	9.01**	9.00**	11.17**	-2.66
K	-0.43	-14.82**	-13.84**	23.66**	7.33**	-3.82*	-1.67	7.34*	-7.17**	1.00
NP	3.17	4.50**	14.82**	-3.00	-9.67**	-0.84	2.35	-20.98**	-8.49**	-15.66**
NK	4.71**	-5.50**	6.18**	4.66**	7.33**	-0.82	-0.33	-4.00*	-16.83**	8.00**
PK	-2.63	-6.50**	-9.16**	-1.34	6.33**	-12.16**	-8.67**	-14.66**	1.15	-6.66**
NPK	3.43*	-1.18	1.50	-8.98**	11.01**	6.16**	-1.33	-8.20**	-0.83	-2.32

Table 14. Estimates of δ^2_G, δ^2_{NG}, δ^2_{GY}, δ^2_{GNY} and δ^2_E and co-efficient of variability for the twelve characters.

	δ^2_G	δ^2_{NG}	δ^2_{GY}	δ^2_{GNY}	δ^2_E	CVδ^2_G	CVδ^2_{NG}	CVδ^2_{GY}	CVδ^2_{GNY}	CVδ^2_E
Panicle length	0.14	-0.08	0.45	0.16	2.88	0.59	-0.34	1.89	0.04	12.13
Primary branches/ panicle	0.66	0.02	0.48	-0.09	1.40	5.72	0.17	4.16	-0.78	12.13
Spikelet number/ panicle	259.09	97.70	156.87	-40.86	724.10	160.63	60.57	97.25	-25.33	448.92
Kernel number/ panicle	309.90	84.61	115.03	-58.56	761.43	221.86	60.57	82.35	-41.92	545.12
100 kernel weight	0.03	0.01	0.001	-0.013	0.048	1.45	0.48	0.05	-0.63	2.32
Yield/ plant	12.05	-6.50	64.59	30.05	153.80	26.59	-14.35	142.55	66.32	339.44
Tiller number	21.81	1.32	1.64	6.47	17.03	101.73	6.16	7.65	30.18	79.43
Fresh shoot weight	224.01	98.43	229.65	305.09	1221.42	163.97	72.05	168.09	223.31	894.03
Dry shoot weight	86.04	40.02	192.37	-17.53	227.56	143.14	66.58	320.03	-29.16	378.57
Fresh root weight	-22.97	-17.92	576.30	44.78	614.66	-26.75	-20.87	66.74	52.15	715.89
Dry root weight	-16.26	13.45	91.48	6.85	113.15	-44.40	36.73	249.81	18.71	308.98
Plant height	65.61	-1.55	15.85	2.30	23.76	74.37	-1.76	17.97	2.61	26.93

Table 15. Results of joint Regression Analysis

Item	D.F.	M.S.	V.R.[1]	V.R.[2]
Panicle length				
Linear Regression	4	7.21	1.99	2.50*
Deviation	56	3.63		
Error	156	2.88		1.26***
Primary branches/panicle				
Linear Regression	4	8.12	5.31	5.80***
Deviation	56	1.53		1.09***
Error	156	1.40		
Spikelet number/panicle				
Linear Regression	4	2012.14	1.89	2.78*
Deviation	56	1062.77		1.47***
Error	156	724.10		
Kernel number/panicle				
Linear Regression	4	1821.75	1.99	2.39*
Deviation	56	915.98		1.20***
Error	156	761.43		
100 kernel weight				
Linear Regression	4	0.05	1.67	1.04
Deviation	56	0.03		0.63
Error	156	0.048		
Yield/plant				
Linear Regression	4	213.34	1.39	1.39
Deviation	56	337.36		2.19***
Error	156	153.80		

Contd.....

Table 15 (Contd.)

Item	D.F.	M.S.	V.R.[1]	V.R.[2]
Tiller number				
Linear Regression	4	61.11	1.47	3.59**
Deviation	56	41.47		2.44***
Error	156	17.03		
Fresh Shoot Weight				
Linear Regression	4	2064.66	1.08	1.69
Deviation	56	1913.49		1.57***
Error	156	1221.42		
Dry Shoot Weight				
Linear Regression	4	632.14	1.07	2.78*
Deviation	56	592.15		2.60***
Error	156	227.56		
Fresh Root Weight				
Linear Regression	4	1269.25	0.77	2.06
Deviation	56	1646.02		2.68***
Error	156	614.66		
Dry Root Weight				
Linear Regression	4	1764.42	8.23***	15.59***
Deviation	56	214.39		1.89***
Error	156	113.15		
Plant height				
Linear Regression	4	79.32	1.61	3.34***
Deviation	56	49.71		2.09***
Error	156	23.76		

$VR^1 = \frac{\text{M.S.}}{\text{Deviation M.S.}}$ $VR^2 = \frac{\text{M.S.}}{\text{Error M.S.}}$

Table 16. Regression co-efficients b_i, S_{b_i}, β_i, stability $\bar{S}_d^2$ and correlation co-efficient (r) for the 5 genotypes grown under 16 different environments.

Genotypes	b_i	S_{b_i}	β_i	$\bar{S}_d^2$	r
			Panicle length		
Chinese	0.38	0.58	-0.62	-1.40	0.17
IR-8	1.43	0.54	0.43	-1.63	0.50
IR-532	0.87	0.49	-0.13	-1.82	0.43
IR-20	1.44	0.59	0.44	-1.37	0.55
IR-5	1.16	0.49	0.16	-1.82	0.53
	Bartlett's $X^2_{(d.f = 4)}$ testing homogenity of S_{b_i} = 0.9577^{NS}				
			Primary branches/panicle		
Chinese	1.90	0.22	0.90	-1.03	0.93
IR-8	1.19	0.17	0.19	-1.18	0.90
IR-532	0.77	0.17	-0.23	-1.22	0.82
IR-20	1.13	0.22	0.13	-1.03	0.82
IR-5	0.01	0.28	-0.99	-0.74	0.01
	Bartlett's $X^2_{(d.f.=4)}$ testing homogenity of S_{b_i} = 5.3925^{NS}				
			Spikelet number/panicle		
Chinese	1.60	0.20	0.60	-366.31	0.92
IR-8	0.59	0.17	-0.41	-473.88	0.73
IR-532	0.92	0.14	-0.08	-596.10	0.92
IR-20	1.08	0.22	0.08	-292.80	0.82
IR-5	0.82	0.14	-0.18	-583.67	0.89
	Bartlett's $X^2_{(d.f.=4)}$ testing homogenity of S_{b_i} = 5.0209^{NS}				

Contd.....

Table 16 (Contd.)

Genotypes	b_i	S_{b_i}	β_i	σ^2_d	r
			Kernel number/panicle		
Chinese	1.76	0.26	0.76	-445.01	0.89
IR-8	0.71	0.24	-0.29	-492.43	0.63
IR-532	0.72	0.17	-0.28	-651.58	0.80
IR-20	1.12	0.26	0.12	-438.16	0.76
IR-5	0.72	0.17	-0.28	-629.61	0.77
Bartlett's $X^2_{(d.f.=4)}$ testing homogenity of S_{b_i} = 5.5739^{NS}					
			100 kernel weight		
Chinese	0.81	0.30	-0.19	-0.035	0.57
IR-8	0.94	0.24	-0.06	-0.040	0.72
IR-532	0.69	0.29	-0.31	-0.037	0.54
IR-20	1.25	0.29	0.25	-0.037	0.76
IR-5	1.21	0.24	0.21	-0.041	0.80
Bartlett's $X^2_{(d.f.=4)}$ testing homogenity of S_{b_i} = 1.4478^{NS}					
			Yield/plant		
Chinese	1.16	0.09	0.16	-87.53	0.96
IR-8	0.61	0.09	-0.39	-93.12	0.88
IR-532	1.04	0.08	0.04	-102.33	0.96
IR-20	1.43	0.06	0.43	-127.56	0.99
IR-5	0.71	0.08	-0.29	-107.33	0.93
Bartlett's $X^2_{(d.f.=4)}$ testing homogenity of S_{b_i} = 72.95***					

Contd.....

Table 16 (Contd.)

Genotypes	b_i	S_{b_i}	β_i	$\bar{D}^2_d$	r
			Tiller number		
Chinese	0.94	0.09	-0.06	-10.66	0.94
IR-8	0.69	0.09	-0.31	-10.59	0.89
IR-532	1.44	0.14	0.44	-3.95	0.95
IR-20	1.20	0.08	0.20	-11.90	0.97
IR-5	0.74	0.14	-0.26	-6.16	0.85
Bartlett's $K^2_{(d.f.=4)}$ testing homogenity of S_{b_i} = 8.9607^{NS}					
			Fresh Shoot Weight		
Chinese	1.15	0.08	0.15	-900.10	0.98
IR-8	1.03	0.10	0.03	-677.44	0.94
IR-532	1.05	0.14	0.05	-121.98	0.90
IR-20	0.96	0.05	-0.04	-1078.88	0.99
IR-5	0.86	0.07	-0.14	-962.53	0.96
Bartlett's $K^2_{(d.f.=4)}$ testing homogenity of S_{b_i} = -34.508***					
			Dry Shoot Weight		
Chinese	0.78	0.07	-0.22	-189.08	0.95
IR-8	1.28	0.11	0.28	-125.19	0.95
IR-532	0.72	0.20	-0.28	97.51	0.69
IR-20	0.87	0.07	-0.13	-192.26	0.96
IR-5	1.37	0.13	0.37	-86.07	0.94
Bartlett's $X^2_{(d.f.=4)}$ testing homogenity of S_{b_i} = 24.3075***					

Contd.....

Table 16 (Contd.)

Genotypes	b_i	S_{b_i}	β_i	$\bar{S}^2_d$	r
			Fresh Root Weight		
Chinese	0.80	0.19	-0.20	-422.83	0.76
IR-8	2.17	0.25	1.17	-256.74	0.92
IR-532	0.39	0.28	-0.61	-166.44	0.35
IR-20	0.36	0.14	-0.64	507.16	0.57
IR-5	1.28	0.24	0.28	305.86	0.82
Bartlett's $X^2_{(d.f.=4)}$ testing homogenity of S_{b_i} = 8.0548^{NS}					
			Dry Root Weight		
Chinese	0.78	0.25	-0.22	-74.00	0.63
IR-8	1.85	0.25	0.85	-72.05	0.89
IR-532	1.05	0.46	0.05	25.17	0.52
IR-20	0.52	0.29	-0.48	-54.22	0.42
IR-5	0.85	0.44	-0.15	12.79	0.46
Bartlett's $X^2_{(d.f.=4)}$ testing homogenity of S_{b_i} = 10.991*					
			Plant Height		
Chinese	1.20	0.11	0.20	-15.99	0.95
IR-8	0.60	0.13	-0.40	-13.40	0.80
IR-532	0.50	0.09	-0.50	-17.72	0.82
IR-20	1.10	0.08	0.10	-19.20	0.97
IR-5	1.58	0.10	0.58	-16.77	0.97
Bartlett's $X^2_{(d.f.=4)}$ testing homogenity of S_{b_i} = 4.1985^{NS}					

Table 17. Results of correlation co-efficients within characters

	Correlations		
	Between mean ($\bar{X}$) and b_i	Between mean($\bar{X}$) and $\bar{S}_d^2$	Between b_i and $\bar{S}_d^2$
Panicle length	0.816	0.422	-0.10
Primary branches/ panicle	0.799	-0.313	-0.524
Spikelet number/ panicle	0.312	0.825	0.538
Kernel number/ panicle	0.139	0.613	0.679
100 kernel weight	0.448	-0.35	-0.16
Yield/plant	0.815	0.064	-0.515
Tiller number	0.793	0.522	0.345
Fresh shoot weight	0.155	0.955**	0.327
Dry shoot weight	0.505	0.66	-0.426
Fresh root weight	0.87*	-0.076	0.306
Dry root weight	0.69	-0.94*	-0.36
Plant height	0.939*	-0.202	-0.248

D.F. = 3

5% = *
1% = **
0.1% = ***

Table 18. Results of correlation co-efficients between responses b_i (upper right) and between stabilities, $\bar{S}^2_d$ (lower left) among characters.

	Panicle length	Primary branches/ panicle	Spikelet number/ panicle	Kernel number/ panicle	100 kernel weight	Yield/ plant	Tiller number	Fresh shoot weight	Dry shoot weight	Fresh root weight	Dry root weight	Plant height
Panicle length	-	-0.55	-0.69	-0.65	0.75	-0.04	-0.04	-0.78	0.45	0.12	0.05	0.03
Primary branches/ panicle	-0.11	-	0.64	0.79	-0.43	0.44	0.08	0.88	-0.56	-0.09	0.009	-0.28
Spikelet number/ panicle	0.99***	-0.08	-	0.95*	-0.22	0.67	0.25	0.58	-0.67	-0.57	-0.67	0.34
Kernel number/ panicle	0.96**	-0.15	0.94*	-	-0.15	0.13	0.006	0.63	-0.53	-0.35	-0.50	0.32
100 kernel weight	0.21	0.01	0.16	0.16	-	0.08	-0.36	-0.79	0.54	-0.08	-0.34	0.66
Yield/plant	-0.15	-0.25	-0.29	-0.04	0.11	-	0.69	0.26	-0.79	-0.86	-0.78	0.07
Tiller number	-0.90*	0.05	-0.91*	-0.98**	-0.03	0.09	-	0.53	-0.84	-0.86	-0.45	-0.42
Fresh shoot weight	-0.60	-0.67	-0.64	-0.62	0.03	0.33	0.71	-	-0.66	-0.14	0.14	-0.48
Dry shoot weight	0.99***	0.15	-0.98**	-0.93*	-0.14	0.15	0.84	0.54	-	0.81	0.47	0.35
Fresh root weight	-0.88*	-0.35	-0.90*	-0.79	-0.08	0.44	0.79	0.86	0.86	-	0.84	-0.08
Dry root weight	-0.78	0.46	-0.71	-0.88*	-0.08	-0.37	0.83	0.26	0.35	-0.66	-	-0.60
Plant height	-0.15	-0.20	-0.22	0.08	-0.005	0.79	-0.16	0.10	-0.27	0.39	-0.73	-

D.F. = 3 * at 5% ** at 1% *** at 0.1%

C. ONE INTERACTION OF SOME MORPHOLOGICAL AND DEVELOPMENTAL CHARACTERS OF EIGHT-PARENTAL LINES OF RICE FOR SEASONS I AND II.

(a) Means and Relative Importance to Different Nutrients

Mean performances of all the five characters over three replications and eight genotypes for each season and each treatment are shown in table 19. The environmental means (table 19) showed that almost all the characters were highly affected by seasons as well as by different nutritional treatments. Maximum shoot and root weights (both fresh and dry) were observed in case of NPK, NP and N. Maximum plant height was observed in NP combination during season II.

Population means over replications, treatments and seasons for all the five characters are shown in table 20. Varied performances were exhibited by different genotypes. In case of shoot weight (both fresh and dry) Naizersail showed the maximum weight followed by Badshabhog and the minimum weight was found in IR-20. Badshabhog showed the maximum fresh and dry root weight and IR-532 showed the minimum root weight. Maximum plant height (PH) was also observed in Badshabhog and the minimum was found in IR-532.

Usual analysis of variance of the data was then made separately and they are represented in table 21. For all the five traits, the items genotypes (G), season (Y) and nutrition (N) were highly significant indicating that a real differences existed among the genotypes which were greatly affected by seasons and a real effect of different nutritional treatments of N, P, K and their combinations existed. The analysis of variance (table 21) also showed that the populations interacted significantly with all the environmental effects (climatic and edaptic) in most of the characters. Among the interactions G X Y was highly significant in all the five traits; G X N was significant in case of dry shoot weight

(DSW) dry root weight (DRW) and plant height (PH) but it was non-significant in fresh shoot weight (FSW) and fresh root weight (FRW). N X Y was significant in case of FSW and DSW whereas it was non-significant in case of FRW, DRW and PH. The third order interaction (G X Y X N) was significant in case of DSW and PH only. The replication was significant in case of FRW and DRW.

Since the analysis of variance indicated that the genotypes in this experiment were highly affected by nutritional treatments as well as seasons, further analysis was carried out to evaluate the individual effect of nutrients in each season for each genotype. As the effects of different nutrients on Chinese, IR-8, IR-532, IR-20 and IR-5 in both the two seasons for these five traits have already been tabulated and discussed (table 13) the effects of nutrients on Naizersail, Badshabhog and Kataribhog only in relation to the five characters are shown in table 22.

Fresh Sheet Weight (FSW) : N had significant positive effect on FSW of the three varieties in both the seasons but the effect was non-significant in case of Badshabhog during Y_2. The effects of P was significantly positive on FSW in case of Naizersoil in both the seasons, in Badshabhog and Kataribhog during Y_1 but its effect on FSW was negative in case of Badshabhog and Kataribhog during Y_2. K significantly decreased the FSW of Badshabhog and of Naizersail during Y_2 whereas it significantly increased the FSW of Badshabhog and Kataribhog during Y_1. The effect due to NP was significant in all the cases but the effect was negative on Naizersail and Kataribhog during Y_2. NK also showed significant positive effect on FSW in all the varieties except Naizersail during Y_2 where it was negatively significant. Significant positive effect of PK was

observed on Naizersail and Kataribhog during Y_1 and on Badshabhog during Y_2. NPK had significant positive effects on FSW in case of Badshabhog during Y_2 and Kataribhog in both the seasons.

Dry Sheet Weight (DSW) : N had significantly positive effect on DSW in all cases indicating that increase of DSW was dependent on the application of N. P also had positive effect and in most of the cases showed significant effect on DSW. The effect of K was significantly negative on Naizersail and Badshabhog in both the seasons. Significant positive effect due to NP was noted in all the varieties except Naizersail during Y_2. NK had significant positive effect on DSW in case of Naizersail and Badshabhog during Y_1 and in case of Kataribhog in both the seasons. The effect of PK was significantly positive on Naizersail and Kataribhog during Y_1 and on Badshabhog during Y_2. NPK had positive and significant effect on Naizersail during Y_2 and on Kataribhog during Y_1.

Fresh Root Weight (FRW) : N significantly increased the FRW of all varieties in both the seasons. The effect of P was significantly positive on Naizersail and Badshabhog during Y_1 and on Kataribhog during Y_1 and Y_2. K had significant negative effect on FRW of Naizersail and Badshabhog in both the seasons and significant positive effect on FRW of Kataribhog during Y_2 only. Significant positive effect due to NP was also found in case of Naizersail and Badshabhog in both the seasons but very small and negative effect on Kataribhog was noted. Significant positive effect of NK was observed on Badshabhog and Kataribhog during Y_2. PK also increased FRW in all the cases. NPK had significant negative effect on FRW of Naizersail during Y_1 and of Badshabhog in both the seasons but only Kataribhog had significantly positive effect on FRW due to NPK in both the seasons.

Dry Root Weight (DRW) : The effects of N was positive and significant on DRW of all the varieties in both the seasons. Significant positive effect of P was also found on all varieties except Badshabhog during Y^2. K had significant negative effect on DRW of Naizersail in both the seasons and significant positive effect on DRW of Kataribhog during Y_2. Except Kataribhog during Y_2 all the varieties had significant positive effect due to NP on DRW in both the seasons. NK also had positive effect on DRW of all the cases except of Naizersail during Y_1. PK significantly increased the DRW of all the varieties in both the seasons. NPK produced significant positive effect on DRW of Naizersail during Y_2 and of Kataribhog during Y_1.

Plant Height (PH) : N had significant positive effect on PH of all the varieties in both the seasons except in case of Naizersail during Y_1. Significant positive effect due to P was found on PH of Naizersail and Badshabhog during Y_2 and of Kataribhog in both the seasons. K had significantly positive effect on PH of Naizersail during Y_1, of Badshabhog in both the seasons and of Kataribhog during Y_2. NP and NK had negative effect on PH of Naizersail and Badshabhog in both the seasons but positive effect on that of Kataribhog. PK significantly decreased the PH of all the varieties in both the seasons. Similarly NPK had negative effect on PH in most of the cases.

(b) Variability

The phenotypic variance was repartitioned into genotypic (δ^2_G), environmental (δ^2_E) and their interaction (δ^2_{NG}, δ^2_{GY} and δ^2_{NGY}) variations. The estimates of δ^2_G, δ^2_{NG}, δ^2_{GY}, δ^2_{NGY} and δ^2_E along with their co-efficients of variability are shown in table 23.

Greater portion of the total phenotypic variation was of genetic in nature in case of dry shoot weight and plant height whereas influences of environment (δ^2_E) were greater than δ^2_G, δ^2_{NG}, δ^2_{GY} and δ^2_{NGY} in case of fresh shoot weight, fresh root weight and dry root weight. The influence of δ^2_{NG} was negative in case of fresh shoot weight and plant height and that of δ^2_{NGY} was negative in case of fresh shoot and root weight and dry root weight. The influence of δ^2_{GY} was greater than δ^2_E in case of plant height. Maximum co-efficient of variability was exhibited by δ^2_G, δ^2_{GY} and δ^2_E in all the five characters.

(c) Regression

Since the interaction item was significant no generalization can be made on the relative performances of these populations and as the analysis of variance can give no useful account of the G X E interaction, the data were subjected to regression analysis. For each population the linear regression of individual values on these sixteen environmental means (8 treatments of NPK and their combination in two years) were computed. The environmental means were measured quantitatively by the mean of the eight genotypes.

The sum of squares measuring the interaction of the populations with the environments were partitioned into linear regression and deviation (joint regression) sum of squares and the results are shown in table 24. The table showed that major part of the genotype-environment variance was due to the difference between the slopes of the linear regression as it responded significantly in most of the characters except fresh shoot weight. The deviation mean square was significantly greater than that of error in case of fresh shoot weight, dry root weight and plant height but the linear regression M.S. was greater than deviation M.S. in case of dry shoot weight, fresh root weight and dry root weight.

Both the linear regression and deviation items were significant when tested by experimental error in case of dry root weight and plant height indicating the presence of relationship between 'g's and 'e's and the variation of G X E interactions within each genotype. Linear regression alone was significant in case of dry shoot weight and fresh root weight but was non-significant in case of fresh shoot weight. The deviation M.S. alone was non-significant in case of dry shoot weight

and fresh root weight, and significant in case of fresh shoot weight only.

The regression co-efficients are in effect measure responses to increaments in an improving environments. Regression co-efficients b_i, β_i, standard error (S_{bi}), stability (S^2_d) and correlation co-efficients(r) between environments in each genotype were measured and are shown in table 25. Both linear and non-linear responses accounted for most of the variations of these genotypes over environments as their high and low correlation co-efficient (r) values.

In case of fresh shoot weight all the seven varieties except Naizersail responded significantly with the environments. Chinese, IR-8, IR-532, IR-20 and Kataribhog showed above average responses and Badshabhog and IR-5 showed below average responses to the environments. The heighest response was detected in IR-532 ($b = 1.33 \pm 0.11$) and the lowest was in Naizersail ($b = 0.47 \pm 0.30$). Except Naizersail all the seven varieties had high correlation co-efficient (r) values.

For dry shoot weight all the eight varieties responded significantly to the environments which indicated that maximum responses were in the good environments. Among the eight genotypes, Naizersail, IR-8, IR-5 and Kataribhog showed above average responses and Badshabhog, Chinese, IR-532 and IR-20 showed below average responses to the environments. Maximum responses was found in case of Kataribhog ($b = 1.35 \pm 0.12$) and the minimum responses was in IR-532 ($b = 0.69 \pm 0.19$). Most of the genotypes had high correlation co-efficient values which indicated the linear responses accounted for most of the variations of the genotypes over environments.

Naizersail, Chinese, IR-8, IR-532, IR-20 and IR-5 had significant linear responses to environments with respect to fresh root weight. The responses of Naizersail and IR-20 were significant at 0.1% (P = 0.001), Chinese and IR-8 at 1% (P = 0.01) and IR-532 and IR-5 at 5% (P = 0.05) level. Maximum response was observed in case of IR-8 (b=2.09 $\pm$ 0.67) and the minimum was in Badshabhog (b = 0.28 $\pm$ 0.39). Most of the genotypes had low correlation co-efficient (r) values indicating that non-linear response was important in genotypic variation over environments.

In case of dry root weight significant linear responses were shown by Naizersail, Badshabhog, IR-8, IR-532, IR-20 and Kataribhog. Above average responses were found in Naizersail, Badshabhog, IR-532 and Kataribhog and below average responses were in Chinese, IR-8 and IR-20. IR-5 responded negatively (b = -0.21 $\pm$ 0.43) to the environment indicating that good environments decreased the dry root weight. Maximum response was found in case of Naizersail (b = 1.73 $\pm$ 0.28) and the minimum response was in case of Chinese (b= 0.08 $\pm$ 0.28). Both high and low correlation co-efficient (r) values indicate that both the linear and non-linear responses were involved in phenotypic variations over environments.

For plant height all the eight genotypes had significant linear responses to the environments. Naizersail, Badshabhog and Kataribhog had above average responses and the other five had below average responses to the environments. Badshabhog had maximum responses (b = 2.41 $\pm$ 0.15) and IR-532 had minimum response (b = 0.26 $\pm$ 0.05) to the environments. Most of the varieties had high correlation co-efficient (r) values.

The standard error (S_{b_i}) was heterogeneous as X^2 in the Bartlett's test (shown at the bottom of each character in table 25) was highly

significant in all the characters. It is, therefore, evident that the extent of the deviation from regression is specific to, and characteristic of particular population. It also indicated that this aspects of the phenotype was under genetic control. As revealved by joint regression and standard error (S_{bi}), the $\bar{S}^2_d$ was highly heterogeneous arround the regression slopes. The values of $\bar{S}^2_d$ was very high in case of fresh shoot weight, dry shoot weight, fresh root weight and dry root weight indicating instability of these genotypes. But in case of plant height moderately high value of $\bar{S}^2_d$ was found which indicated that the genotypes had considerable stability in this character.

The actual regression line of the performance of every genotype under all the different nutritional treatments against the corresponding overall environmental mean for all the five characters are shown in Fig. 20-24. Crossing of regression lines were very marked in most of the cases which indicated that GXE interaction was very marked in these characters. In case of fresh shoot weight Naizersail and Badshabhog showed good response to the poor environments. In case of dry root weight IR-5 responded negatively to the good environments. For plant height (Fig. 24) regression lines were close together in poor environments and spread out in good environments.

Explanation to the Figs. 20-24.

Fig. 20. Regression of individual population mean on environmental mean for eight parental lines in fresh shoot weight.

Fig. 21. Regression of individual population mean on environmental mean for eight parental lines in dry shoot weight.

Fig. 22. Regression of individual population mean on environmental mean for eight parental lines in fresh root weight.

Fig. 23. Regression of individual population mean on environmental mean for eight parental lines in dry root weight.

Fig. 24. Regression of individual population mean on environmental mean for eight parental lines in plant height.

The genotypes in the graphs (represented by their serial numbers) are as follows : 1 = Naizersail, 2 = Badshabhog, 3 = Chinese, 4 = IR-8, 5 = IR-532, 6 = IR-20, 7 = IR-5 and 8 = Kataribhog.

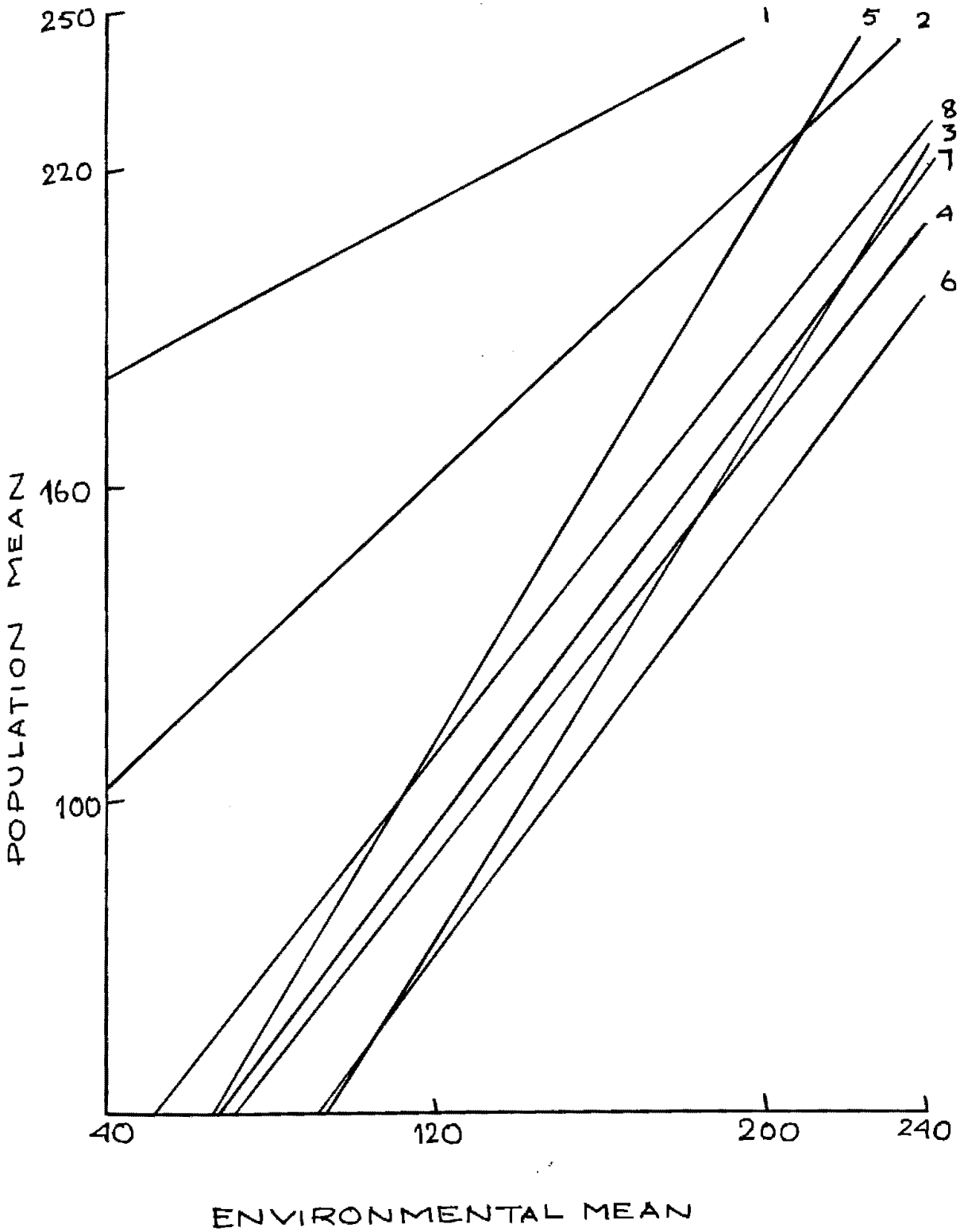

250
220
160
100
POPULATION MEAN
40
120
200
240
ENVIRONMENTAL MEAN
1
5
2
8
3
7
4
6

FIG. 20

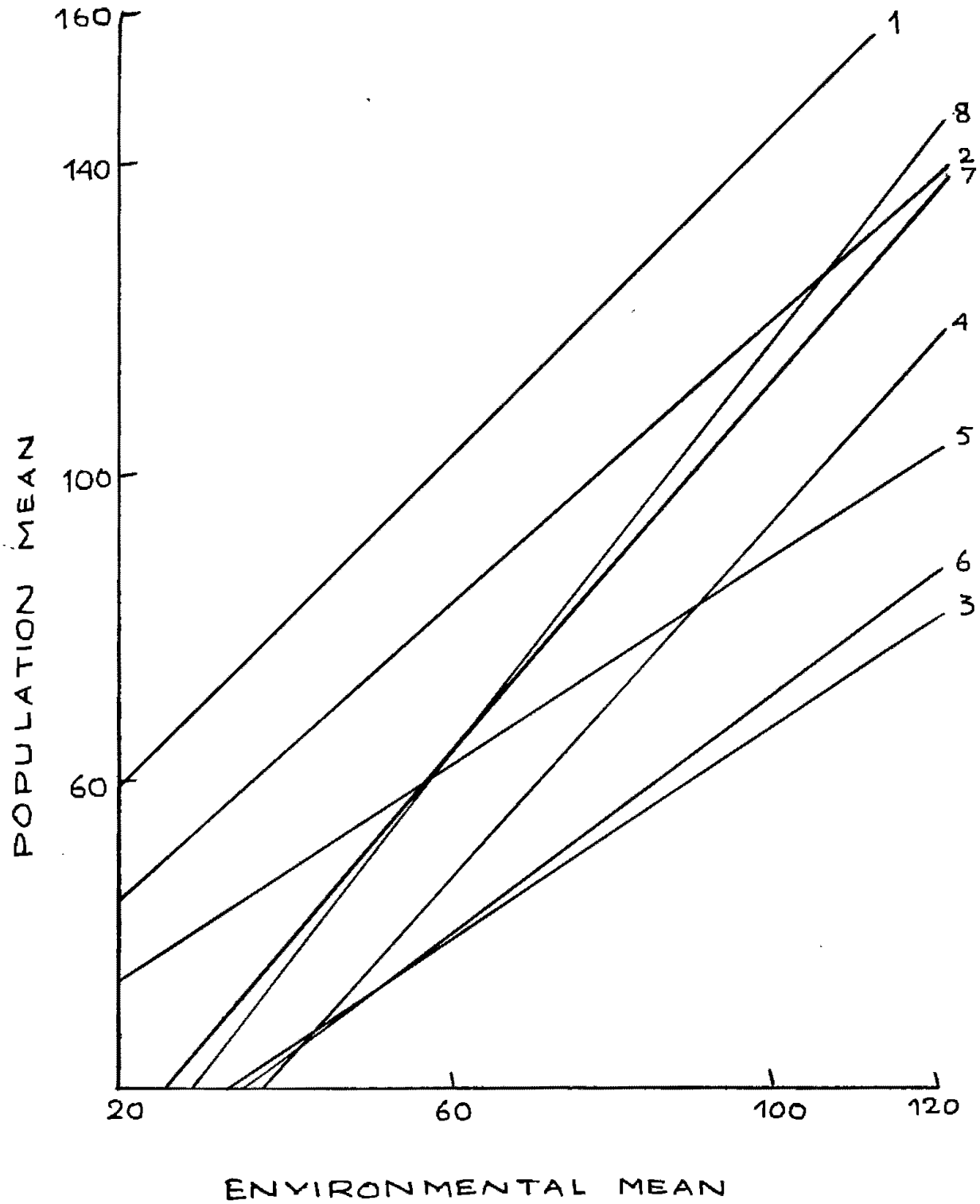

160
140
100
60
POPULATION MEAN
1
8
2/7
4
5
6
3
20
60
100
120
ENVIRONMENTAL MEAN

FIG. 21

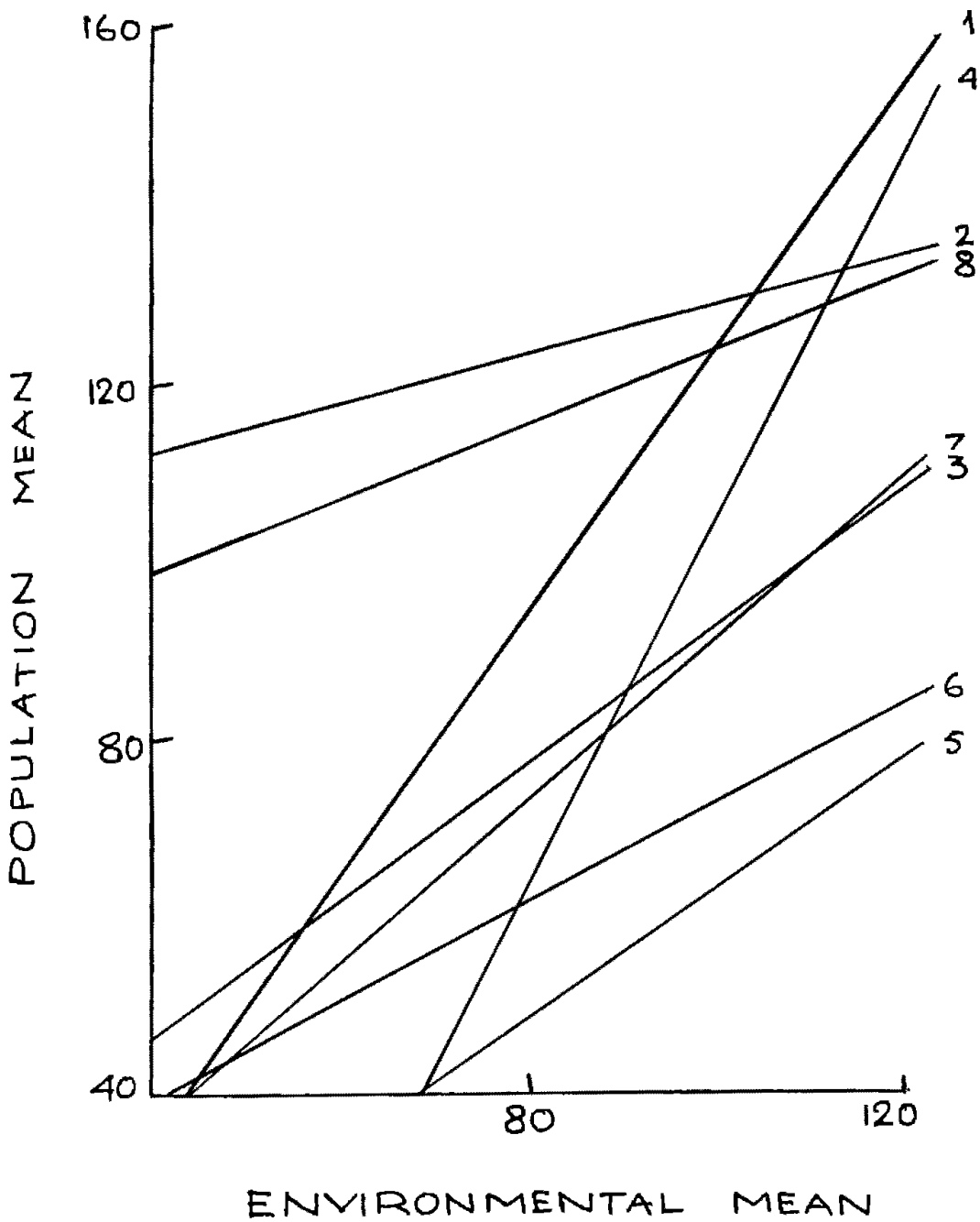

160
120
80
40
80
120
POPULATION MEAN
ENVIRONMENTAL MEAN
1
4
2
8
7
3
6
5

FIG. 22

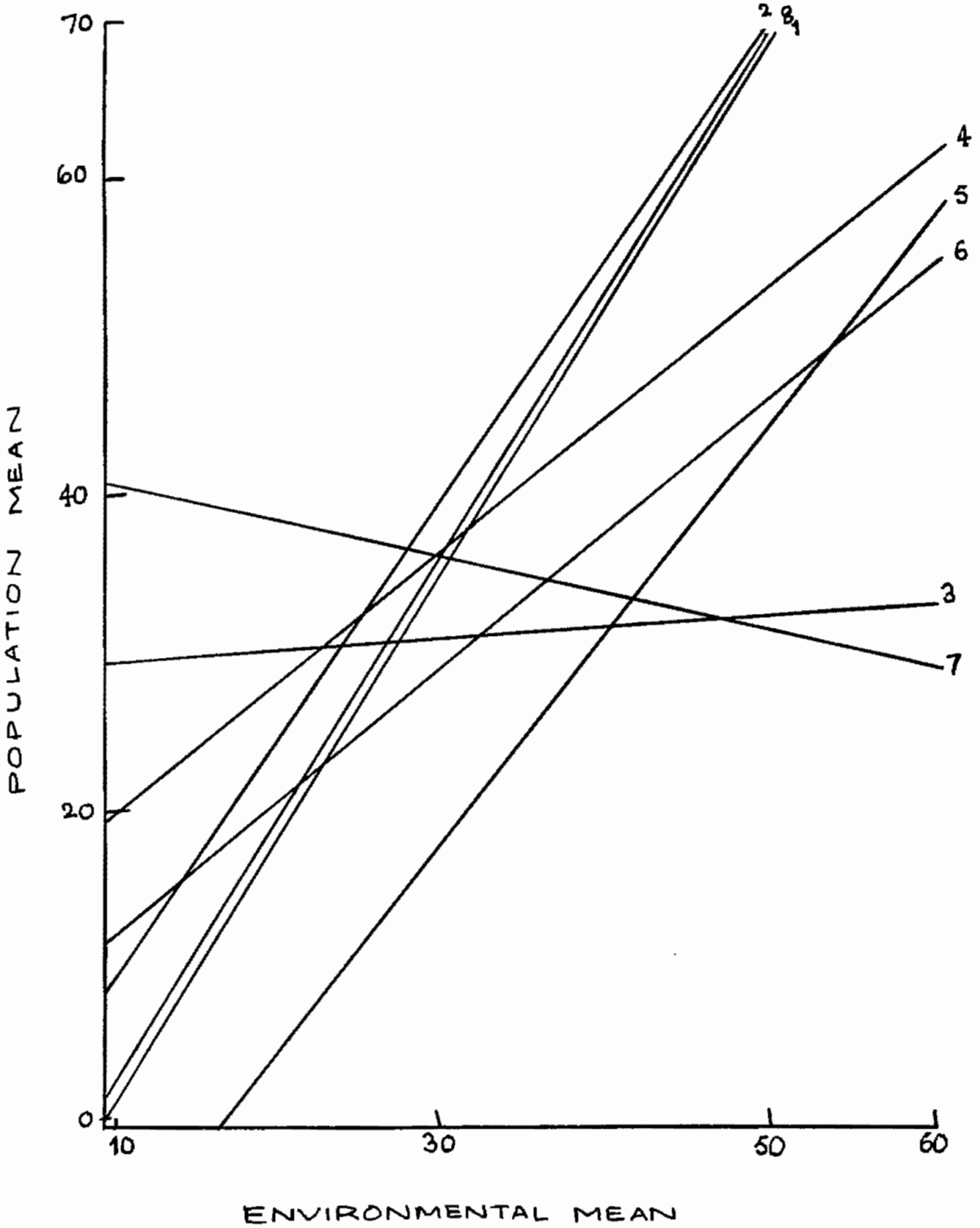

70
60
40
20
0
10
30
50
60
POPULATION MEAN
ENVIRONMENTAL MEAN
2 B_1
4
5
6
3
7

FIG. 23

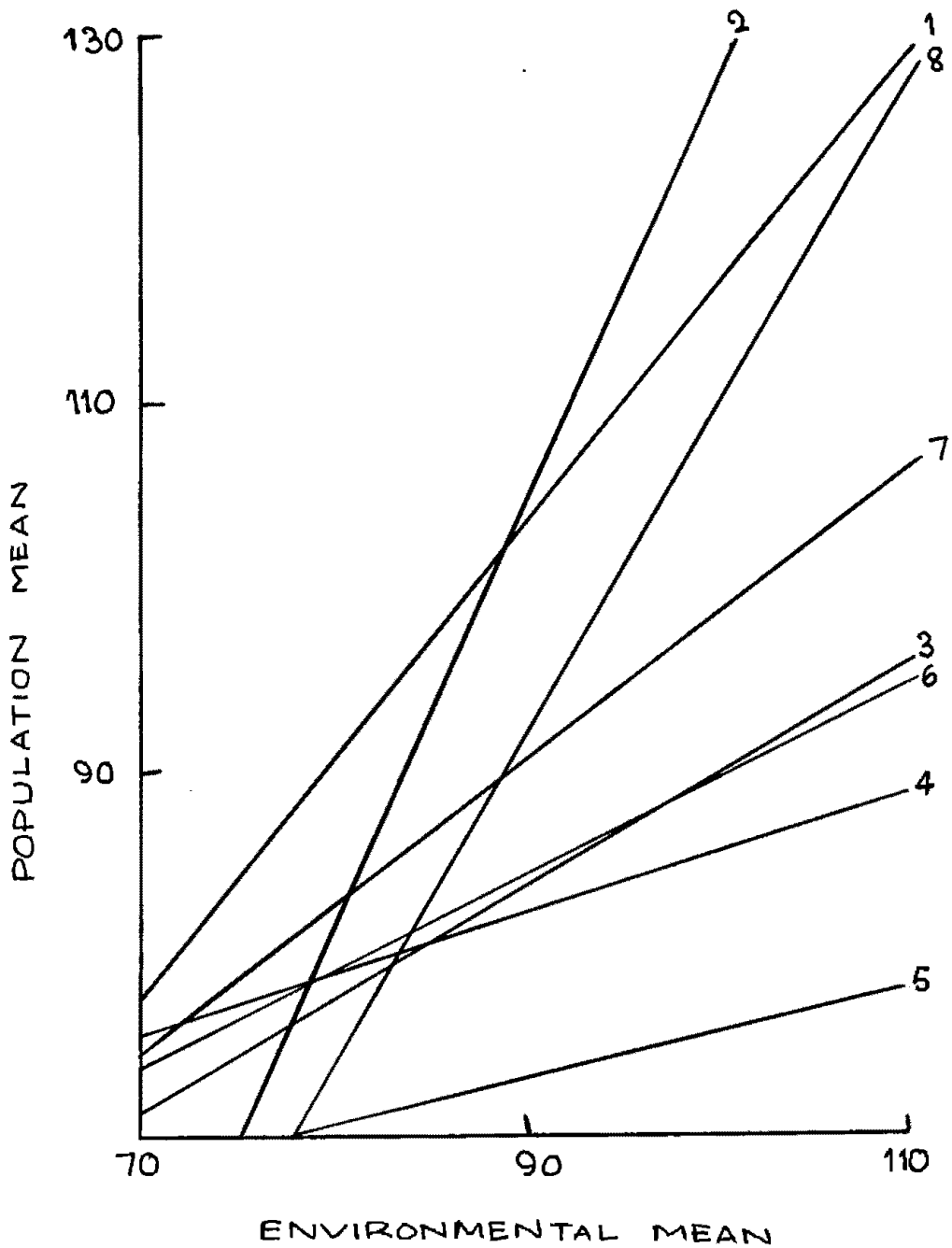

130
110
90
70
90
110
POPULATION MEAN
ENVIRONMENTAL MEAN
1
2
3
4
5
6
7
8

FIG. 24

(d) Correlation

Correlation co-efficient (r) "within" and "between" characters were measured and are shown in table 26 and 27 respectively.

The correlation co-efficient(r) between mean ($\bar{X}$) and response (b_i), between mean ($\bar{X}$) and stability ($\bar{S}^2_d$) and between response (b_i) and stability ($\bar{S}^2_d$) within a character were tabulated in table 26. Mean performance was negative and significantly correlated with response in case of fresh shoot wight whereas significantly positive correlations were found in case of dry root weight and plant height. The mean performance ($\bar{X}$) was also significantly correlated with $\bar{S}^2_d$ in case of plant height and negatively correlated in case of fresh shoot weight. The correlation co-efficient between response (b_i) and stability ($\bar{S}^2_d$) was positive and significant in case of fresh root weight and the rests were non-significant. As most of the characters showed non-significant correlation co-efficient (r) values between mean ($\bar{X}$) and response (b_i), between mean ($\bar{X}$) and stability ($\bar{S}^2_d$) and between response (b_i) and stability ($\bar{S}^2_d$) it was suggested that these aspects of phenotypes were independent to each other and they were under different gene control.

Correlation co-efficient(r) between responses (b_i) and between stabilities ($\bar{S}^2_d$) among characters were calculated and are shown in table 27. Most of the characters showed negative co-relation co-efficient values and except plant height with fresh shoot weight all the characters had non-significant correlation co-efficients between the responses (bi) which indicated that variation of a character was not correlated with other characters. Correlation co-efficients between $\bar{S}^2_d$ among characters were significant and positively correlated only incase of dry root

weight with fresh root weight and plant height with fresh shoot weight. Most of the characters showed non-significant correlation co-efficients (r) between responses (b_i) and between stabilities ($\bar{\sigma}^2_d$) which indicated that they are independent to each other.

Table 19. Environmental means over replications and genotypes.

Seasons	Treatments							
	O	N	P	K	NP	NK	PK	NPK
Fresh Shoot Weight								
1977	152.09	206.65	161.73	119.46	231.13	199.13	122.80	293.94
1978	120.53	143.07	133.55	100.71	150.23	140.65	109.65	154.69
Dry Shoot Weight								
1977	70.77	98.88	75.15	53.63	111.57	92.92	55.86	132.73
1978	55.11	66.96	62.90	41.48	70.65	63.96	46.00	73.17
Fresh Root Weight								
1977	96.23	107.23	101.05	85.52	135.52	103.75	86.73	134.50
1978	91.15	100.15	89.30	80.94	103.94	104.36	79.27	120.59
Dry Root Weight								
1977	38.94	41.74	36.05	35.43	49.38	35.80	33.03	53.61
1978	46.67	47.69	39.81	38.89	48.14	49.41	38.35	59.83
Plant Height								
1977	109.30	111.76	113.45	112.57	114.11	112.30	112.32	111.96
1978	82.01	86.76	88.63	85.55	91.26	90.51	87.84	97.93

Table 20. Population means over replications, treatments and seasons.

Genotypes	Fresh shoot weight(FSW)	Dry shoot weight(DSW)	Fresh root weight(FRW)	Dry Root weight(DRW)	Plant height(PH)
Kaizersail	236.33	113.52	125.53	53.45	117.62
Badshabhog	197.05	93.66	130.33	55.89	129.69
Chinese	128.31	47.25	94.05	32.24	90.51
IR-8	134.76	60.02	105.03	45.91	85.79
IR-532	168.57	69.84	63.69	32.03	75.66
IR-20	116.23	45.90	73.82	38.59	89.74
IR-5	135.19	77.53	92.69	34.31	99.39
Kataribhog	153.55	78.14	125.16	53.97	110.73

Table 21. Results of Analysis of variance of different characters.

Items	D.F.	Fresh Shoot Weight M.S.	Fresh Shoot Weight V.R.	Dry Shoot Weight M.S.	Dry Shoot Weight V.R.
Season (Y)	1	282344.16	159.23***	66876.49	172.06***
Nutrition(N)	7	72.47.44	40.63***	17864.12	45.96***
N X Y	7	20885.24	11.78***	3673.40	9.45***
Genotypes(G)	7	78665.76	44.36***	25300.61	65.09***
G X Y	7	34192.96	19.28***	3317.41	8.53***
G X N	49	1584.21		424.87	1.09***
G X Y X N	49	1730.69	0.98	395.61	1.02***
Replication in years	4	1524.03		641.44	1.65
Error	252	1773.16		388.69	

		Fresh Root Weight		Dry Root Weight	
Season (Y)	1	9639.04	9.17***	3013.36	14.28***
Nutrition(N)	7	12325.04	11.73***	2312.32	10.95***
N X Y	7	1145.27	1.09	212.64	1.01
Genotype(G)	7	29510.80	28.08***	5035.05	23.85***
G X Y	7	17785.84	16.92***	4242.77	20.10***
G X N	49	1034.86	0.98	236.20	1.12***
G X Y X N	49	853.43		163.98	
Replications in years	4	2495.22	2.37*	592.26	2.81*
Error	252	1050.92		211.08	

Contd.....

Table 21 (Contd.)

Items	D.F.	Plant height	
		M.S.	V.R.
Season (Y)	1	58388.47	1578.66***
Nutrition (N)	7	209.02	5.65***
N X Y	7	42.13	1.14
Genotypes (G)	7	15749.95	425.83***
G X Y	7	4159.62	112.46***
G X N	49	40.39	1.09***
G X Y X N	49	45.63	1.23***
Replications in year	4	73.42	1.99
Error	252	36.99	

*, ** and *** significant at 5%, 1% and 0.1% level.

Table 22. Results of effects of Nutrients on genotypes

Genotypes		N	P	K	NP	NK	PK	NPK
				Fresh Shoot Weight (FSW)				
Naizersail	Y_1	462.50***	112.84*	-24.50	55.84**	207.82*	192.84*	6.84
	Y_2	75.01**	105.01**	-78.33*	-54.99*	-98.33*	-15.01	-201.33**
Badshabhog	Y_1	375.49***	131.17**	53.83*	102.83*	165.49*	11.17	10.83
	Y_2	22.50	-42.50*	-47.16*	75.82*	37.84*	102.34*	37.84*
Kataribhog	Y_1	385.00***	103.00***	87.00**	86.34*	116.98*	182.34**	145.00***
	Y_2	191.67**	-4.35	21.33	-70.67**	58.33*	-64.33*	32.67*
				Dry Shoot Weight (DSW)				
Naizersail	Y_1	255.35**	4.67	-78.67**	36.01**	105.99**	98.67**	-47.99**
	Y_2	54.45*	61.47*	-51.53***	0.47	7.47	5.81	30.13*
Badshabhog	Y_1	194.16**	54.16*	-19.16*	59.16*	39.16*	-4.16	-5.84
	Y_2	51.66*	0.68	-70.68	29.00	-3.00	28.66*	10.34
Kataribhog	Y_1	235.83**	92.51**	0.83	64.17**	62.49**	72.49**	97.51**
	Y_2	26.68*	32.34*	1.84	28.34*	57.84*	-9.00	7.00
				Fresh Root Weight (FRW)				
Naizersail	Y_1	216.66**	80.00**	-138.34*	90.00**	-11.66	78.32**	-95.00**
	Y_2	46.66*	-0.66	- 86.32*	32.32*	21.34	52.66*	19.00
Badshabhog	Y_1	111.17**	93.83**	-24.51*	126.17**	17.83	7.17	-47.17**
	Y_2	87.37**	-109.97**	-31.63*	74.37**	70.71**	56.05**	-44.97**
Kataribhog	Y_1	49.99*	89.99**	20.01	0.01	-3.33	16.67	133.33**
	Y_2	195.83**	65.83**	47.49**	-7.49	27.49*	44.17**	24.17*

Contd.....

Table 22. (contd.)

Genotypes		N	P	K	NP	NK	PK	NPK
					Dry Root Weight (DRW)			
Naizersail	Y_1	85.68**	43.00**	-46.32**	57.68**	-21.00**	36.32**	1.84
	Y_2	42.34*	11.20*	-18.06**	19.06*	39.12**	51.74**	39.20**
Badshabhog	Y_1	34.51**	31.49**	2.83	52.17**	13.51*	37.17**	-8.63
	Y_2	51.30**	-68.50**	-1.30	30.30**	18.82**	27.42**	-47.50**
Kataribhog	Y_1	16.84**	18.82**	5.18	27.50**	1.50	17.16*	23.84**
	Y_2	53.83**	10.83*	13.15*	-2.49	11.83*	30.83**	-10.49*
					Plant Height (PH)			
Naizersail	Y_1	-7.04**	-3.24	6.56**	-2.22	-19.10**	-17.70**	-7.76**
	Y_2	23.50**	24.15**	-2.18	-23.50**	-15.15**	-30.50**	-4.16
Badshabhog	Y_1	5.49*	-7.29**	24.37**	-17.03**	-12.97**	-12.71**	-0.69
	Y_2	33.01**	16.01**	5.67**	-12.67**	-7.01**	-9.33**	4.67*
	Y_1	21.32**	16.00**	-11.00**	2.00	1.00	-4.32*	8.32**
	Y_2	11.51**	29.49**	8.49**	16.17**	1.17	-10.17**	-8.17**

*, **, and *** significant at 5%, 1% and 0.1% level.

Table 23. Estimates of δ^2_G, δ^2_{NG}, δ^2_{GY}, δ^2_{NGY} and δ^2_E and the co-efficient of variability for the five characters.

	Fresh Shoot Weight	Dry Shoot Weight	Fresh Root Weight	Dry Root Weight	Plant Height
δ^2_G	929.57	457.37	240.49	15.00	241.57
δ^2_{NG}	-24.41	4.88	30.24	12.04	-0.87
δ^2_{GY}	1352.59	121.74	705.52	169.95	171.42
δ^2_{NGY}	-14.16	2.31	-65.83	-15.70	2.88
δ^2_E	1773.16	388.69	1050.92	211.08	36.99
$CV\delta^2_G$	585.52	624.48	237.47	34.64	240.32
$CV\delta^2_{NG}$	-15.38	6.66	29.86	27.81	-0.87
$CV\delta^2_{GY}$	851.97	166.22	696.67	392.49	170.53
$CV\delta^2_{NGY}$	-8.92	3.15	-65.00	-36.26	2.87
$CV\delta^2_E$	1116.88	530.71	1037.74	487.48	36.80

Table 24. Results of Joint Regression

Item	D.F.	M.S.	V.R.[1]	V.R.[2]
Fresh Shoot Weight				
Linear Regression	7	2127.26	0.54	1.20
Deviation	98	3947.86		2.23***
Error	252	1773.16		
Dry Shoot Weight				
Linear Regression	7	5104.22	18.06***	13.13***
Deviation	98	282.61		0.73
Error	252	388.69		
Fresh Root Weight				
Linear Regression	7	2874.71	3.32***	2.74**
Deviation	98	866.37		0.82
Error	252	1050.92		
Dry Root Weight				
Linear Regression	7	512.11	1.10	2.43*
Deviation	98	466.57		2.21***
Error	252	211.08		
Plant Height				
Linear Regression	7	173.01	0.52	4.68***
Deviation	98	333.89		9.03***
Error	252	36.99		

$$VR^1 = \frac{\text{M.S.}}{\text{Deviation M.S.}} \qquad VR^2 = \frac{\text{M.S.}}{\text{Error M.S.}}$$

Table 25. Regression co-efficients b_i, S_{b_i}, β_i, Stability $\bar{S}^2_d$ and Correlation co-efficient(r) for eight Genotypes grown under 16 environments.

Genotypes	b_i	S_{b_i}	β_i	$\bar{S}^2_d$	r
			Fresh Shoot Weight		
Naizersail	0.47	0.30	-0.53	1680.15	0.39
Badshabhog	0.75	0.12	-0.25	-1219.65	0.86
Chinese	1.31	0.14	0.31	-1054.23	0.93
IR-8	1.05	0.20	0.05	-213.90	0.81
IR-532	1.33	0.11	0.33	-1315.23	0.96
IR-20	1.08	0.11	0.08	-1325.03	0.94
IR-5	0.98	0.11	-0.02	-1348.03	0.94
Kataribhog	1.02	0.10	0.02	-1354.46	0.94

Bartlett's $X^2_{(d.f.=7)}$ testing homogenity of S_{b_i} = 38.5185***

			Dry Shoot Weight		
Naizersail	1.05	0.18	0.05	-92.95	0.84
Badshabhog	0.94	0.09	-0.06	-316.26	0.94
Chinese	0.72	0.07	-0.28	-344.87	0.94
IR-8	1.19	0.12	0.19	-263.71	0.94
IR-532	0.69	0.19	-0.31	-75.43	0.70
IR-20	0.80	0.08	-0.20	-338.27	0.95
IR-5	1.25	0.15	0.25	-189.38	0.91
Kataribhog	1.35	0.12	0.35	-259.98	0.95

Bartlett's $X^2_{(d.f.=7)}$ testing homogenity of S_{b_i} = 27.0298***

Contd.....

Table 25 (Contd.)

Genotypes	b_i	S_{b_i}	β_i	$\bar{S}^2_d$	r
			Fresh Root Weight		
Naizersail	1.49	0.33	0.49	-539.06	0.77
Dadghabbog	0.28	0.39	-0.72	-588.34	0.24
Chinese	0.77	0.25	-0.23	-788.85	0.64
IR-8	2.09	0.67	1.09	-175.46	0.78
IR-532	0.73	0.28	-0.27	-707.57	0.57
IR-20	0.55	0.12	-0.45	-984.46	0.76
IR-5	0.90	0.40	-0.10	-343.01	0.51
Kataribhog	0.42	0.58	-0.58	515.87	0.19

Bartlett's $X^2_{(d.f.=7)}$ testing homogenity of S_{b_i} = 48.2385***

			Dry Root Weight		
Naizersail	1.73	0.28	0.73	-145.37	0.86
Dadshabbog	1.56	0.40	0.56	-74.12	0.72
Chinese	0.08	0.28	-0.92	-143.41	0.08
IR-8	0.87	0.43	-0.13	-55.74	0.48
IR-532	1.38	0.29	0.38	-138.57	0.79
IR-20	0.88	0.17	-0.12	-187.46	0.82
IR-5	-0.21	0.43	-1.21	-53.07	-0.13
Kataribhog	1.71	0.55	0.71	51.09	0.64

Bartlett's $X^2_{(d.f.=7)}$ testing homogentiy of Sb_i = 28.3568***

Contd.....

Table 25 (Contd.)

Genotypes	b_i	S_{b_i}	β_i	$\bar{S}^2_d$	r
			Plant Height		
Kaizersail	1.29	0.11	0.29	-5.86	0.95
Badshahbhog	2.41	0.15	1.41	14.65	0.98
Chinese	0.63	0.07	-0.37	-24.15	0.95
IR-8	0.33	0.07	-0.67	-26.86	0.80
IR-532	0.26	0.05	-0.74	-30.96	0.79
IR-20	0.56	0.08	-0.44	-20.90	0.88
IR-5	0.84	0.07	-0.16	-24.62	0.95
Kataribhog	1.78	0.10	0.78	-12.96	0.98

Bartlett's $X^2_{(d.f.=7)}$ testing homogenity of S_{b_i} = 26.8129***

Table 26. Results of correlation co-efficients within characters

Character	Correlations		
	Between mean and b_i	Between mean and $\bar{S}_d^2$	Between b_i and $\bar{S}_d^2$
Fresh Shoot Weight	-0.76*	-0.47	0.34
Dry Shoot Weight	0.37	0.57	0.06
Fresh Root Weight	0.059	0.52	0.91***
Dry Root Weight	0.84**	0.66	0.26
Plant Height	0.95***	0.85**	0.74

Table 27. Results of correlation co-efficients between responses, b_i (upper right) and between stabilities, $\bar{S}_d^2$ (lower left) among characters.

	Fresh Shoot Weight	Dry Shoot Weight	Fresh Root Weight	Dry Root Weight	Plant Height
Fresh Shoot Weight	-	-0.41	-0.20	-0.52	-0.87***
Dry Shoot Weight	-0.37	-	0.27	0.08	0.34
Fresh Root Weight	0.49	0.13	-	-0.12	-0.48
Dry Root Weight	0.38	-0.04	0.89**	-	0.56
Plant Height	0.85**	-0.35	0.57	0.42	-

*, **, *** at 5%, 1% and 0.1% level D.F. = 6

D. G X E INTERACTION OF YIELD AND YIELD COMPONENTS OF $5F_2$S AND THEIR 5-PARENTS OF RICE.

(a) Means and Relative Importance to Different Nutrients

Mean performances of all the seven characters under different nutritional treatments over six replications and ten genotypes (A=5 F_2S plus 5 parents) and 5 parents (B) are shown in table 28. The table shows that almost all the characters were affected by the nutritional treatments which were treated as environments. The environmental means (table 28) also suggest that population in general gave better yield performances in the treatments having N. The highest yield performance was found in NPK and lowest was found in nil and K treatments. Primary branches/panicle and 100 kernel weight were found to remain more or less unaffected by nutritional treatments.

Population means over replications and treatments for all the characters are given in table 29. Among the parents IR-8 and Kataribhog showed the highest panicle length whereas among parents and F_2S, IR-8 X Kataribhog gave the highest panicle length. Most of the F_2S showed higher panicle length than their parents. The number of primary branches/panicle among parents was more in Naizersail and Chinese but among F_2S, IR-8 X Kataribhog and IR-8 X Chinese showed maximum primary branche number. Almost all the F_2S showed more primary branch number than parents. The highest number of spikelet/panicle was found in case of IR-20 and Kataribhog among the parents but crosses IR-8 X Kataribhog and Chinese X Naizersail showed the highest spikelet number. IR-20 showed the highest kernel number whereas IR-8 X Kataribhog showed the highest kernel number/ panicle among F_2S. Among the parents IR-20 and among the F_2S IR-8 X Kataribhog showed highest yield performances. Kataribhog and the cross IR-8 X Kataribhog exhibited the highest tiller number.

An analysis of variance was done for all the characters and are shown in table 30. The table showed that all the main items were highly significant against experimental error in most of the characters. The item, F_2 genotypes was non-significant in case of spikelet number/panicle and tiller number whereas the item ($P-F_2$) was non-significant in case of tiller number only. The item P X N was non-significant in case of spikelet number/panicle and the item ($P-F_2$) X N was non-significant in case of panicle length, spikelet number/panicle, kernel number/panicle and 100 kernel weight. The item population (G) was highly significant in case of all the characters studied indicating that a real difference existed among the genotypes. As the item nitrition (N) was highly significant in all the cases, it indicated that a real effect of different nutritional treatments on the genotypes were present. The analysis of variance further showed that the genotypes interacted significantly with all environment, as the item genotype X environment (G X N) was highly significant in all the seven characters. Since all the interactions were significant, no immediate generalisation can be made on the relative performances of the populations over a range of environmental contrast, valid comparisons only be made under each environment separately.

As the analysis of variance showed that all the genotypes responded siguificantly under different treatments, it was very essential to evaluate the effects of individual nutrients on the genotypes. In the present study the effects of N,P,K and their combinations on 10 populations,5 parents and 5F_2S were calculated separately and are given in table 31.

In case of panicle length N and P had significant effects on populations, parents and F_2S. Only parents showed significant effect due to K and NP. NP had negative effect on F_2S. NK and NPK had positive effects on all the cases but the effects were non-significant. PK had negative effects in all the cases.

For primary branches/panicle N and P had significant positive effects in all the cases except N on F_2S. K had also positive effects in all the cases but the effects were non-significant. NP had positive effects on parents and populations but negative significant effect on combined F_2S. NK showed positive effects on 5 parents and 10 populations but negative effect on $5F_2S$. PK and NPK had positive effects in all the cases but the effects were non-significant.

N, P and NPK significantly increased the spikelet number/panicle in all the cases but the maximum effect was due to N only. K had positive effect on population and F_2S but negative effect on parents. Positive effect due to NP was observed in all the cases but the effect was significant in case of parents and population. NK and PK also had positive effects in all the cases.

Significant positive effect on kernel number per panicle was found in all the three cases due to N,P and NPK. Except F_2S the two others showed negative effect due to K. NP, NK, and PK also had positive effect in all the cases.

In case of 100 kernel weight N had negative and practically no effect in parents, population and F_2S. P had significant positive effect in the parents population and F_2S. K had positive effect in all the cases but the effect was very small and non-significant. NP and NPK had negative effect on parents and population but positive effect on F_2S. NK had non-significant positive effect and PK had significant negative effect in the three cases.

N, P and NP significantly increased the yield of parents, population and F_2S separately. K and PK had positive effect but the effect was non-significant. NK and NPK had positive significant effect in case of F_2S only.

N, P and NP increased the tiller number of parents, population and F_2S but the maximum effect was due to N. K significantly decreased the tiller number of parents and population. NK had non-significant negative effect on all the cases. PK showed negative effect on parents and population but positive effect on F_2S. NPK had both non-significant positive and negative effect.

(b) Variability

The estimates of variance components (δ^2_G, δ^2_{GE} and δ^2_E) along with the co-efficient of variability are shown in table 32. Genetic variation (δ^2_G) was greater than both δ^2_{GE} and δ^2_E in case of 100 kernel weight only. The environmental variations (δ^2_E) were greater than δ^2_G and δ^2_{GE} in majority cases. Highest co-efficient of variability for δ^2_G were shown by kernel number/panicle followed by spikelet number/panicle whereas that for δ^2_{GE} were shown by yield/plant followed by tiller number. Uncontrolled variation (δ^2_E) was high in kernel number/panicle, spikelet number/panicle and yield/plant.

(c) Regression

The presence of the genotype-environment interaction indicated that a dynamic relationship existed between genotype and environmental effects (Finlay and Wilkinson, 1963). In the analysis two kinds of assessment of the environment were determined which are shown in table 28. Firstly the mean performances of all the ten genotypes (both parents and F_2s) were used to provide an independent assessment of the environment. Secondly the mean performances of the five parental lines were used to provide an independent assesement of the environments. The two kinds of assessments of the environment were highly correlated (Significant at 0.1% level) in all the seven characters and the co-rrelation co-efficients (r) were 0.98, 0.89, 0.97, 0.98, 0.95, 0.98 and 0.99 (table 28) for panicle length, primary branches/panicle, spikelet number/panicle, kernel number/panicle, 100 kernel weigth, yield/plant and tiller number respectively. Thus both the two assessments were obviously providing satisfactory assessment of the environment. In this analysis, the genotype X environment interaction was, therefore, measured by means of all the ten populations.

The sum of squares measuring the interaction of the population with the environments were repartitioned into linear regression and deviation item and are shown in table 33. A major part of the genotype-environment interaction was due to the difference btweeen the slopes of the linear regression as the item was significant in all the cases except spikelet number/panicle, kernel number/panicle and 100 kernel weight. The deviation M.S. was significantly greater than error M.S. in all the cases and the linear regression mean squares were also greater than those of

deviation in all the seven trisits. Both the linear regression and deviation items were significant in case of panicle length, primary branches/panicle, yield/plant and tiller number when tested by experimental error. This suggested that there was relationship between genotype and environment and the presence of G X E interaction within each genotype. Deviation M.S. alone was significant in case of spikelet number/panicle, kernel number/panicle and 100 kernel weight. But when the regression item was tested by residual item then all the characters showed non-significant.

For each variety and F_2S linear regression of individual values on these eight environmental means were computed. The regression co-effieients b_i, β_i, standard error (S_{b_i}), Stability ($\bar{S}^2_d$) and the correlation co-efficient(r) between environmental mean of each genotype were measured and are shown in table 34. The distribution of ten b_i values were heterogenous as revealed by joint regression (table 33) and hence all these genotypes had different responses to different environments. The range of b_i values among F_2S exceeded the parental range in both directions in most of the cases. It suggested that this aspect of phenotype was not simply inherited. High and low correlation co-efficient(r) indicated that both linear and non-linear regression accounted for most of the variation over environments.

Panicle Length : Except Chinese X Naizersail all other nine population showed significant linear response to the environments. Among the parents Chinese, IR-20 and Naizersail but among F_2S IR-8 X Chinese and IR-8 X Kataribhog showed above average responses to the environments. Other had below average responses. The lowest response was observed by Chinese X Naizersail ($b_i = 0.33 \pm 0.26$) and the highest was by IR-8 X Chinese ($b_i = 1.66 \pm 0.33$) among all the populations. Both high and low

correlation co-efficients (r) were found in this trait.

Primary Branches/panicle : Significant linear responses were observed by Chinese, IR-8, Naizersail, Kataribhog, IR-8 X Chinese and IR-20 X Kataribhog. Highest response was found in case of Chinese (b_i = 2.31 ± 0.77). Chinese, Naizersail and Kataribhog showed above average responses and all other populations showed below average responses to the environments. The F_2 Chinese X Kataribhog responded negatively to the environments (b_i = -0.24 ± 0.48). Chinese X Naizersail practically had no response (b_i = 0.04 ± 0.52) to the environments. Most of the genotypes had low correlation co-efficient values indicating non-linear variations.

Spikelet Number/panicle : All the genotypes responded significantly to the environments but Chinese and IR-20 among parents and IR-8 X Chinese and IR-20 X Chinese among F_2S showed above average responses to the environments. The other population showed below average responses but the responses were more or less similar. Most of the genotypes had high correlation co-efficient values (r) which indicated the linear regression accounted for variation over environments.

Kernel Number/panicle : In this case significant linear responses were also observed by all the populations. Chinese (b_i = 1.35 ± 0.18), IR-20 (b_i = 1.08 ± 0.20) and Kataribhog (b_i = 1.46 ± 0.28) among parents and IR-8 X Chinese (b_i = 1.15 ± 0.43) and IR-8 X Kataribhog (b_i=1.06 ± 0.34) among F_2S showed above average responses to the environments. Other genotypes had below average responses. Both high and low correlation co-efficients (r) were observed.

100 Kernel Weight : Chinese, IR-8, Naizersail, IR-8 X Chinese and IR-20 X Kataribhog showed significant linear responses to the environments

and they had above average responses. The highest response was found in IR-8 (b_i = 2.36 ± 0.58) among parents and IR-8 X Chinese (b_i = 2.21 ±0.95) among F_2S. Kataribhog responded negatively to the environments (b_i = 0.31 ± 0.40) and the Chinese X Kataribhog had practically no response to the environments (b_i = 0.02 ± 0.60). Most of the genotypes had low correlation co-efficient (r) values for this characters.

Yield/plant : Highly significant linear responses were found in all the population to the environments. Among parent IR-20 only had above average responses. But among F_2S, all the F_2 populations had above average responses which indicated that the F_2 populations were highly responsive to the environments with respect to yield performance. Maximum response was observed in case of IR-8 X Kataribhog (b_i = 1.61 ± 0.18). All the genotypes had high correlation co-efficient (r) values indicating the linear response accounted for most of the variations over the environments.

Tiller Number : In this case also, all the ten genotypes had significant responses to the environments. IR-20 (b_i = 1.02 ± 0.04), IR-8 (b_i = 1.05 ± 0.04) Kataribhog (b_i = 1.53 ± 0.13), IR-8 X Chinese (b_i = 1.04 ± 0.01) and IR-8 X Kataribhog (b_i = 1.08 ± 0.11) showed above average responses and the other five genotypes showed below average responses to the environments. High correlation co-efficients (r) were found for all the genotypes.

The standard error (S_{b_i}) proves to be heterogenous as X^2 in the Bartlett's test (shown at the bottom of each character in table 34) was significant in all the cases except spikelet number/panicle and yield/plant. Thus it indicated that there were distinct difference between the populations in the amount of deviation arround to regression slopes and

suggested that this attribute is under gene control. Another measure of variation around the regression slopes was $\bar{S}^2_d$ which was also shown in table 34. The $\bar{S}^2_d$ was highly heterogenous in these characters as revealed by joint regression (table 33) and standard error (S_{b_i}). Among the seven characters, panicle length, primary branches/panicle and 100 kernel weight were considerably stable as shown by their low $\bar{S}^2_d$ values. The other characters had high $\bar{S}^2_d$ values indicating their unstability of the genotypes.

The actual regression line of the performance of every genotype under the different treatments of N, P, K and their combinations against the corresponding over all treatment mean are shown in Figs. 25, 26, 27, 28, 29, 30 and 31 for panicle length, primary branches/panicle, spikelet number/panicle, kernel number/panicle, 100 kernel weight yield/plant and tiller number respectively. Individual points were not plotted in the figures. Crossing of regression lines were very marked incase of panicle length, primary branches/panicle and 100 kernel weight which indicated that G X E interactions were very marked in these characters. But for yield/plant (Fig. 30) and tiller number (Fig. 31) the regression lines were very close together in poor environments and spread out rapidly in good environments. Chinese X Kataribhog gave minimum primary branches/ panicle in good environments (Fig. 26).

Explanation to the Figs. 25-31.

Fig. 25. Regression of individual population mean on environmental mean for five parental lines and their five F_2s in panicle length.

Fig. 26. Regression of individual population mean on environmental mean for five parental lines and their five F_2s in primary branches/panicle.

Fig. 27. Regression of individual population mean on environmental mean for five parental lines and their five F_2s in spikelet number/panicle.

Fig. 28. Regression of individual population mean on environmental mean for five parental lines and their five F_2s in kernel number/panicle.

Fig. 29. Regression of individual population mean on environmental mean for five parental lines and their five F_2s in 100 kernel weight.

Fig. 30. Regression of individual population mean on environmental mean for five parental lines and their five F_2s in yield/plant.

Fig. 31. Regression of individual population mean on environmental mean for five parental lines and their five F_2s in tiller number/plant.

The population in the graphs (represented by their serial numbers) are as follows : 1 = Chinese, 2 = IR-20, 3 = IR-8, 4 = Malmereail, 5 = Katarithog, 6 = 1 X 5, 7 = 3 X 1, 8 = 2 X 5, 9 = 1 X 4 and 10 = 3 X 5.

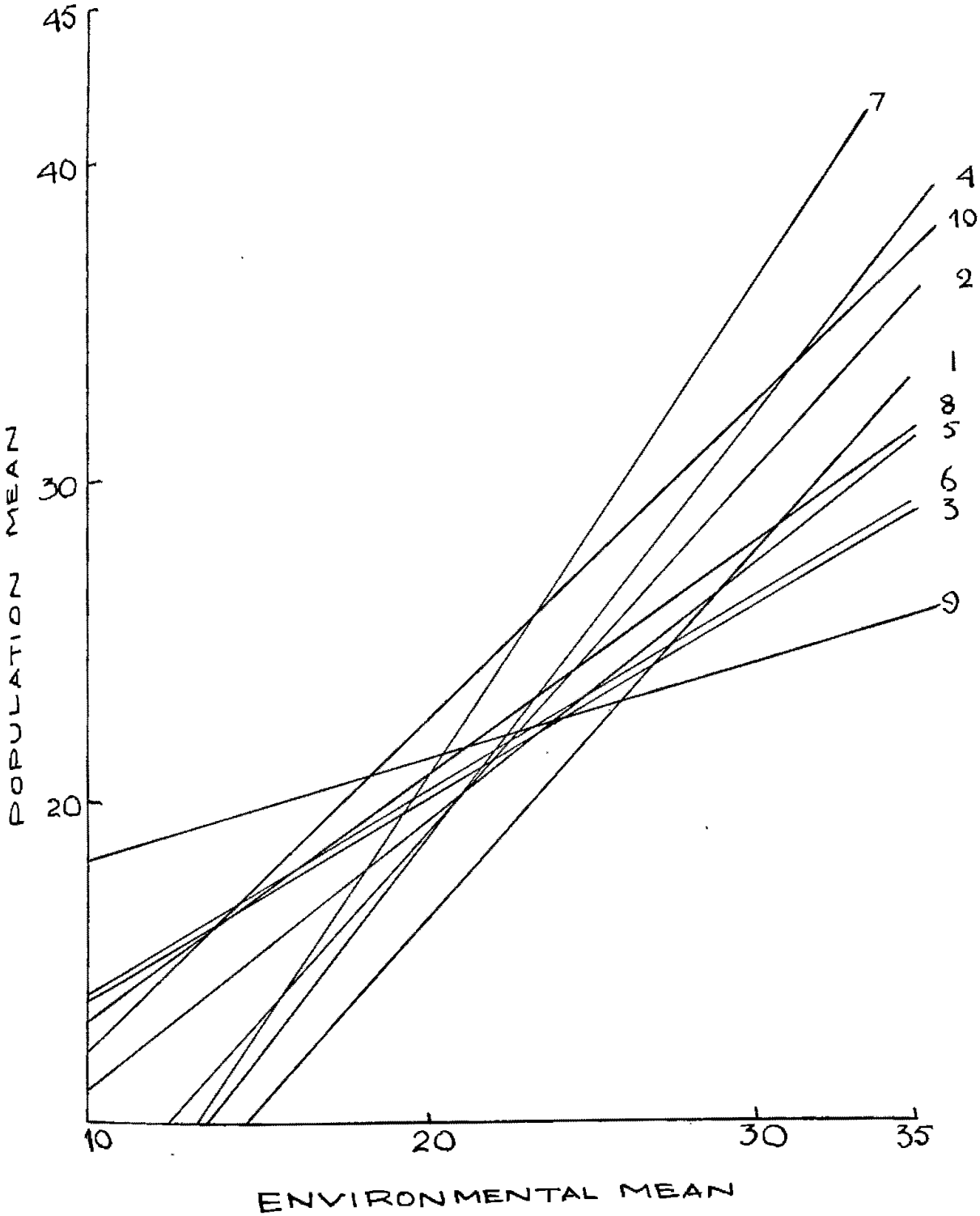

45
40
30
20
POPULATION MEAN
7
4
10
2
1
8
5
6
3
9
10
20
30
35
ENVIRONMENTAL MEAN

FIG. 25

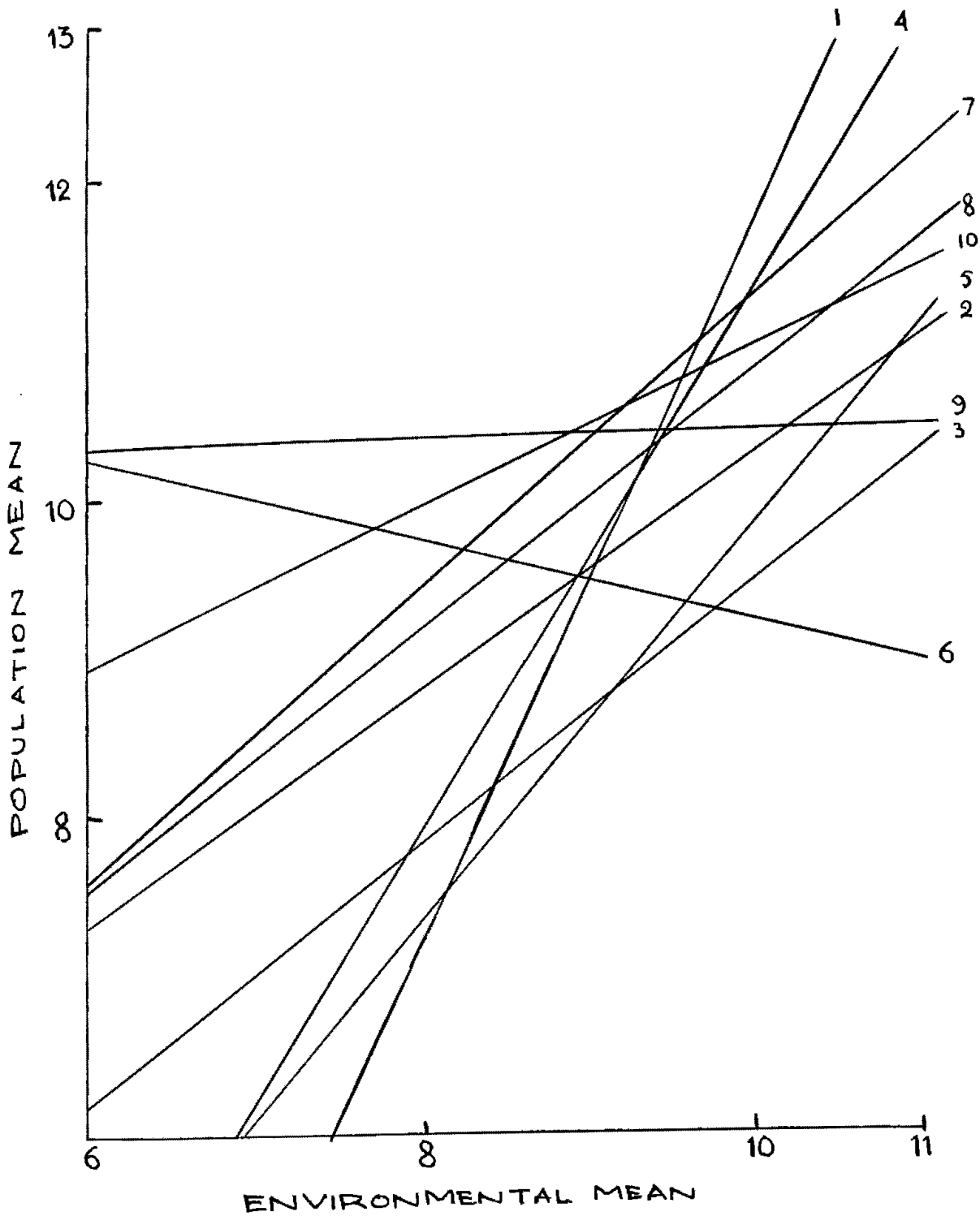

13
12
10
8
POPULATION MEAN
1
4
7
8
10
5
2
9
3
6
6
8
10
11
ENVIRONMENTAL MEAN

FIG. 26

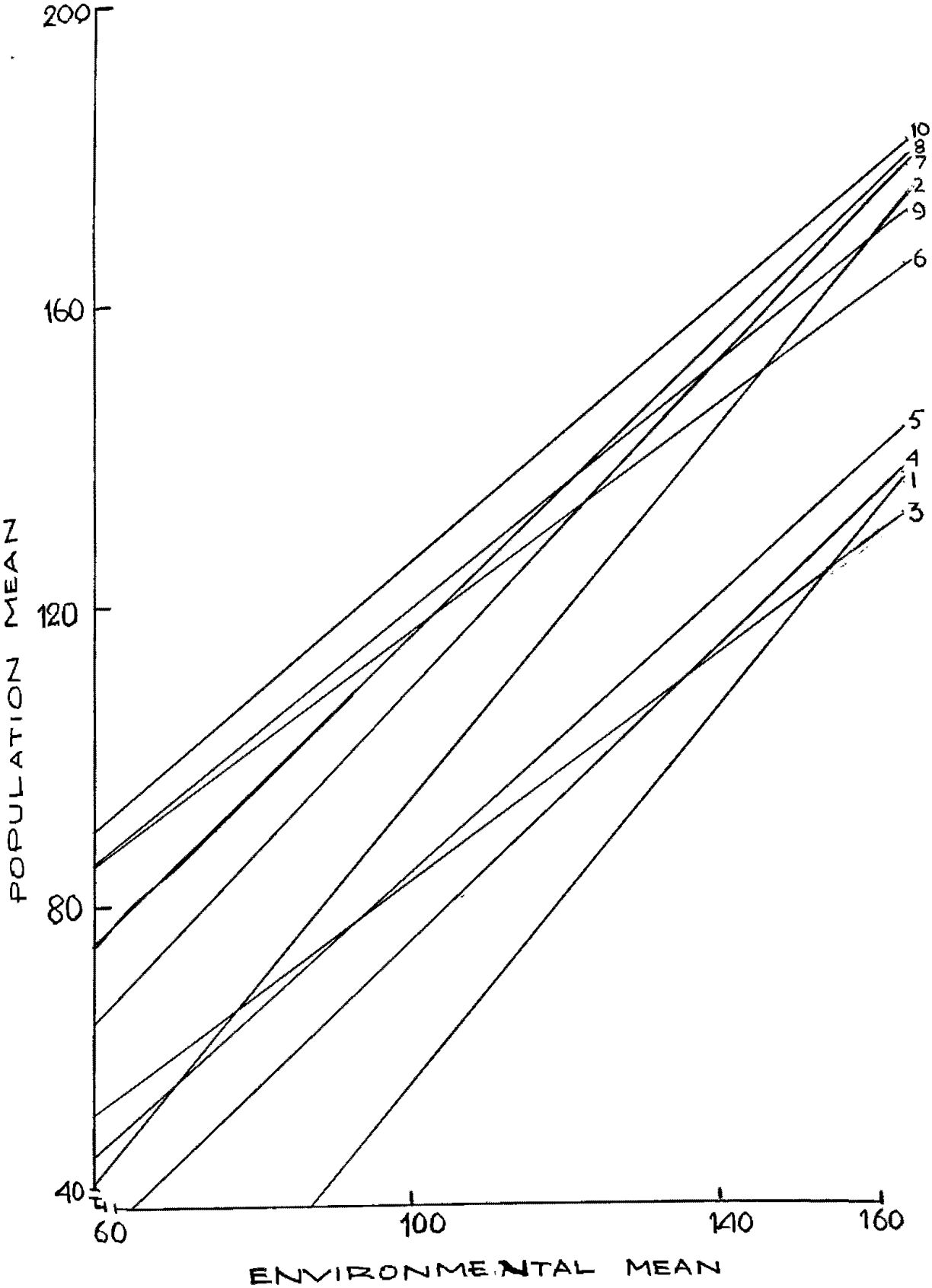

200
160
120
80
40
POPULATION MEAN
60
100
140
160
ENVIRONMENTAL MEAN
10
8
7
2
9
6
5
4
1
3

FIG. 27

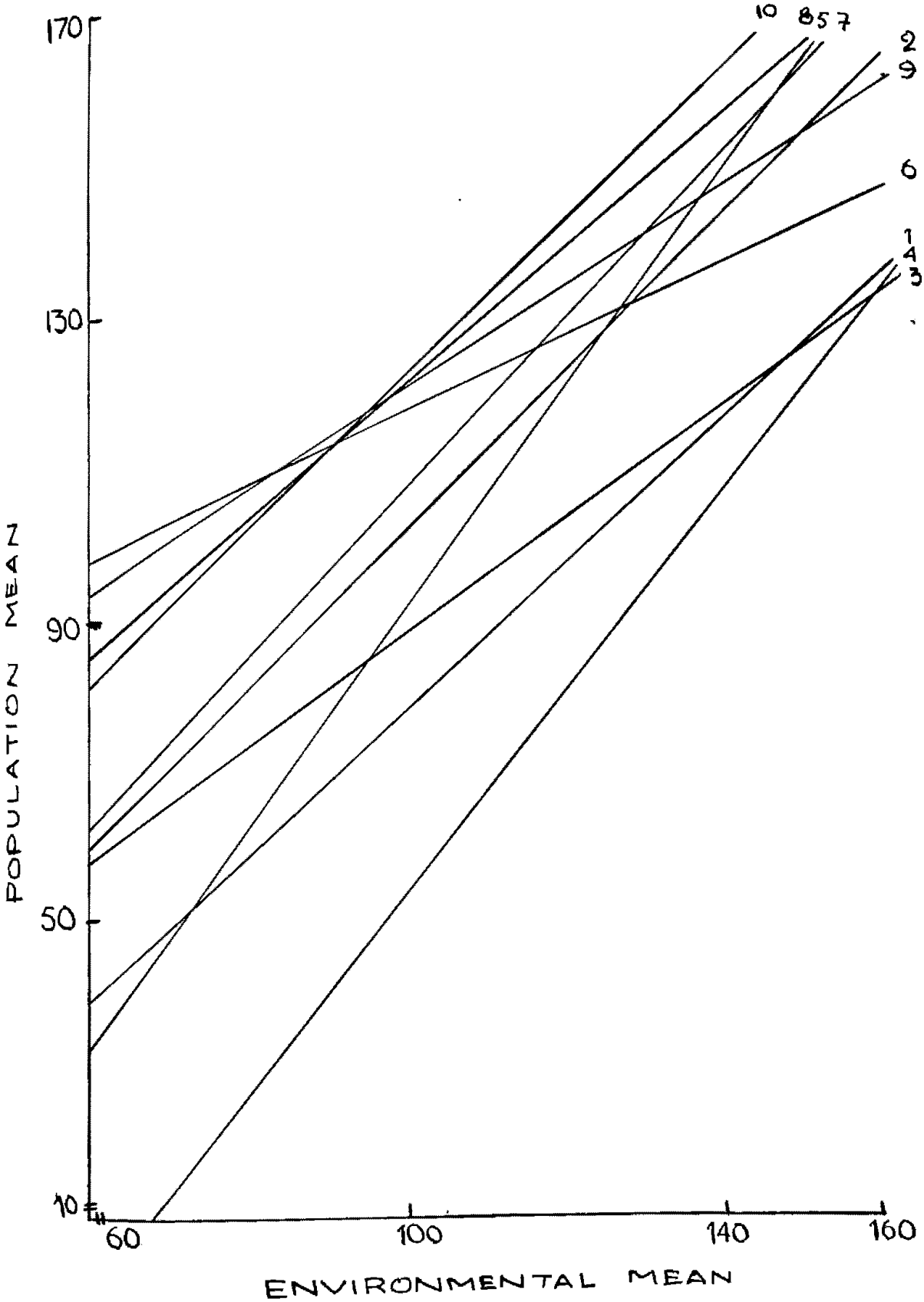

170
130
90
50
10
POPULATION MEAN
60
100
140
160
ENVIRONMENTAL MEAN
10
8
5
7
2
9
6
1
4
3

FIG. 28

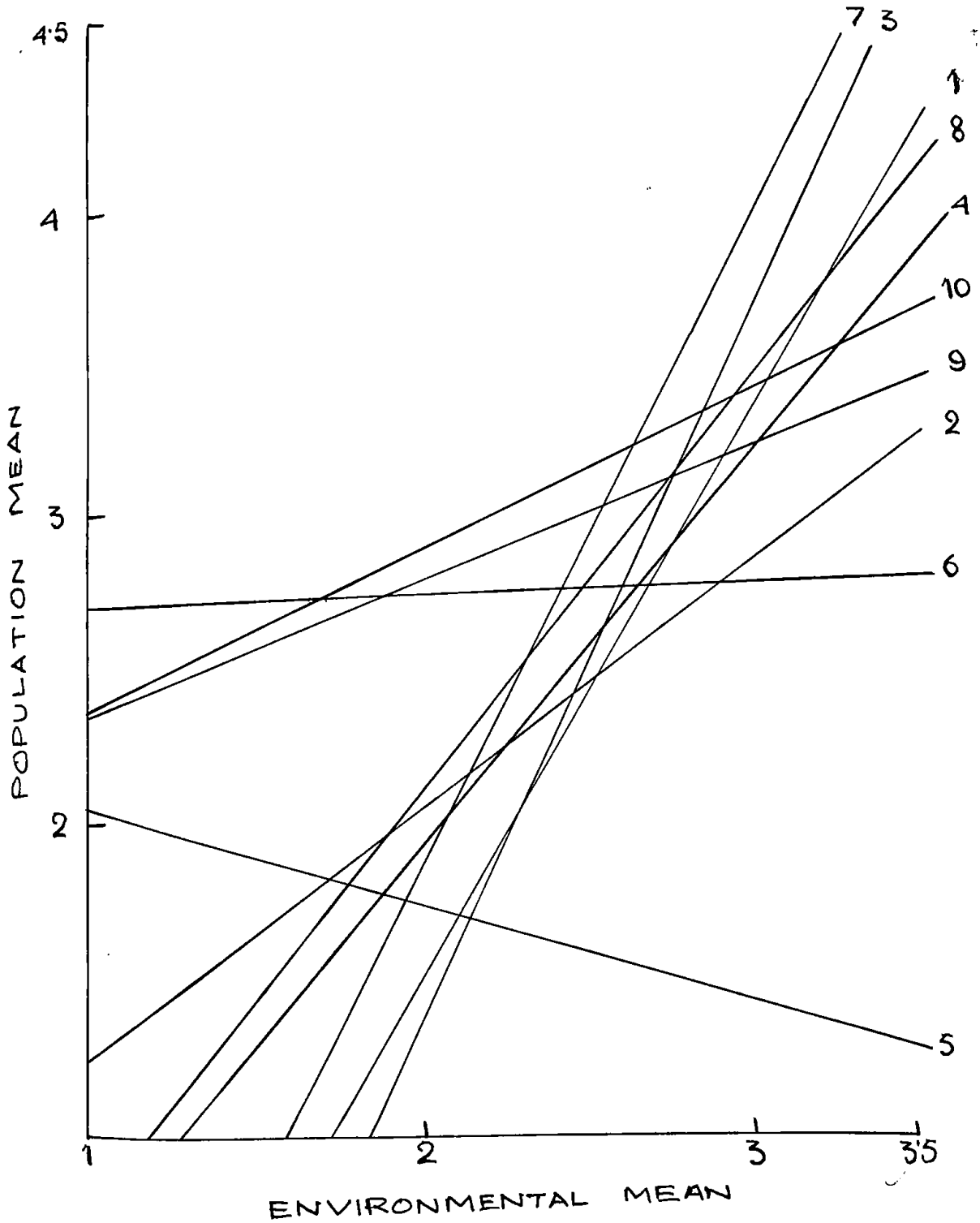

4·5
4
3
2
POPULATION MEAN
7
3
1
8
4
10
9
2
6
5
1
2
3
3·5
ENVIRONMENTAL MEAN

FIG. 29

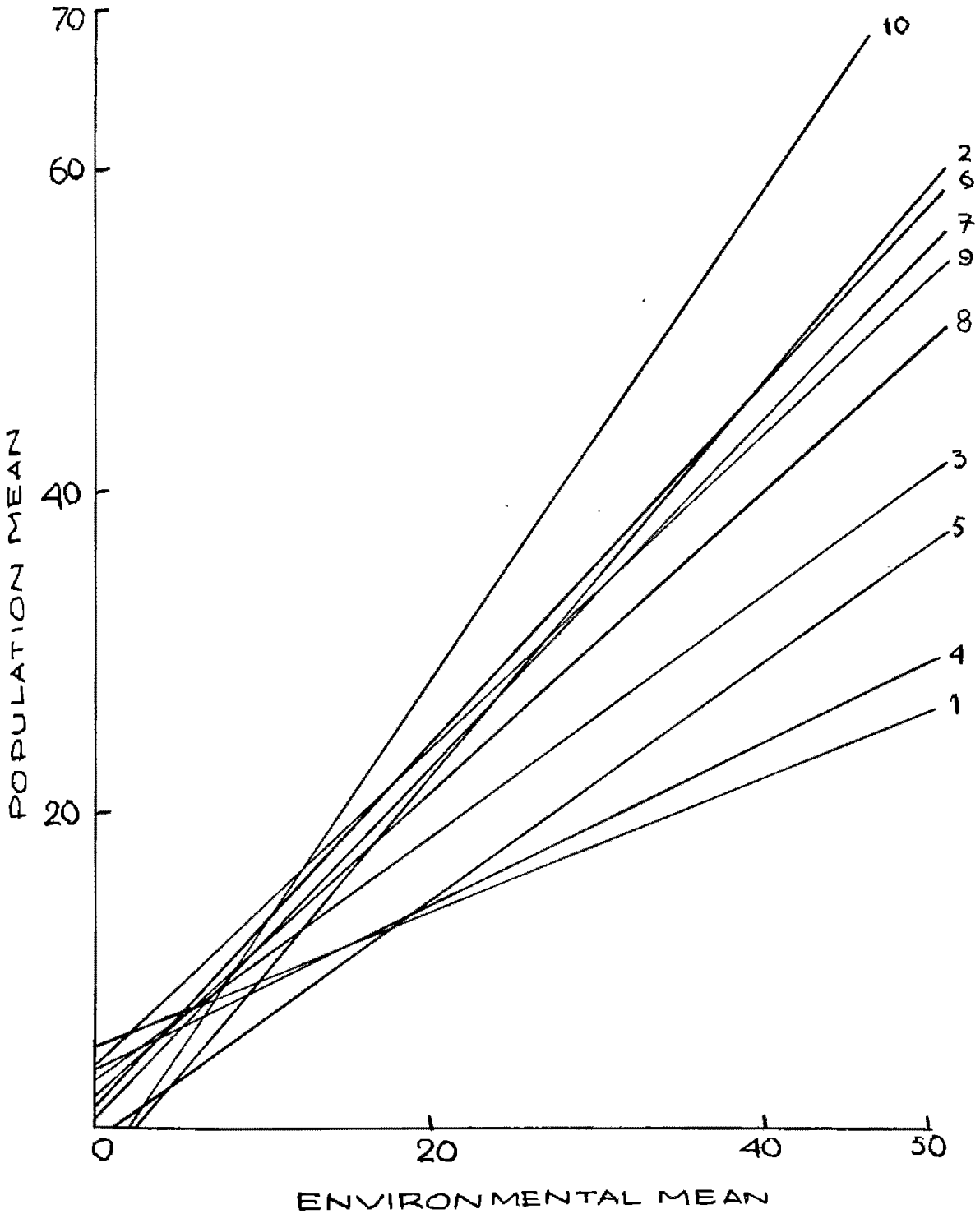

70
60
40
20
POPULATION MEAN
0
20
40
50
ENVIRONMENTAL MEAN
10
2
6
7
9
8
3
5
4
1

FIG. 30

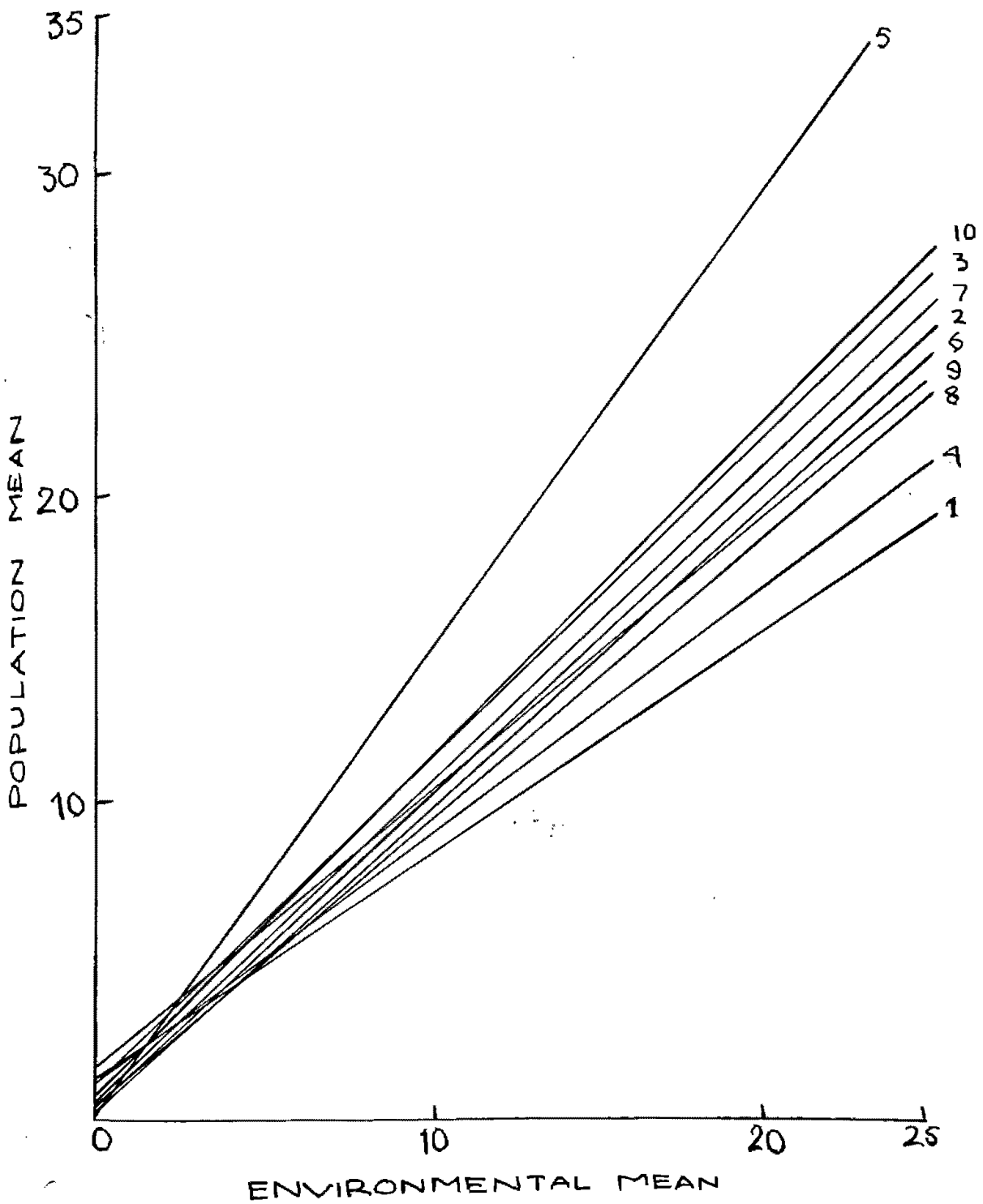

35
30
20
10
POPULATION MEAN
5
10
3
7
2
6
9
8
4
1
0
10
20
25
ENVIRONMENTAL MEAN

FIG. 31

(d) Correlation

Results of correlation co-efficients "within" and "between" characters were given in table 35 and 36 respectively. Within a character, correlation between means ($\bar{X}$) and response (b_i), between means ($\bar{X}$) and stability ($\bar{S}^2_d$) and between response (b_i) and stability ($\bar{S}^2_d$) were measured separately for all the seven characters and they are shown in table 35. In case of yield/plant and tiller number the means ($\bar{X}$) were high and significantly correlated with the responses (b_i). Except 100 kernel weight, for other four characters the means ($\bar{X}$) were negatively correlated with the responses (b_i) indicating that there is no association between mean ($\bar{X}$) and response (b_i) in these characters. Correlation co-efficients between mean performance ($\bar{X}$) and stability ($\bar{S}^2_d$) were significant in cases of 100 kernel weight, yield/plant and tiller number which indicated that the increase or decrease of the mean performances was associated with the increase or decrease of stability values. But in other cases the correlation co-efficient values were non-significant indicating non association between mean ($\bar{X}$) and stability ($\bar{S}^2_d$) and they were independent to each other. The degree of association between response (b_i) and stability ($\bar{S}^2_d$) was significant in case of primary branches/panicle, yield/plant and tiller number which indicated that with the increase in the linear sensitivity of the genotypes, stability values also increased and vice versa. In other characters the two aspects were independent to each other.

Correlation between responses (b_i) and between stabilities ($\bar{S}^2_d$) among all the characters were calculated and are shown in table 36. In case of correlation between responses (b_i) among characters, panicle length was correlated with primary branches/panicle and spikelet number/panicle; primary branches/panicle was correlated positively with kernel number/panicle and negatively with yield/plant while spikelet number was positively correlated with kernel number/panicle. The other characters showed that the fluntuation in the responses of a character with changing environments was not correlated with that of another character. Correlation co-efficients between the stabilities ($\bar{S}^2_d$) of various characters was measured and observed that the variation of $\bar{S}^2_d$ values of one character was independent of that of another character in most of the cases (Table 36). Only the $\bar{S}^2_d$ values of kernel number/panicle was positively and significantly correlated with that of spikelet number/panicle, yield/plant was negatively and positively correlated with primary branch/panicle and 100 kernel weight respectively.

(e) Genetic Parameters

(i) Partition of Variation

Stability parameters were constructed from following expression of Eberhart and Russell (1966) :

$$Yij = \mu_i + \beta_i I_j + \delta^2_{ij}$$

where μ_i is the mean of the ith variety over all environments, β_i is the regression co-efficient that measures the response of the ith variety to the varying environments against environmental index, I_j which is obtained as the mean of all varieties in the ith environment and δ^2_{ij} is the deviation from regression of the ith variety in the jth environment.

Methods of describing and measuring components of variation (Mather 1949) have been extended by Mather and Jones (1958) to include parameters specifying environmental effects and the interaction of genotype with environment. These have been adapted by Bucio Alanis (1966) to the analysis of difference in height between two inbred lines of Nicotiana rustica grown over a number of seasons and in a number of locations. Variation in a character was partitioned into a constant genetic difference $[d] = 1/2$ (the mean parental difference), an environmental effect e, which is measured as the deviation of μ from the mid-parental value in each environment and the interaction of genotype and environment. β_d which is the deviation of the parental difference from $[d]$ in each environment. All values were expressed as deviation from the overall mid-parent (μ), so the phenotypic values in a particular environment may be written as

$$P_1 = \mu + [d] + e + \beta_d$$
$$P_2 = \mu - [d] + e - \beta_d.$$

It was found that the genotype-environmental interaction β_d was a linear function of the effect of the environment e. The phenotypic value of F_2 generation in any specific environment is presented by the following expression (Bucio Alanis and Hill, 1966 and Bucio Alanis, Perkins and Jinks, 1969).

$$F_2 = \mu + 1/2\ [h] + e + 1/2\ \beta_h$$

Where μ is the mean of all parental values, [h] is the mean deviation of F_2 from μ and the genotype-environment interaction β_h is the deviation from [h] in that environment.

The function of the environment β_d and β_h was estimated from the absolute phenotypic values of the two inbred lines and F_2 by using procedures of Bucio Alanis and Hill (1966). The procedures were as follows:

$$V_e = 1/4\ V\ (\bar{F}_1 + \bar{F}_2)$$

$$V\beta_d = 1/4\ V\ (\bar{F}_1 - \bar{F}_2)$$

$$Cov_{ed} = 1/4\ (V\bar{F}_1 - V\bar{F}_2)$$

$$\beta_d = Cov_{ed}/V_e$$

$$V\beta_h = 1/2\ V\ [2\bar{F}_2 - (\bar{F}_1 + \bar{F}_2)]$$

$$Cov_{eh} = (V\bar{F}_2 - V_e - 1/4\ V\beta_h)$$

$$\beta_h = Cov_{eh}/V_e$$

μ, [d], [h] and ej were calculated as follows :

$$= (\Sigma n_1\bar{F}_1 + \Sigma n_2\bar{F}_2)/(\Sigma n_1 + \Sigma n_2)$$

$$[d] = 1/2 \ (\bar{F}_1 - \bar{F}_2)$$

$$[h] = 2 \ (\bar{F}_2 - \mu) \text{ and}$$

$$ej = 1/2 \ (\bar{F}_1 + \bar{F}_2) - \mu$$

Results obtained for [d] , [h] , [h] / [d] , β_d and β_h for all the seven characters are shown in table 37. Both the genetic components [d] and [h] were significant in most of the crosses under each of the seven characters. [d] was non-significant in IR-20 X Kataribhog and IR-8 X Kataribhog of panicle length, in Chinese X Naizersail and IR-8 X Kataribhog of primary branches/panicle, in IR-8 X Kataribhog of spikelet number/panicle in IR-8 X Chinese of 100 kernel weight, in Chinese X Naizersail of both yield/plant and tiller number. The relationship between environment e and $([d] + \gamma d)$ and $([h] + \gamma h)$ can be found from the regression co-efficients β_d and β_h and from the scatter diagrams of figures 32-38 for panicle length, primary branches/panicle, spikelet number/panicle, kernel number/panicle, 100 kernel weight, yield/plant and tiller number respectively. In the figures $([d] + \gamma d)$ and $([h] + \gamma h)$ have been plotted against e, which were measured on the function of the effects of the environment on [d] and [h] respectively. Both $([d] + \gamma d)$ and $([h] + \gamma h)$ were linearly related to e as expected from the previous phenotypic regression, but the linearity varied from crosses to crosses in all the characters.

Estimates of [h] / [d] are shown in table 37. The table shows that overdominance in all the cases except Chinese X Kataribhog and IR-8 X Chinese in tiller number where it showed partial dominance.

The regression co-efficient β_d was non-significant in all the five crosses for spikelet number/panicle, kernel number panicle, and panicle

length except IR-8 X Kataribhog in panicle length. The co-efficient was also non-significant in the crosses of IR-20 X Kataribhog, Chinese X Naizersail and IR-8 X Kataribhog for primary branches; in IR-8XChinese for 100 kernel weight, in Chinese X Naizersail and IR-8 X Kataribhog for tiller number. Thus non-significant β_d in those cases indicated that [d] + γd did not appear to be linear function of the environment and [d] appear to be constant in all these characters. The magnitude of β_d was less than 1.0 in all the cases except IR-20 X Kataribhog for 100 kernel weight (β_d = 1.02).

The regression co-efficient β_h was non-significant in all the crosses for spikelet number and kernel number except Chinese X Kataribhog for kernel number/panicle. Crosses IR-8 X Kataribhog for panicle length, IR-20 X Kataribhog for primary branches, Chinese X Kataribhog, IR-8 X Chinese and IR-8 X Kataribhog for 100 kernel weight, IR-20 X Kataribhog for yield/plant and Chinese X Naizersail for tiller number also showed non-significant β_h. These non-significant β_h indicated the non-linear type of genotype-environment interaction associated with [h] in those crosses. The crosses which showed significant β_h indicated the([h] + γh) was a linear function of the environment. The magnitude of β_h was more than 1.0 in majority cases.

A t-test was used to test the difference between β_d and β_h and the values of 't' are also included in table 37. In most of the cases ($\beta_d - \beta_h$) was significant which indicated that β_d and β_h were of different function of the environment. 't' was however, non-significant in all the crosses for spikelet number except Chinese X Kataribhog. 't'

't' was also non-significant in IR-8 X Kataribhog for panicle length, IR-20 X Kataribhog for primary branches, IR-8 X Chinese and IR-8 X Kataribhog for kernel number and 100 kernel weight; and ChineseX Kataribhog and IR-8 X Kataribhog for tiller number.

Explanation to the Figs. 32-38.

Fig. 32. The effect of environments on additive and dominance variation for two parents and their F_2S in panicle length.

Fig. 33. The effect of environments on additive and dominance variation for two parents and their F_2S in primary branches/panicle.

Fig. 34. The effect of environments on additive and dominance variation for two parents and their F_2S in spikelet number/panicle.

Fig. 35. The effect of environments on additive and dominance variation for two parents and their F_2S in kernel number/panicle.

Fig. 36. The effect of environments on additive and dominance variation for two parents and their F_2S in 100 kernel weight.

Fig. 37. The effect of environment on additive and dominance variation for two parents and their F_2S in yield/plant.

Fig. 38. The effect of environment on additive and dominance variation for two parents and their F_2S in tiller number.

Each fig. contents

a = Chinese, Kataribhog and their F_2S.

b = IR-8, Chinese and their F_2S.

c = IR-20, Kataribhog and their F_2S.

d = Chinese, Naisersail and their F_2S.

e = IR-8, Kataribhog and their F_2S.

FIG. 32

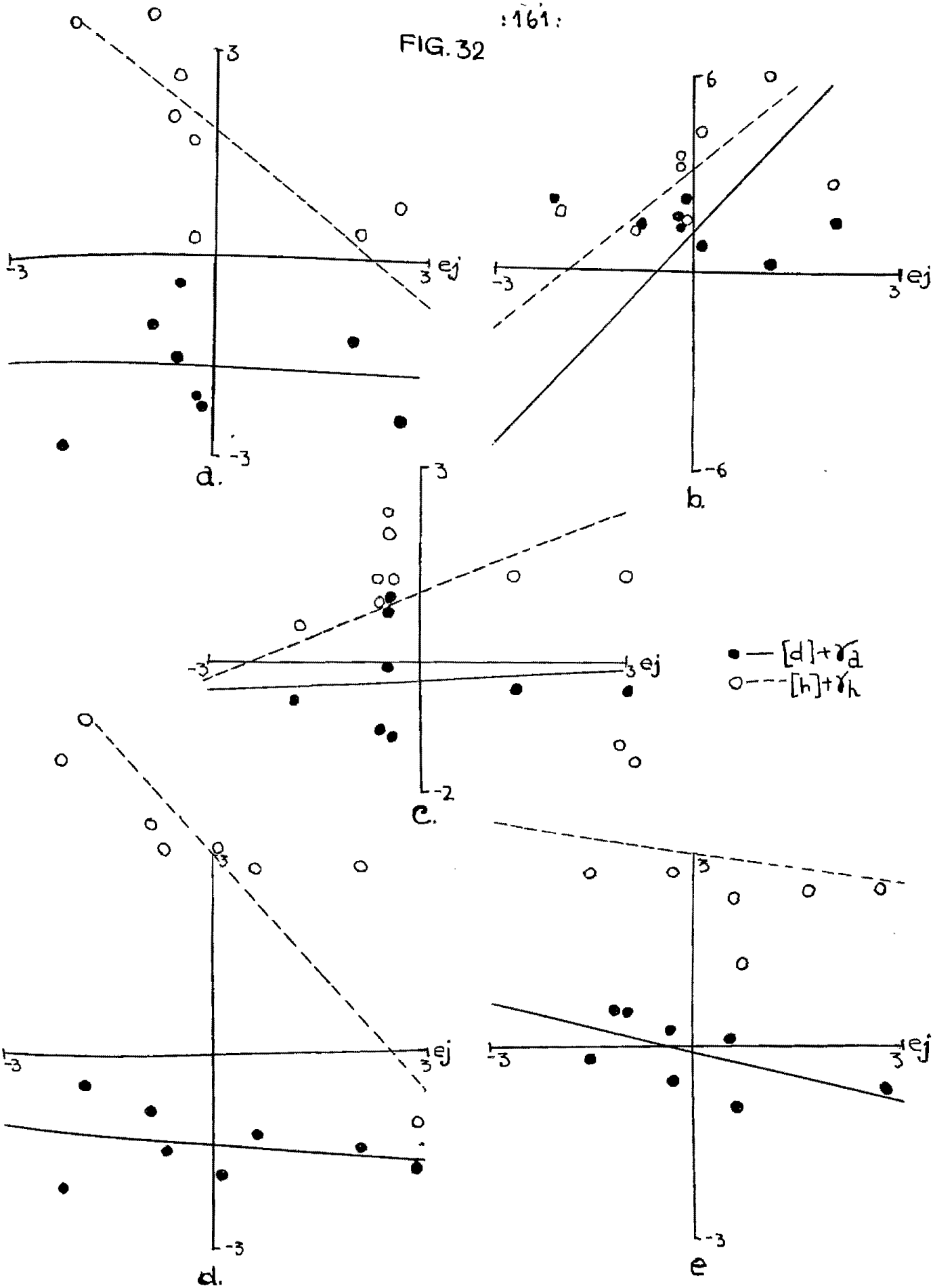
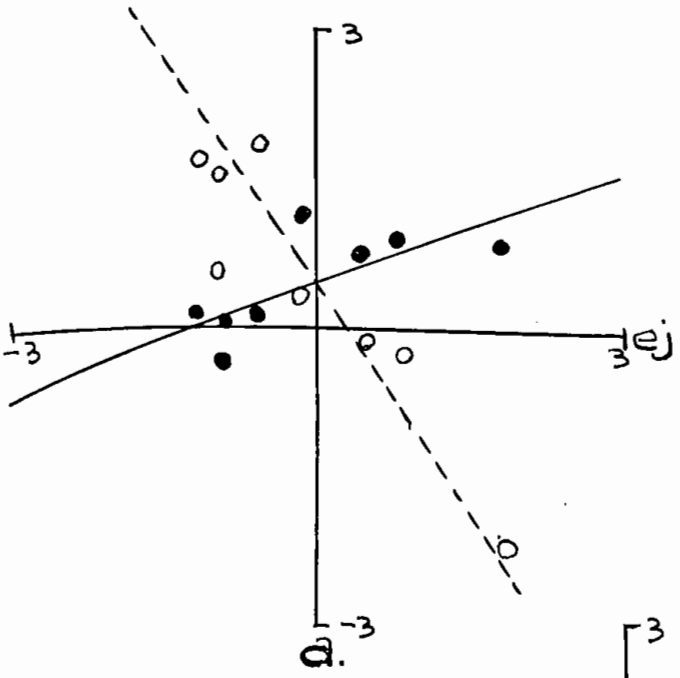
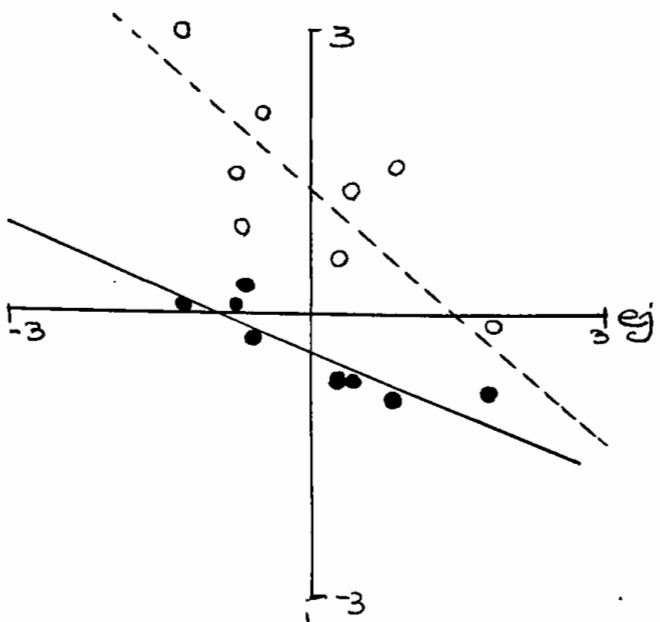


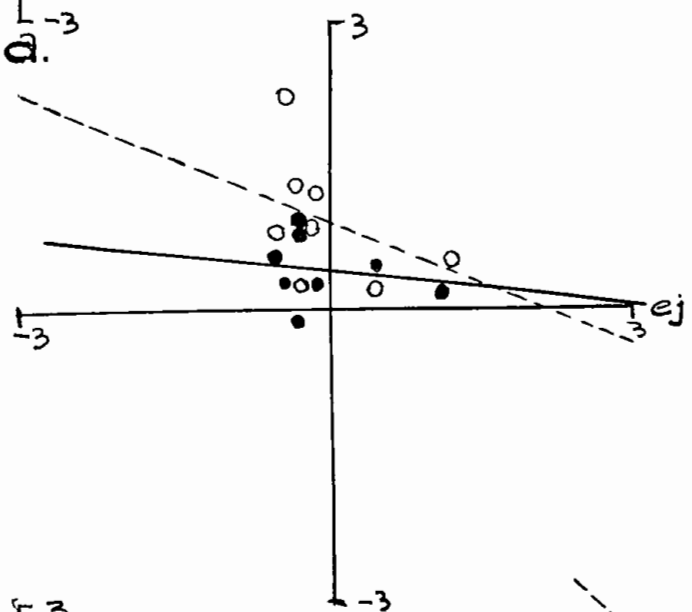
FIG.33



a.



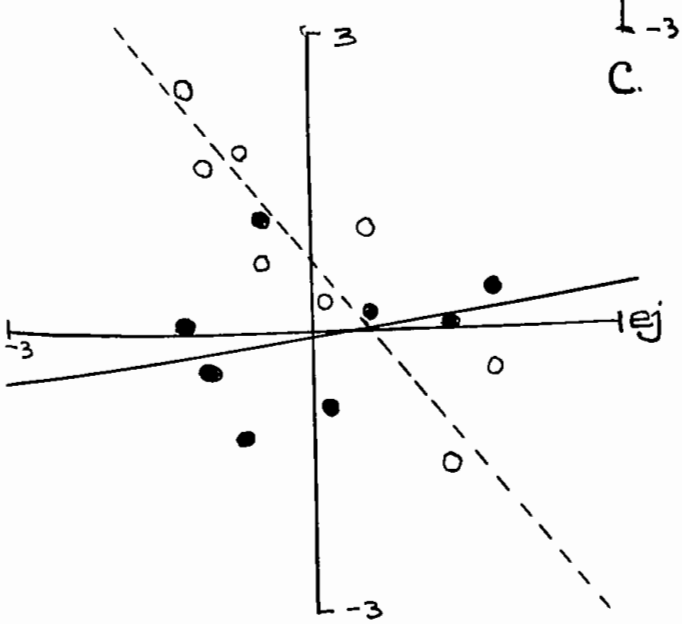
b.



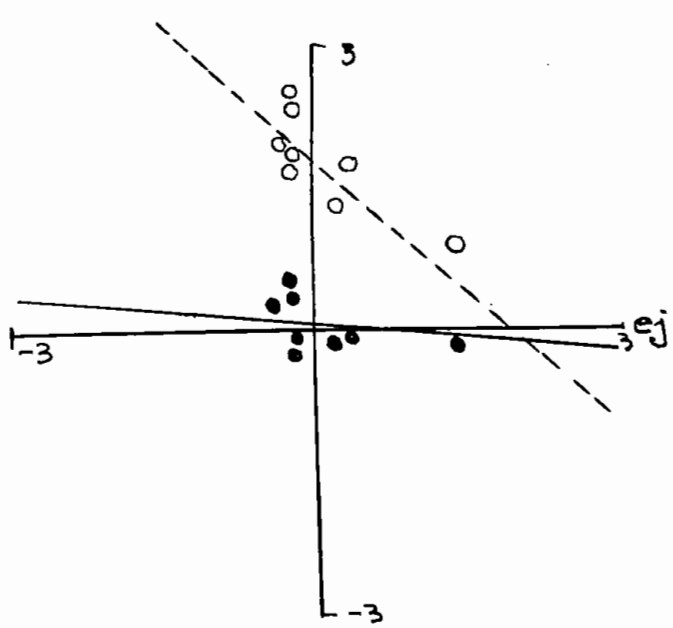
c.

$\bullet$ — $[d]+\gamma_d$

o --- $[h]+\gamma_h$



d.



e.

FIG. 34

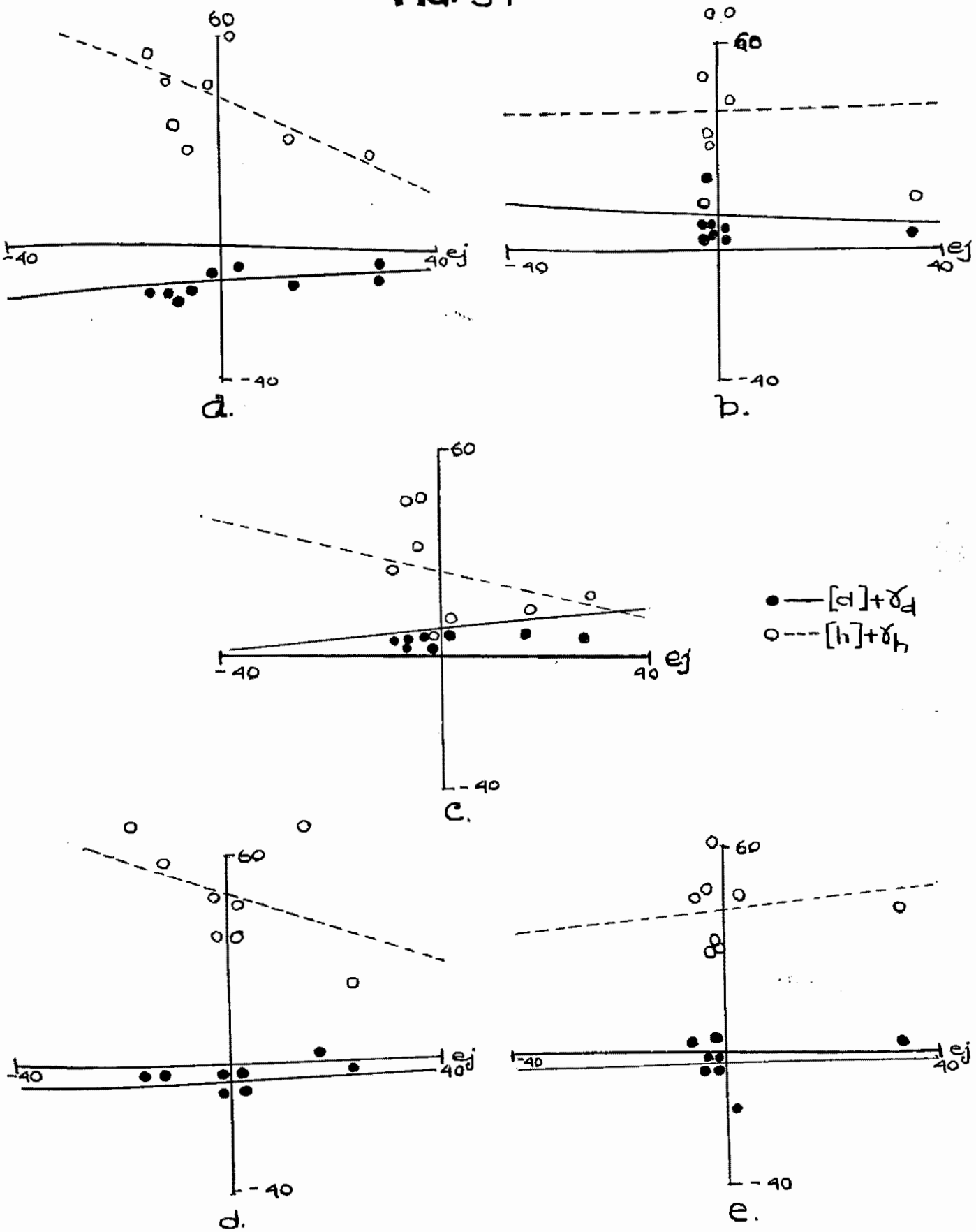


FIG. 35

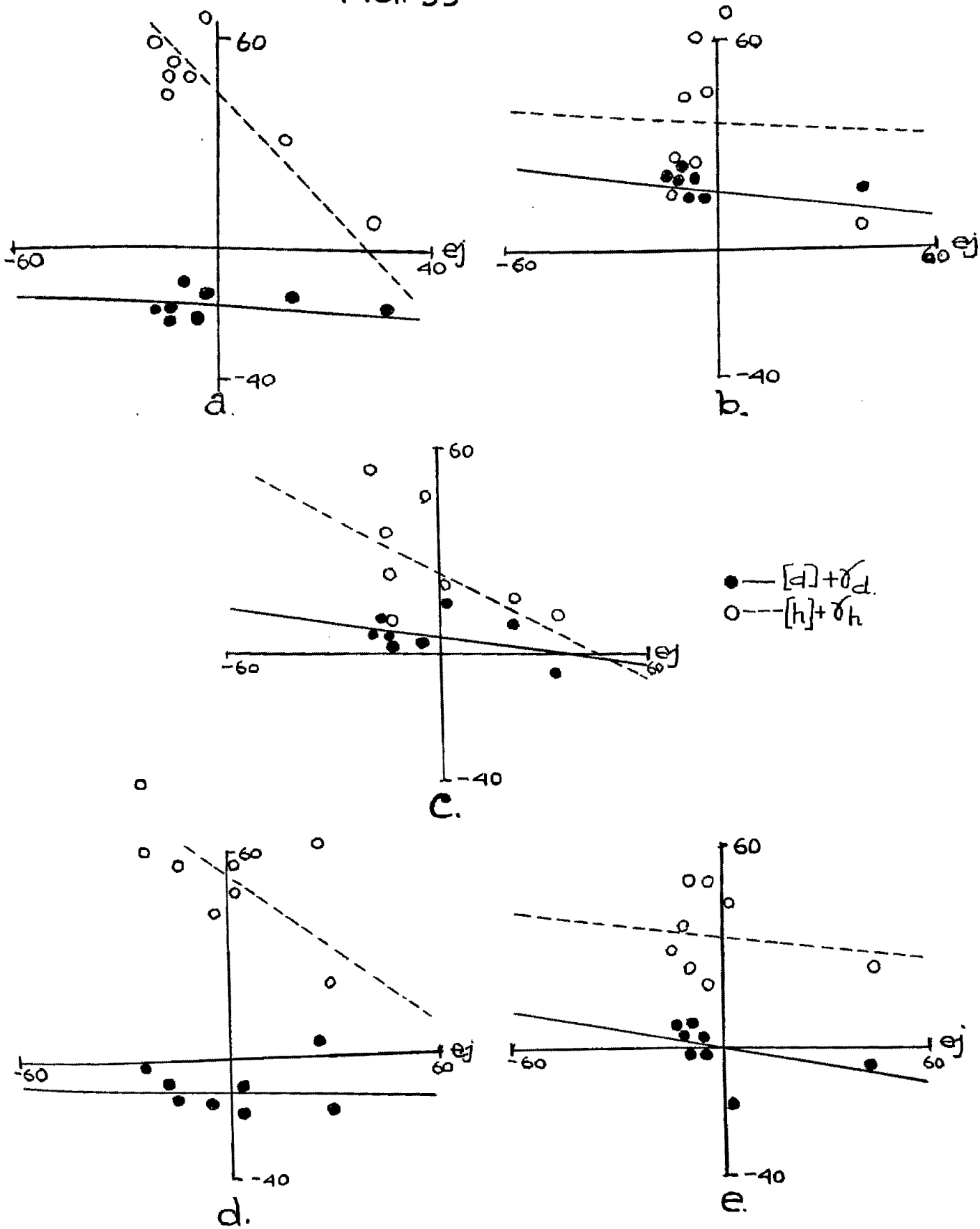

60
-60
40
ej
-40
a.
60
-60
60
ej
-40
b.
60
-60
60
ej
-40
c.
● — [d] + γd.
○ --- [h] + γh
60
-60
60
ej
-40
d.
60
-60
60
ej
-40
e.

FIG.36

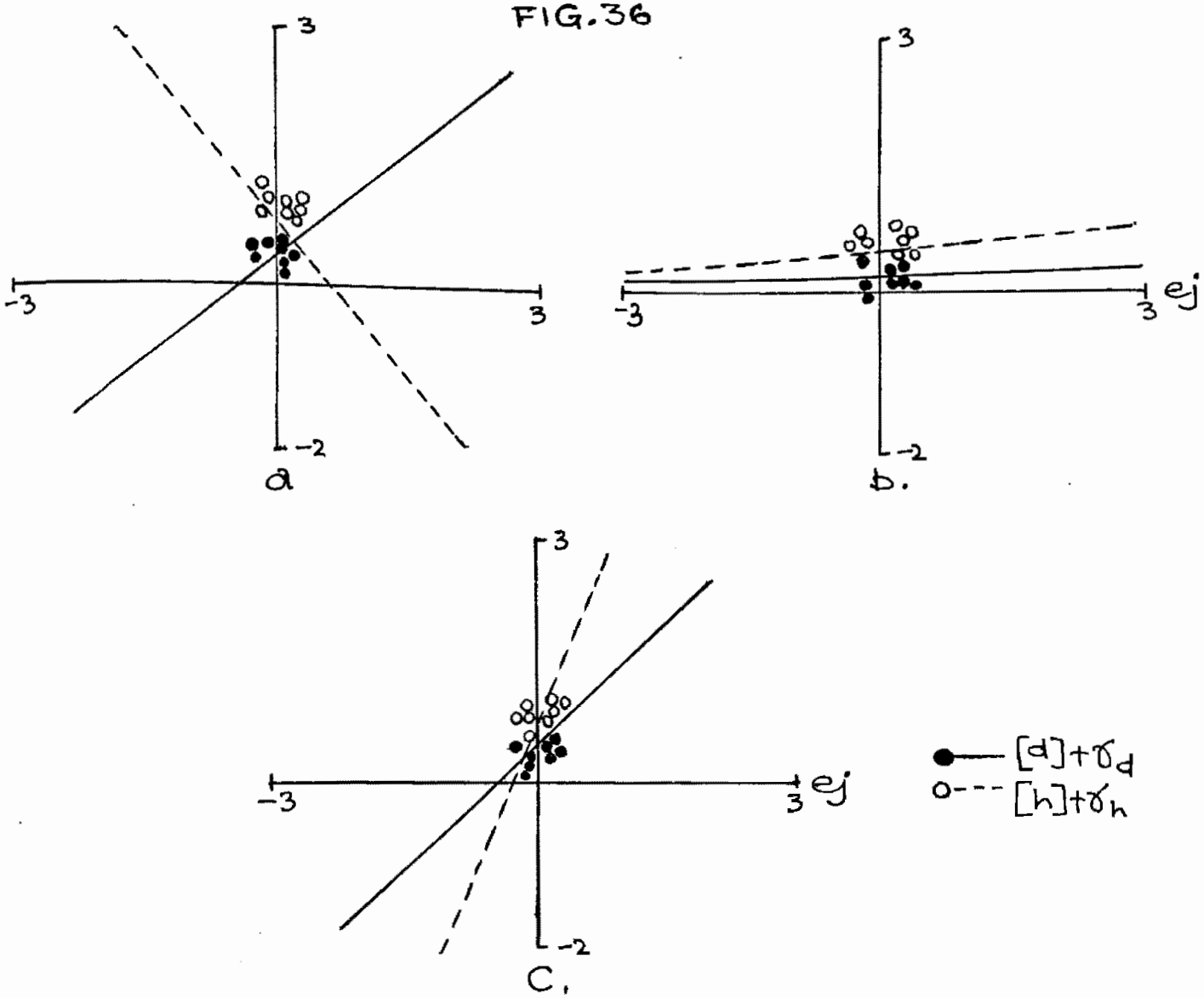


FIG. 37

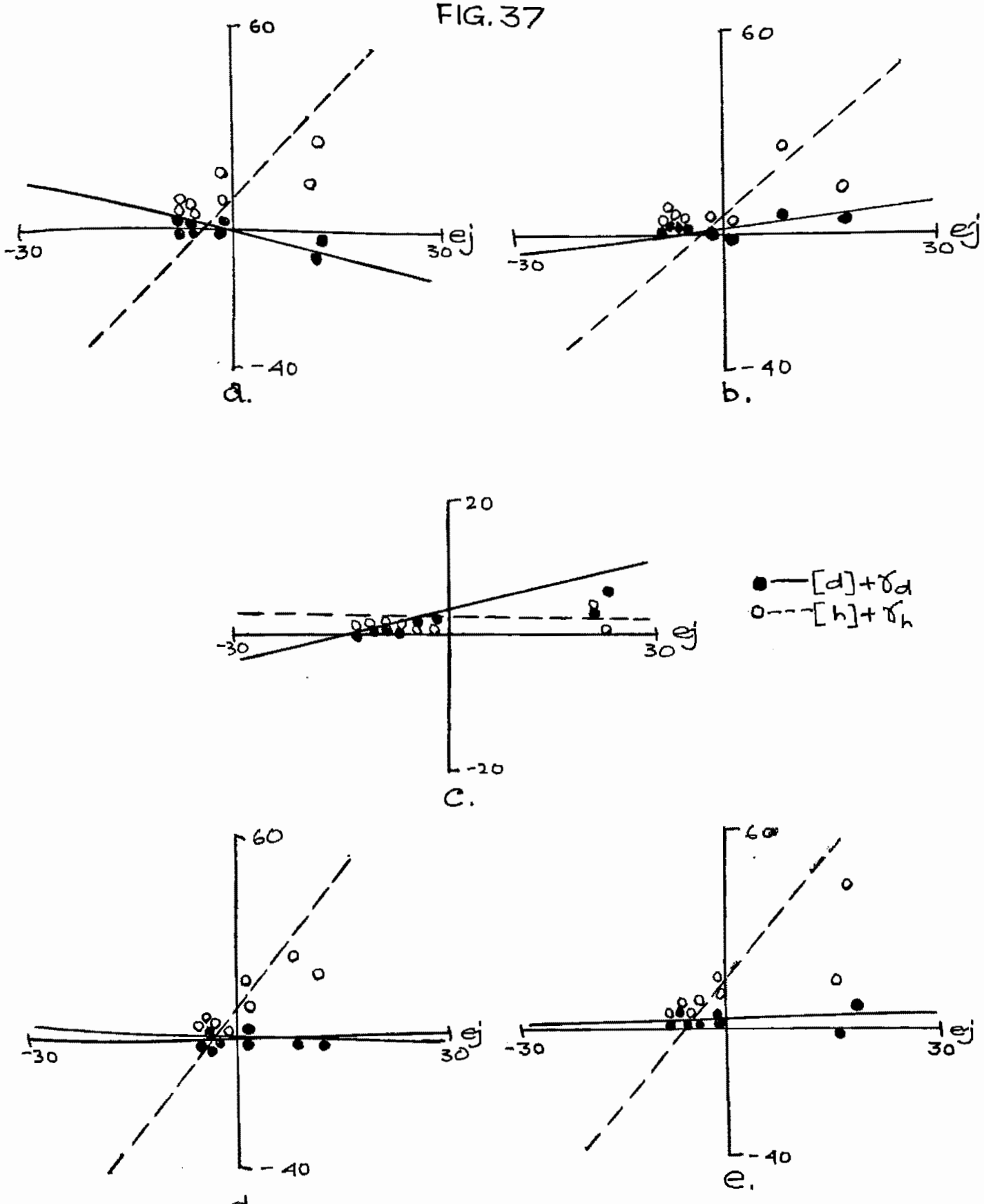
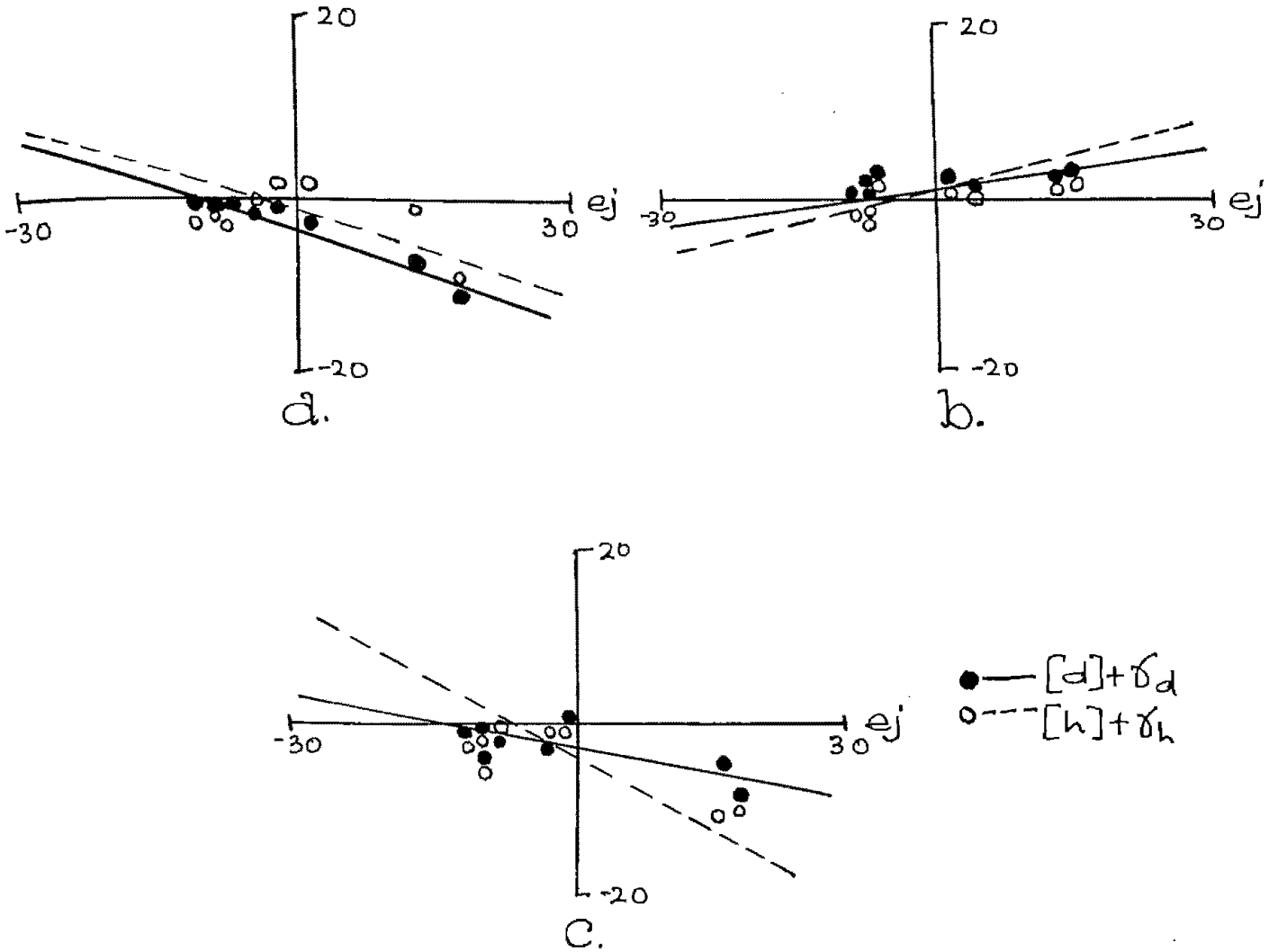


FIG. 38



(ii) Potence Ratio

Potence ratio which measures the potence of parental gene sets may be determined by the ratio of algebric sum of [h] effects to that of [d] within an environment. But due to the presence of genotype-environment interaction components β_d (for homozygotes) and β_h (for heterozygotes) that effected the [h] and [d] the potence ratio would be determined as the ratio of $([h] + \gamma h)$ to the $([d] + \gamma d)$. The observed values for $([h] + \gamma h)$ and $([d] + \gamma d)$ were calculated as follows :-

$([h] + \gamma h) = 2 (F_2 - 1/2 P_1 - 1/2 P_2)$

$([d] + \gamma d) = 1/2 (P_1 - P_2)$; and the expected values of $([h] + \gamma h)$ and $([d] + \gamma d)$ were calculated as

$([h] + \gamma h) = [h] + \beta_h ej$ and

$([d] + \gamma d) = [d] + \beta_d ej$

Where [d],[h] and ej were same as those given under genetic parameters. The results of expected potence ratio $([h] + \gamma h) / ([d] + \gamma d)$ were plotted against environmental means separately for panicle length, primary branches, spikelet number, kernel number, 100 kernel weight, yield/plant and tiller number. They are shown in figures 39-45. Potence ratios were usually high under poor environment and relatively low under good environment in most of the characters. In case of panicle length all except IR-8 X Kataribhog showed high potence ratios under good environments. High potence ratios under good environments were found in IR-20 X Kataribhog for primary branches/panicle, in IR-8 X Chinese for spikelet number/panicle, kernel number/panicle and yield/plant and in other crosses except IR-8 X Kataribhog and Chinese X Kataribhog for tiller number.

Explanation to the Figs. 39-45.

Fig. 39. Potence ratio plotted against the corresponding ej for panicle length.

Fig. 40. Potence ratio plotted against the corresponding ej for primary branches/panicle.

Fig. 41. Potence ratio plotted against the corresponding ej for spikelet number/panicle.

Fig. 42. Potence ratio plotted against the corresponding ej for kernel number/panicle.

Fig. 43. Potence ratio plotted against the corresponding ej for 100 kernel weight.

Fig. 44. Potence ratio plotted against the corresponding ej for yield/plant.

Fig. 45. Potence ratio plotted against the corresponding ej for tiller number.

1 X 5 = Chinese X Katribhog, 3 X 1 = IR-8 X Chinese

2 x 5 = IR-20 X Kataribhog, 1 X 4 = Chinese X Naizersail and

3 x 5 = IR-8 X Kataribhog in the Figures .

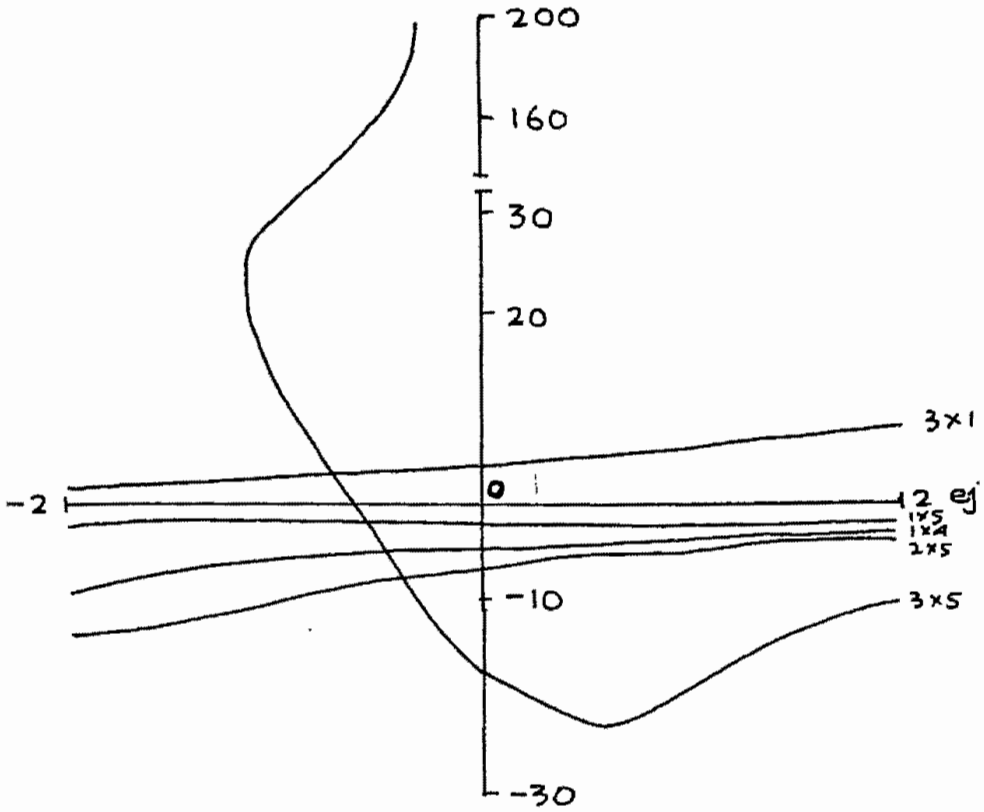

200
160
30
20
3×1
-2
0
2 ej
1×5
1×4
2×5
-10
3×5
-30

FIG. 39

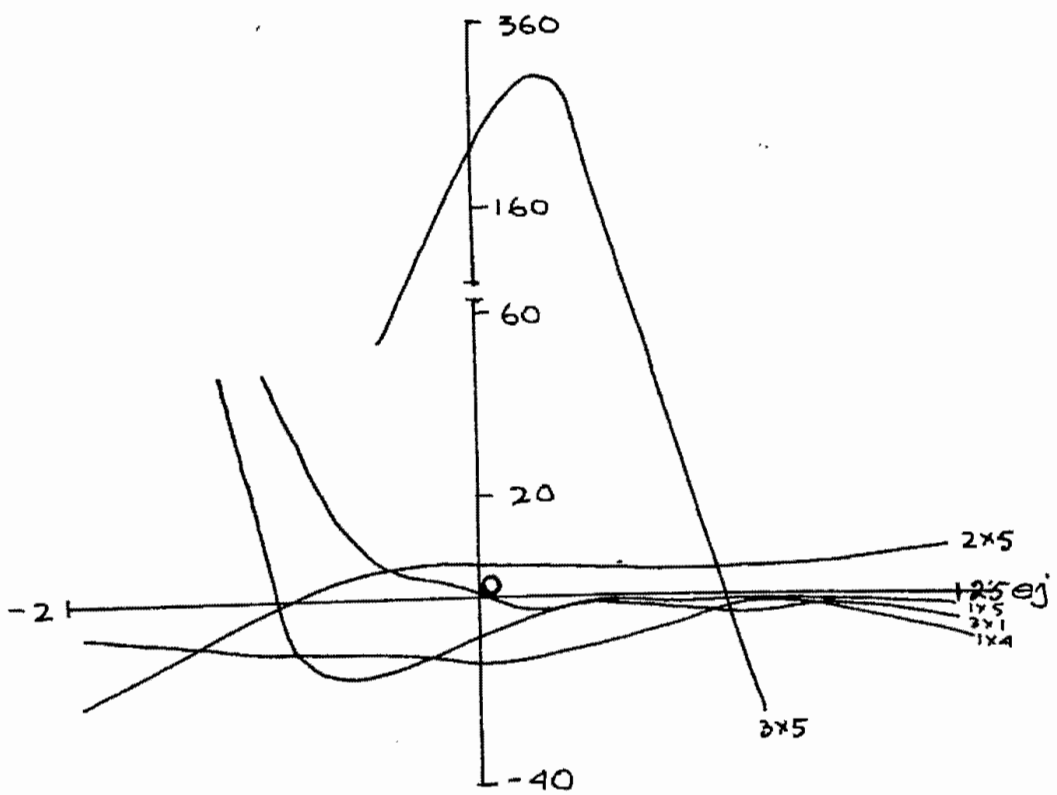

360
160
60
20
2×5
-2
1·25 ej
1×5
3×1
1×4
3×5
-40

FIG. 40

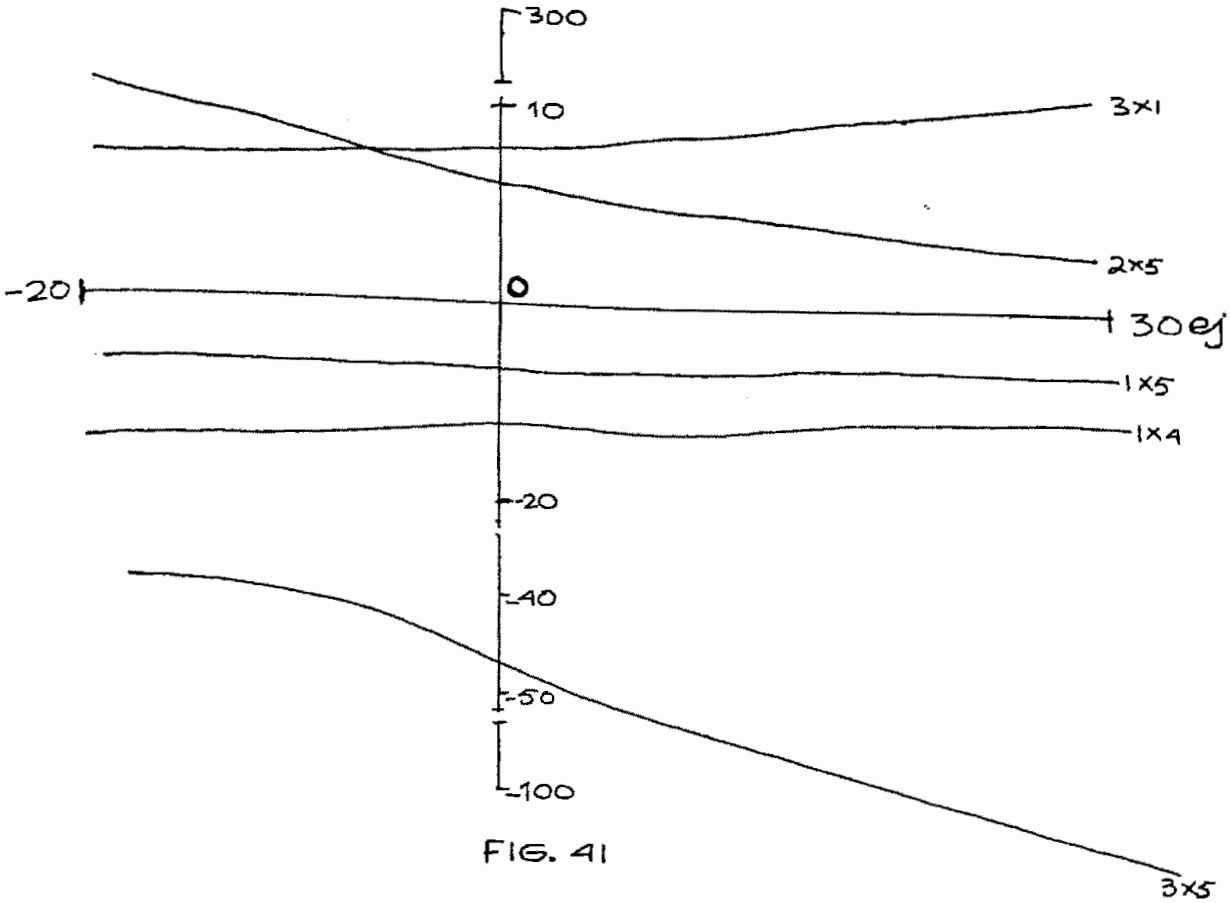
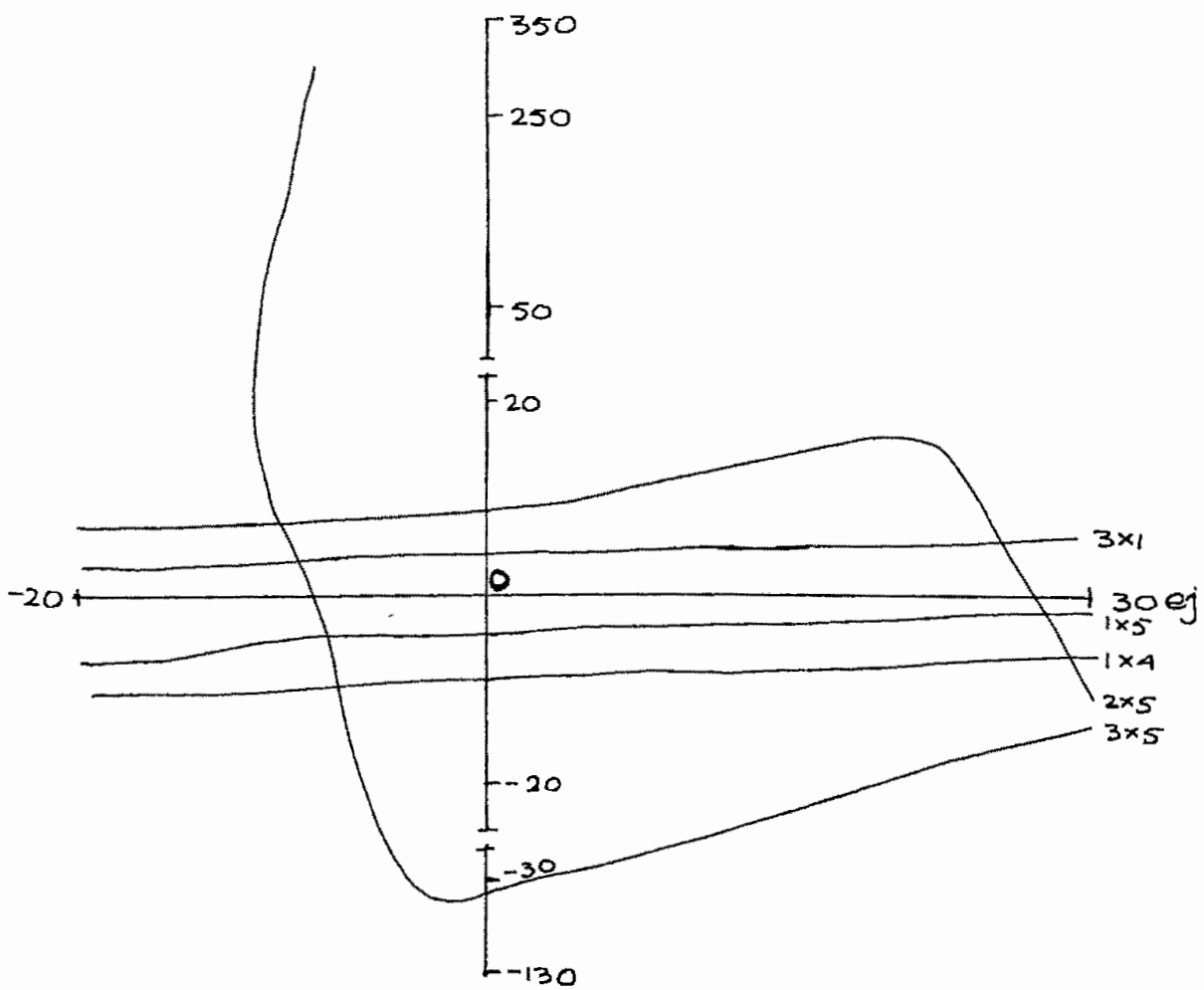

300
10
3x1
2x5
-20
0
30ej
1x5
1x4
-20
-40
-50
-100
3x5

FIG. 41


350
250
50
20
3x1
-20
0
30ej
1x5
1x4
2x5
3x5
-20
-30
-130

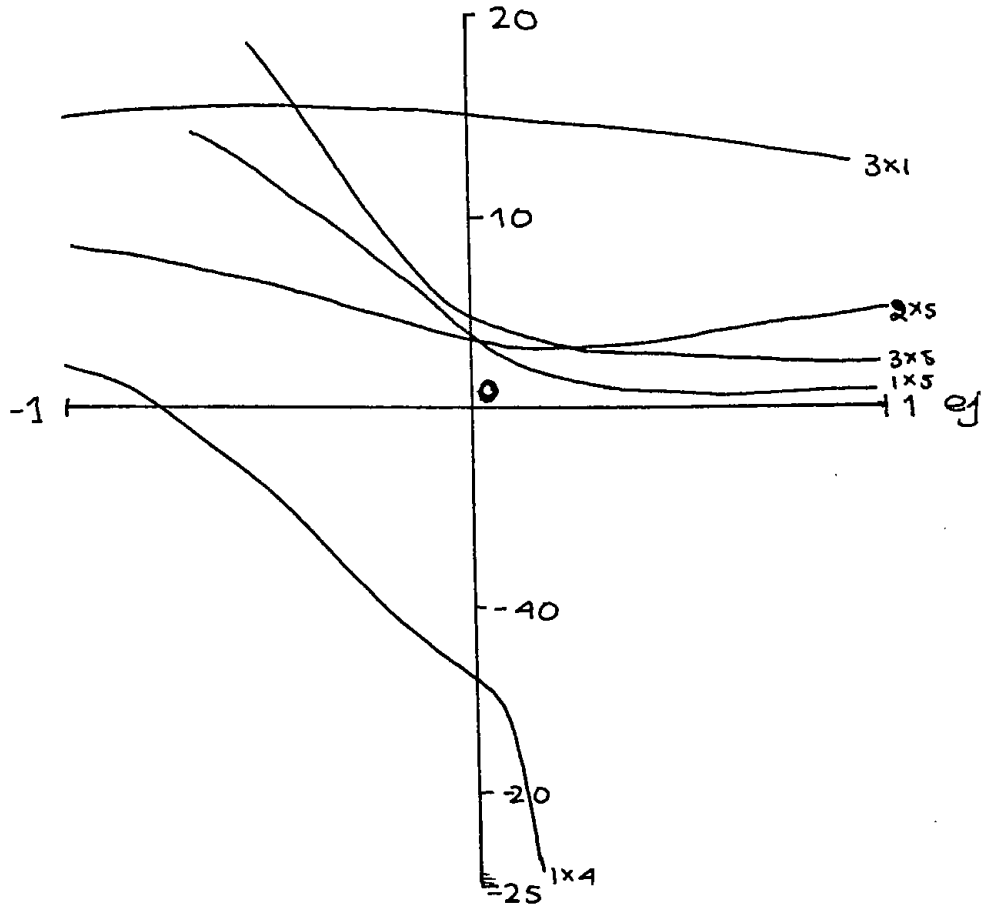

20
10
-40
-20
-25
3x1
2x5
3x5
1x5
1x4
-1
1 ej

FIG. 43

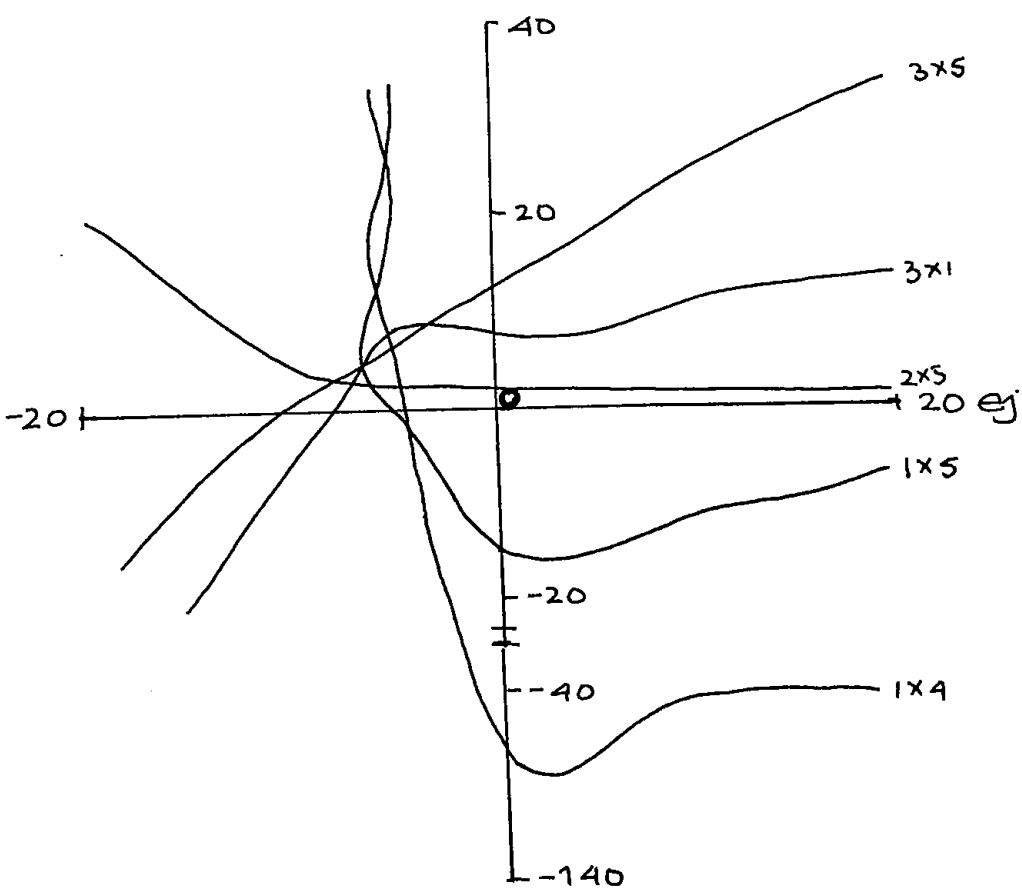

40
20
-20
-40
-140
3x5
3x1
2x5
1x5
1x4
-20
20 ej

FIG. 44

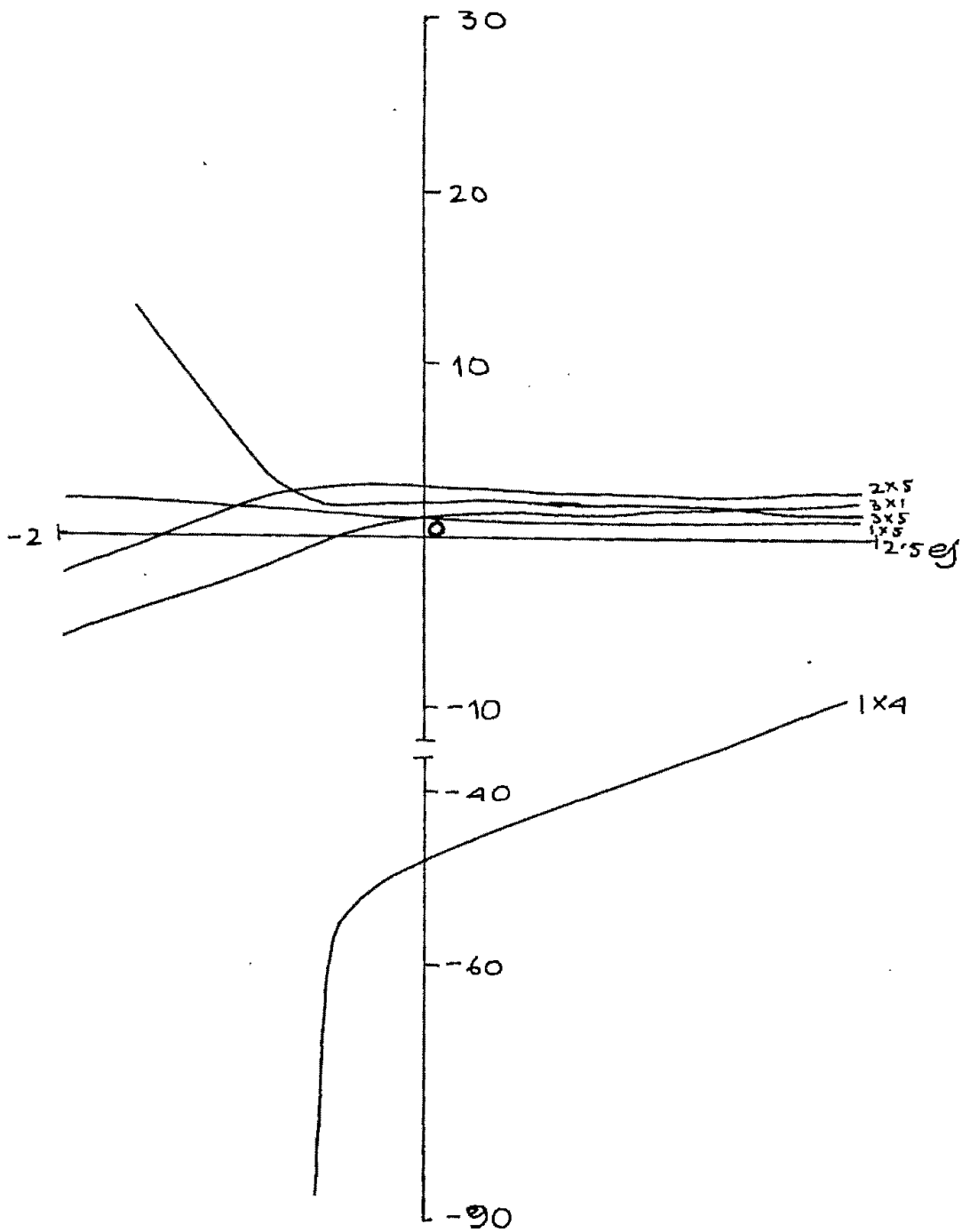


FIG. 45

Table 28. Environmental means over replications and genotypes.

Characters	Treatments								
	Nil	N	P	K	NP	NK	PK	NPK	r
Panicle length									
A	19.51	21.04	21.21	20.05	22.88	21.66	20.86	23.43	0.98*
B	18.28	19.60	20.00	19.03	21.95	20.18	19.86	22.72	
Primary branches/ panicle									
A	9.26	9.62	9.80	9.18	10.18	9.82	9.71	10.61	0.89*
B	8.77	9.00	9.09	8.52	10.05	9.43	8.85	10.75	
Spikelet number/ panicle									
A	98.09	116.59	114.14	99.96	129.37	110.34	106.91	142.32	0.97*
B	85.41	99.84	90.21	79.27	113.57	91.81	82.97	125.81	
Kernel number/ panicle									
A	86.17	104.36	103.93	88.84	117.59	96.38	96.49	130.11	0.98*
B	72.37	86.27	81.01	68.54	102.91	78.07	73.54	117.84	
100 kernel weight									
A	2.59	2.56	2.76	2.65	2.71	2.69	2.66	2.65	0.95*
B	2.26	2.26	2.46	2.28	2.43	2.41	2.38	2.35	
Yield/plant									
A	9.59	20.51	12.28	9.51	38.91	19.74	10.92	43.85	0.98*
B	8.48	16.00	10.19	8.21	31.43	14.72	9.18	35.23	
Tiller number									
A	3.82	13.92	4.94	3.80	26.29	12.82	4.12	24.87	0.99*
B	4.27	12.44	5.41	4.21	28.20	12.24	4.04	25.04	

A = Means of ten genotypes. B = Means of 5 parents.

* = Significant values.

Table 29. Population means over replication and treatments.

Genotypes	Characters						
	Panicle length	Primary branches/ panicle	Spikelet number/ panicle	Kernel number/ panicle	100 kernel weight	Yield/ plant	Tiller number
1. Chinese	17.68	9.63	76.44	56.40	2.45	13.70	9.30
2. IR-20	20.57	9.57	115.61	104.47	2.53	22.38	11.61
3. IR_8	21.05	8.80	96.80	90.40	2.58	18.50	12.74
4. Naizersail	20.55	9.81	91.24	80.65	2.60	14.02	9.49
5. Kataribhog	21.16	8.74	100.47	93.42	1.62	14.84	16.78
6. 1 X 5	21.33	9.57	130.30	120.70	2.78	24.73	11.22
7. 3 X 1	22.74	10.49	127.78	110.28	3.00	23.17	11.80
8. 2 X 5	21.90	10.11	132.28	124.43	2.83	21.73	10.90
9. 1 X 4	22.12	10.47	133.99	123.47	3.04	24.51	11.55
10. 3 X 5	24.19	10.55	142.26	125.61	3.21	29.12	12.88

Table 30. Results of Analysis of Variance of different characters.

	D.F.	Panicle length		Primary branches/panicle	
		M.S.	V.R.	M.S.	V.R.
Nutrition(N)	7	104.56	24.49***	13.06	7.55***
Population(G)	9	137.14	32.12***	20.43	11.81***
P	4	99.27	23.25***	12.10	6.99***
F_2	4	57.26	13.41***	8.07	4.67***
(P-F_2)	1	608.18	142.43***	103.13	59.61***
G X N	63	6.03	1.41***	2.85	1.65***
P X N	28	5.998	1.404***	2.85	1.65***
F_2X N	28	6.54	1.53***	1.91	1.11***
(P-F_2) X N	7	4.14	0.97	6.57	3.80***
Replication	5	8.20	1.92	1.59	0.92
Error	395	4.27		1.73	
		Spikelet number/panicle		Kernel number/panicle	
Nutrition(N)	7	13330.65	17.48***	13030.85	16.89***
Population(G)	9	23427.30	30.71***	24951.26	32.34***
P	4	9722.70	12.75***	15788.64	20.47***
F_2	4	1454.93	1.91^{Ns}	1848.78	2.40*
(P-F_2)	1	166135.21	217.79***	154011.71	199.64***
G X N	63	884.21	1.16***	972.99	1.26***
P X N	28	743.74	0.98^{Ns}	875.19	1.14***
F_2X N	28	1006.07	1.32***	1066.53	1.38***
(P-F_2)XN	7	958.65	1.26^{Ns}	990.08	1.28^{Ns}
Replication	5	868.93	1.14	1507.93	1.96
Error	395	762.84		771.44	

Contd.....

Table 30 (Contd.)

	D.F.	100 Kernel weight		Yield/plant	
		M.S.	V.R.	M.S.	V.R.
Nutrition(N)	7	0.253	3.56***	11004.80	100.89***
Populations(G)	9	9.37	131.97***	1304.39	11.96***
P	4	8.27	116.48***	662.34	6.07***
F_2	4	1.46	20.56***	369.09	3.39**
$(P-F_2)$	1	45.45	640.14***	7613.75	69.81***
G X N	63	0.095	1.34***	205.39	1.88***
P X N	28	0.0836	1.18***	156.49	1.44***
F_2X N	28	0.121	1.71***	178.84	1.64***
$(P-F_2)$ X N	7	0.043		507.17	4.65***
Replication	5	0.121	1.71	36.44	
Error	395	0.071		109.07	
		Tiller number			
Nutrition(N)	7	5313.72	299.70***		
Population(G)	9	211.60	11.94***		
P	4	445.63	25.14***		
F_2	4	27.55	1.55Ns		
$(P-F_2)$	1	11.72			
G X N	63	43.39	2.45***		
P X N	28	64.29	3.63***		
F_2X N	28	19.12	1.08***		
$(P-F_2)$ X N	7	56.86	3.21***		
Replication	5	17.93	1.01		
Error	395.	17.73			

Table 31. Results of effects of nutrients on over all 5 varieties, 10 populations and 5 F_2s.

Genotypes	N	P	K	NP	NK	PK	NPK
			Panicle length				
5 Parents	7.28**	7.44**	1.96*	2.34*	0.74	-0.70	1.08
10 Populations	7.38**	6.12**	1.36	1.10	0.98	-0.96	0.82
5 F_2s	7.50**	4.80**	0.76	-0.12	1.20	-1.26	0.54
			Primary branches/panicle				
5 Parents	4.00**	3.02**	0.64	1.72**	1.62**	0.28	0.26
10 Populations	2.36**	2.42**	0.46	0.28	0.80	0.22	0.24
5 F_2s	0.56	1.82**	0.30	-1.16*	-0.04	0.18	0.24
			Spikelet number/panicle				
5 Parents	93.17**	56.23**	-9.18	39.23**	17.59	19.17*	21.37*
10 Populations	79.52**	67.76**	1.34	21.76*	12.65	10.10	28.30**
5 F_2s	65.90**	79.30**	11.84	4.30	6.56	1.04	35.24**
			Kernel number/panicle				
5 Parents	89.63**	70.05**	-4.57	42.77**	18.03	19.49*	26.77**
10 Populations	73.01**	72.37**	-0.23	21.55*	9.31	10.39	30.61**
5 F_2s	56.36**	74.76**	4.10	0.36	0.56	1.30	34.44**

Contd.....

Table 31. (Contd.)

Genotypes	N	P	K	NP	NK	PK	NPK
				100 Kernel weight			
5 Parents	0.07	0.41***	0.01	-0.19	0.13	-0.33***	-0.13
10 Populations	-0.05	0.29**	0.03	-0.07	0.11	-0.35***	-0.03
5 F_2s	-0.14	0.22*	0.06	0.02	0.10	-0.34***	0.02
				Yield/plant			
5 Parents	61.32***	38.62***	1.24	33.26***	3.80	4.34	5.82
10 Populations	80.71***	46.61***	2.73	38.41***	5.61	4.43	6.99
5 F_2s	100.10***	54.60***	4.24	43.58***	7.42*	4.52	8.18*
				Tillor number/plant			
5 Parents	59.99***	29.53***	-4.79**	27.59***	-1.93	-4.09**	-1.65
10 Populations	61.22***	25.86***	-3.36*	22.98***	-1.68	-1.12	0.48
5 F_2s	62.43***	22.17***	-1.91	18.37***	-1.43	2.03	2.63

*, **, and *** significant at 5%, 1% and 0.1% level.

Table 32. Estimates of δ^2_G, δ^2_{GS} and δ^2_E and the co-efficient of variability for the seven characters.

	δ^2_G	δ^2_{GS}	δ^2_E	$CV\delta^2_G$	$CV\delta^2_{GS}$	$CV\delta^2_E$
Panicle length	2.73	0.29	4.27	0.13	0.02	0.20
Primary branches/ panicle	0.38	0.19	1.73	0.04	0.02	0.176
Spikelet number/ panicle	469.65	20.23	762.84	4.09	0.176	6.65
Kernel number/ panicle	499.55	33.59	771.44	4.85	0.33	7.49
100 kernel weight	0.193	0.004	0.071	0.072	0.002	0.027
Yield/plant	22.89	16.05	109.07	1.10	0.77	5.25
Tiller number	3.50	4.28	17.73	0.30	0.36	1.50

Table 33. Results of Joint Regression Analysis

Item	D.F.	M.S.	VR_1	VR_2
Panicle length				
Linear Regression	9	9.24	1.49	2.16*
Deviation	54	6.22		1.46***
Error	395	4.27		
Primary branches/panicle				
Linear Regression	9	3.19	1.14	1.84*
Deviation	54	2.79		1.61***
Error	395	1.73		
Spikelet number/panicle				
Linear Regression	9	1224.00	1.48	1.60
Deviation	54	827.57		1.08***
Error	395	762.84		
Kernel number/panicle				
Linear Regression	9	1104.00	1.16	1.43
Deviation	54	951.15		1.23***
Error	395	771.44		
100 Kernel Weight				
Linear Regression	9	0.104	1.11	1.46
Deviation	54	0.0935		1.32***
Error	395	0.071		

Contd.....

Table 33. (Contd.)

Item	D.F.	M.S.	VR_1	VR_2
Yield/Plant				
Linear Regression	9	247.32	1.25	2.27^{**}
Deviation	54	198.40		1.82^{***}
Error	395	109.07		
Tiller number				
Linear Regression	9	49.71	1.17	2.80^{***}
Deviation	54	42.34		2.39^{***}
Error	395	17.73		

$$VR_1 = \frac{\text{M.S.}}{\text{Deviation M.S.}} \qquad VR_2 = \frac{\text{M.S.}}{\text{Error M.S.}}$$

Table 34. Regression co-efficients b_i, S_{b_i}, β_i, stability ($\bar{S}^2_d$) and correlation co-efficients(r) for the ten genotypes grown in 8 environments.

	b_i	S_{b_i}	β_i	$\bar{S}^2_d$	r
			Panicle length		
1. Chinese	1.22	0.18	0.22	-3.86	0.94
2. IR-20	1.19	0.19	0.19	-3.80	0.93
3. IR-8	0.63	0.23	-0.37	-3.60	0.75
4. Naizersail	1.40	0.30	0.40	-3.14	0.88
5. Kataribhog	0.95	0.39	-0.05	-2.29	0.69
6. 1 X 5	0.65	0.22	-0.35	-3.68	0.77
7. 3 X 1	1.66	0.33	0.66	-2.88	0.90
8. 2 X 5	0.77	0.20	-0.23	-3.75	0.84
9. 1 X 4	0.33	0.26	-0.67	-3.46	0.47
10. 3 X 5	1.05	0.17	0.05	-3.94	0.93
			Primary branches/panicle		
1. Chinese	2.31	0.77	1.31	-0.74	0.78
2. IR-20	0.72	0.42	-0.28	-1.43	0.57
3. IR-8	0.86	0.38	-0.14	-1.48	0.67
4. Naizersail	1.77	0.64	0.77	-1.03	0.75
5. Kataribhog	1.29	0.32	0.29	-1.27	0.85
6. 1 X 5	-0.24	0.48	-1.24	-1.34	-0.20
7. 3 X 1	0.94	0.43	-0.06	-1.41	0.66
8. 2 X 5	0.83	0.40	-0.17	-1.46	0.65
9. 1 X 4	0.04	0.52	-0.96	-1.28	0.03
10. 3 X 5	0.50	0.58	-0.50	-1.61	0.61

Bartlett's $X^2_{(d.f.=9)}$ testing homogenity of S_{b_i} = 42.44*** (Panicle length)

Bartlett's $X^2_{(d.f.=9)}$ testing homogenity of S_{b_i} = 41.38*** (Primary branches/panicle)

Contd.....

Table 34. (Contd.)

	b_i	S_{b_i}	β_i	$\bar{s}^2_d$	r
			Spikelet number/panicle		
1. Chinese	1.23	0.22	0.23	-688.00	0.92
2. IR-20	1.31	0.21	0.31	-689.35	0.93
3. IR-8	0.78	0.35	-0.22	-575.72	0.68
4. Kaizersail	0.97	0.37	-0.03	-544.69	0.73
5. Kataribhog	0.96	0.21	-0.04	-693.34	0.88
6. 1 X 5	0.79	0.21	-0.21	-676.15	0.81
7. 3 X 1	1.14	0.42	0.14	-491.87	0.75
8. 2 X 5	1.03	0.28	0.03	-643.89	0.84
9. 1 X 4	0.87	0.37	-0.13	-551.08	0.69
10. 3 X 5	0.92	0.33	-0.08	-596.82	0.76
Bartlett's $X^2_{(d.f.=9)}$ testing homogenity of S_{b_i} = 8.42^{NS}					
			Kernel number/panicle		
1. Chinese	1.35	0.18	0.35	-721.06	0.99
2. IR-20	1.08	0.20	0.08	-714.36	0.92
3. IR-8	0.78	0.33	-0.22	-600.21	0.69
4. Kaizersail	0.98	0.43	-0.02	-488.25	0.68
5. Kataribhog	1.46	0.28	0.46	-652.28	0.90
6. 1 X 5	0.51	0.23	-0.49	-692.78	0.68
7. 3 X 1	1.15	0.43	0.15	-495.35	0.74
8. 2 X 5	0.95	0.30	-0.05	-636.22	0.79
9. 1 X 4	0.69	0.34	-0.31	-599.86	0.65
10. 3 X 5	1.06	0.34	-0.06	-597.45	0.79
Bartlett's $X^2_{(d.f. = 9)}$ testing homogenity of S_{b_i} = 42.395^{***}					

Contd

Table 34. (Contd.)

		b_i	S_{b_i}	β_i	$\bar{\sigma}^2_d$	r
				100 Kernel weight		
1.	Chinese	1.88	0.79	0.88	-0.053	0.69
2.	IR-20	0.71	0.72	-0.29	-0.056	0.37
3.	IR-8	2.36	0.58	1.36	-0.061	0.86
4.	Naizersail	1.29	9.33	0.29	-0.067	0.84
5.	Kataribhog	-0.31	0.40	-1.31	-0.066	-0.28
6.	1 X 5	0.02	0.60	-0.98	-0.061	0.01
7.	3 X 1	2.21	0.95	1.21	-0.045	0.68
8.	2 X 5	1.32	0.56	0.31	-0.061	0.68
9.	1 X 4	0.44	0.62	-0.56	-0.06	0.27
10.	3 X 5	0.53	1.01	-0.47	-0.042	0.20

Bartlett's $\chi^2_{(d.f.=9)}$ testing homogenity of S_{b_i} = 46.17***

				Yield/plant		
1.	Chinese	0.45	0.08	-0.55	-101.79	0.93
2.	IR-20	1.29	0.13	0.29	-87.04	0.97
3.	IR-8	0.82	0.08	-0.18	-100.90	0.97
4.	Naizersail	0.56	0.06	-0.44	-104.63	0.97
5.	Kataribhog	0.77	0.11	-0.23	-93.04	0.94
6.	1 X 5	1.17	0.15	0.17	-79.74	0.95
7.	3 X 1	1.13	0.15	0.13	-82.21	0.95
8.	2 X 5	1.02	0.12	0.02	-91.13	0.96
9.	1 X 4	1.03	0.14	0.03	-84.67	0.95
10.	3 X 5	1.61	0.18	0.61	-65.06	0.96

Bartlett's $\chi^2_{(d.f.=9)}$ testing homogenity of S_{b_i} = 12.68^{Ns}

Contd.....

Table 34. (Contd.)

		b_i	S_{b_i}	β_1	$\bar{S}^2_d$	r
				Tiller number		
1.	Chinese	0.76	0.03	-0.24	-17.38	0.99
2.	IR-20	1.02	0.04	0.02	-16.61	0.94
3.	IR-8	1.05	0.04	0.05	-16.78	0.99
4.	Kaizersail	0.78	0.06	-0.22	-15.19	0.98
5.	Kataribhog	1.53	0.13	0.53	-6.77	0.97
6.	1 X 5	0.98	0.09	-0.02	-12.80	0.97
7.	3 X 1	1.04	0.01	0.04	-17.16	0.99
8.	2 X 5	0.88	0.03	-0.12	-17.12	0.99
9.	1 X 4	0.89	0.09	-0.11	-13.14	0.97
10.	3 X 5	1.08	0.11	0.08	-10.90	0.97

Bartlett's $X^2_{(d.f. = 9)}$ testing homogenity of $S_{b_i} = 52.26^{***}$

For correlation co-efficients

$P < 0.05 = 0.71$

$P < 0.01 = 0.83$

$P < 0.001 = 0.93$

Table 35. Results of correlation co-efficients within characters.

	Between Means and response (b_i)	Between Means and stability ($\bar{S}^2_d$)	Between response (b_i) and stability ($\bar{S}^2_d$).
Panicle length	-0.12	0.074	0.25
Primary branches/panicle	-0.289	-0.169	0.787**
Spikelet number/panicle	-0.25	0.23	-0.24
Kernel number/panicle	-0.52	0.11	-0.066
100 kernel weight	0.29	0.98***	0.47
Yield/plant	0.94***	0.92***	0.92***
Tiller number	0.98***	0.76**	0.75*

D.F. = 8

* at 5%
** at 1%
*** at 0.1%

Table 36. Results of co-rrelation co-efficients between responses, b_i (upper right) and between stabilities, $\bar{S}^2_d$ (lower left) among characters.

	Panicle length	Primary branches/ panicle	Spikelet number/ panicle	Kernel number/ panicle	100 kernel weight	Yield/ plant	Tiller number
Panicle length	-	0.65*	0.66*	0.61	0.41	-0.11	-0.06
Primary branches/ panicle	0.09	-	0.56	0.82**	0.54	-0.82**	-0.18
Spikelet number/ panicle	0.19	-0.20	-	0.63*	0.26	-0.08	-0.17
Kernel number/ panicle	0.41	-0.15	0.92***	-	0.08	-0.29	0.38
100 kernel weight	-0.56	-0.57	0.39	0.13	-	-0.36	-0.53
Yield/plant	-0.22	-0.65*	0.08	-0.02	0.99***	-	0.22
Tiller number	0.49	-0.17	-0.25	-0.08	-0.27	0.36	-

Table 37. Estimated values for genetic parameters [d], [h], [h]/[d], βd, βh and t-for ($\beta d - \beta h$) for the five crosses.

Crosses	[d]	[h]	[h]/[d]	βd	βh	t for($\beta d - \beta h$)
			Panicle length			
1 x 5	-1.74***	3.82***	-2.19	-0.02	-0.85*	4.50***
3 x 1	1.68***	6.76***	4.02	-0.26	1.95***	-12.27***
2 x 5	-0.29	2.08***	-7.17	-0.04	-0.43***	5.73***
1 x 4	-1.43***	6.02***	-4.20	-0.10	-1.22***	8.89***
3 x 5	-0.05	6.18***	123.60	-0.26***	-0.16	-0.53
			Primary branches			
1 x 5	0.44***	0.78***	1.77	0.38*	-1.57**	10.26***
3 x 1	-0.41***	2.56***	-6.24	-0.43***	-0.93*	3.17**
2 x 5	0.41***	1.90***	4.63	-0.12	-0.42	1.07
1 x 4	-0.09	1.50***	-16.66	0.16	-1.32***	7.04***
3 x 5	0.03	3.56***	118.66	-0.10	-0.95**	6.07***
			Spikelet number			
1 x 5	-12.01***	83.70***	-6.96	0.10	-0.57	4.81***
3 x 1	10.18***	82.32***	8.08	-0.09	0.01	-0.30
2 x 5	7.57***	48.48***	6.40	0.13	-0.34	2.47
1 x 4	-7.40***	100.30***	-13.55	0.002	-0.47	1.95
3 x 5	-1.83	87.26***	-47.68	0.03	0.17	-0.60
			Kernel number			
1 x 5	-18.51***	91.58***	-4.94	-0.06	-1.10***	10.90***
3 x 1	17.00***	73.76***	4.33	-0.13	-0.08	-0.15
2 x 5	5.52***	50.98***	9.23	-0.16	-0.56	2.22
1 x 4	-12.12***	109.90***	9.06	-0.009	-0.79	3.56**
3 x 5	-1.51*	67.40***	-44.63	-0.20	-0.12	-0.47

Contd.....

Table 37. (Contd.)

Crosses	[d]	[h]	[h]/[d]	β_d	β_h	t for(β_d-β_h)
				100 kernel weight		
1 x 5	0.42***	1.50***	3.57	0.80***	-1.25	5.26***
3 x 1	0.065	0.98**	15.08	0.011	0.066	-0.156
2 x 5	0.46***	1.52***	3.30	1.02*	2.52***	-3.96**
1 x 4	-0.07*	1.04***	-14.85	0.30*	-1.25*	6.50***
3 x 5	0.48***	2.22***	4.63	0.93**	0.86	0.15
				Yield/plant		
1 x 5	-1.14***	20.92***	-18.35	-0.27*	2.31***	-12.28***
3 x 1	2.40***	14.14***	5.89	0.27***	1.76***	-8.30***
2x5	3.77***	6.24***	1.66	0.24***	-0.003	4.59***
1 x 4	-0.16	21.30***	-133.12	-0.08	2.68**	-8.09***
3 x 5	1.83***	24.90***	13.61	0.02	2.58**	-7.93***
				Tiller number		
1 x 5	-3.74***	-3.64***	0.97	-0.34*	-0.31*	-0.37
3 x 1	1.72***	1.56***	0.91	0.16	0.29***	-3.96**
2 x 5	-1.58***	-6.58***	2.55	-0.21	-0.58***	4.11**
1 x 4	-0.09	4.32***	48.00	-0.01	0.31	-4.16
3 x 5	-2.02***	-3.76***	1.86	-0.19***	-0.33*	2.15

1 = Chinese, 2 = IR-20, 3 = IR-8, 4 = Naizersail and 5 = Kataribhog.

DISCUSSION

A knowledge of the nature and relative magnitude of the various types of genotype-environment interaction is important in making decisions concerning breeding methods, selection programmes and testing procedures in crops. Plant breeders are well aware of the problems posed by genotype-environment interaction in breeding better varieties but until recently there was no agreement about its analytical approaches. There are two approaches – one is purely statistical (Yates and Cochran, 1938; Finlay and Wilkinson, 1963; Eberhart and Russell, 1966) and the other based on the biometrical genetics (Mather and Jones, 1958; Jinks and Stevens, 1959; Bucio Alanis, 1966; Bucio Alanis and Hill, 1966; Perkins and Jinks, 1968a). Similar kind of results are obtained by these two types of analyses which show that genotype-environment interaction component is often a linear function of the environmental means. In the present work, a major part of the genotype-environment interaction both in parental lines and segregating generations was accounted for by the linear function of the environmental means, although a smaller but significant part was non-linear and independent of this linear component in some characters.

A plant breeder pins his hope for crop improvement upon evidence of genetic variation for the character being selected. Accurate estimates of the genetic variance will be obtained only if such estimates are unbiased by variation due to GE interactions.

nutritional effects that a wide range of environments gave ample opportunity for the manifestation of genotype-environment interaction.

The magnitude of the genotypic variation was greater than that of environmental and GXE in case of primary branches/panicle, spikelet number/panicle and 100 kernel weight whereas environmental variation was greater than genotypic and GXE variation in other four characters (table 5). Variation due to environment was greater in most of the cases except tiller number and plant height where δ^2_G was high (table 14). Genotypic variation also was greater in case of dry shoot weight and plant height (table 23) and 100 kernel weight (table 32). Magnitude of the co-efficient of variability for genotype, environment and GXE varied from characters to characters. Bhattacharyya (1978) also found high and low genotypic and environmental variation in rice.

Eberhart and Russell (1966) defined both the linear and non-linear functions of the genotype-environment interactions as "stability parameters", β_i (linear regression, b_i) and $\bar{S}^2_d$ (deviation from regression) respectively. Perkins and Jinks (1968a) observed that these two components of genotype-environment interactions are independent and presumably subjected to the control of different gene systems. In the present experiments significant β_i values greater than 1.00 were observed for those F_2S which involved one or both of the parents having β_i values greater than unity in the same characters. It indicated that linear response was under genetic control and subjected to dominance. The relative proportions of estimates of $\bar{S}^2_d$ for parents and F_2S suggested that non-linear components were also

under genetic control (Perkins and Jinks, 1968b; Khaleque, 1975). Both high and low correlation co-efficient (r) within environmental means of each genotype indicated linear and non-linear variations of the genotypes. High (r) values also implied that the regression co-efficient accounted for a large proportion of the genotype-environment interactions (Walton, 1968).

Finlay and Wilkinson (1963), in their discussion of the regression of cultivar mean yield on site mean yield, have opined that a cultivar having a regression co-efficient less than unity had an above average stability of response to environmental influences. A regression co-efficient equal to unity indicates average stability and a regression co-efficient greater than unity suggests less than average stability. In the present investigations the regression co-efficients were heterogenous (as revealed by joint regression analysis) so the varieties responded differently under different environments. The range of b_i values among the F_2s exceeded the parental range in both the directions in most of the cases suggesting that this aspects of phenotype was not simply inherited. In this it was also found that IRRI varieties with $b_i < 1.00$ in most the characters would be less and most of the local varieties with $b_i > 1.00$ would be more responsive varieties to the changes in environments. Eberhart and Russell (1966) state that a stable cultivar is one which performs relatively well in poor environments and relatively poorly in favourable environments. They proposed that the criteria for stability should be a regression co-efficient of unity and a minimum $\bar{S}^2_d$. A cultivar with high mean yield and fulfilling the above two criteria would perform well in all environments.

In the light of the above statements it may be said that firstly, a genotype for a particular character having higher mean performance, average regression co-efficient (b_i) and low $\bar{S}^2_d$ value will be suitable under favourable environments. Secondly, the genotypes having comparatively low b_i and $\bar{S}^2_d$ values with moderately high mean performance will be specially adopted to low yielding environments. These genotypes are so insensitive that they are unable to exploit high yielding environments. Lastly, the genotypes that have low values for mean performance, b_i and $\bar{S}^2_d$ will be consistantly lower yielders under all environments. However, the genotypes which have high $\bar{S}^2_d$ yet they deserve inclusion to suitable environments because of the presence of high b_i and high mean performance and these genotypes are very sensitive to environmental change. The genotypes IR-20, Chinese and IR-532 though had a high deviation around their regressions but due to the high b_i value and high mean yield performances, it is suggested that their inclusion under suitable environments (tables 7 and 16) may be worthwhile. Naizersail, Badshabhog, IR-5 and Kataribhog on the other hand had comparatively low b_i and high $\bar{S}^2_d$ values together with moderately high yield performances may be suitable under inferior environments (table 7).

Among the parents and F_2s, IR-20, IR-8 X Kataribhog and Chinese X Kataribhog with high b_i values with high mean yield and high $\bar{S}^2_d$ values indicated that they are likely to be suitable under favourable environments. The other genotypes IR-8 X Chinese, IR-20 X Kataribhog, Chinese X Naizersail and IR-8 had average b_i values with moderately high mean performances and high $\bar{S}^2_d$ values are likely to be suitable under inferior environments.

The standard error (S_{b_i}) of regression co-efficient is a measure of "stability response" exhibited by each population. It was heterogenous as indicated by $\bar{S}^2_d$ and joint regression analysis. As in the present study, when the linear regression co-efficient gives a more definite and measurable responses to the environment, it is not so much important to consider the component of GXE interaction for stability response (Finlay and Wilkinson, 1963). Both regression co-efficients (b_i) and $\bar{S}^2_d$ were used to measure the stability by Eberhart and Russell (1966). Compared to parental lines the segregating progenies were associated with greater amount of unprodictable irregularities in response to environments.

The correlation between mean ($\bar{X}$) and response (b_i) indicated that they were independent of each other in most of the cases except yield/plant and tiller number (tables 8 and 35), fresh root weight and plant height (table 17) and dry root weight and plant height (table 26). Fresh shoot weight showed significantly negative correlation between mean ($\bar{X}$) and response (b_i) (table 26). Negative correlation between $\bar{X}$ and b_i was found in a few other characters. A positive correlation between mean performance ($\bar{X}$) and linear sensitivity (b_i) was reported in a number of previous studies (Eberhart and Russell, 1966, Perkins and Jinks 1968a, Westerman 1971 and Busch et al. 1976). Mean performance ($\bar{X}$) and stability ($\bar{S}^2_d$) were also found to be independent of each other in most of the cases except kernel number/panicle and tiller number (table 8), fresh shoot weight and dry root weight (table 17), plant height (table 26) and 100 kernel weight, yield/plant and tiller number (table 35). Busch et al.(1976)

also reported the independent nature of mean performance ($\bar{X}$) and stability ($\bar{S}_d^2$). Association of b_i and $\bar{S}_d^2$ was positive and significant only in the case of fresh root weight (table 26) and primary branch/panicle, yield/plant and plant height (table 35). Eberhart and Russell (1966), Perkins and Jinks (1968a), Westerman and Lawrence (1970) and Westerman (1971) reported positive relationship between response (b_i) and stability ($\bar{S}_d^2$). Therefore, the three aspects of a phenotype, mean ($\bar{X}$), response (b_i) and stability ($\bar{S}_d^2$) may or may not be associated with one another and the association when exists may take any sign. The present study further indicated that prediction about linear response as well as stability of either parental lines or of segregating progenies under different environments would not be possible on the basis of their mean performances. This is contrary to the reports made by Jinks and Mather (1955), Perkins and Jinks (1968) and Paroda and Hays (1971).

The response (b_i) of one character was not correlated with that of other character in most of the cases except spikelet number/panicle with primary branches panicle (table 9), spikelet number/panicle with kernel number/panicle (table 18), panicle length with primary branches/panicle and spinelet number/panicle, kernel number/panicle with primary branches/panicle and spikelet number/panicle (table 36). Negative relationship existed in the some of the cases. Similarly $\bar{S}_d^2$ of one character may or may not be correlated with that of the other characters and the nature of the relationship may be positive or negative.

Both dominant and additive components of variation was found to interact with the environment. Similar reports have been made by several

workers (Rajas and Sprague, 1952, Matzinger et al. 1959, Paroda and Joshi, 1970 and Khaleque, 1975). The characters were polygenically inherited and were governed by both dominant and additive genes. The contribution of dominant genes was greater in all the cases except Chinese X Kataribhog and IR-8 X Chinese in tiller number. Khaleque(1975) also reported the greater contribution of dominance genes in rice. Jinks and Mather(1955), Jinks and Stevens (1959), Bucio Alanis and Hill (1966), Bucio Alanis et al. (1969) Jinks and Perkins (1969) and Breese (1969) also reported that dominance component was more sensitive than the additive component. In the present investigation it was found that both dominant and additive components of gene effects interacted with environments and the relative sensitivity of both dominant and additive effects varied from cross to cross in the characters studied. It is, therefore, considered that genetic studies be carried out under environments closely allied to these in which the information is going to be applied.

With respect to a character potence ratios (a measure of dominant effect) varied from cross to cross under different environments. For a particular character, some crosses showed high potence ratios under poor environments while considerably low values for potence ratios were met under good environments and reverse was also observed in some other crosses. The variation of potence ratios of the same crosses under different environments may be explained by assuming that in cases of higher values dominant genes with unidirectional effects were active while in the cases of lowest values dominant genes with bi-directional effects were likely to be active. Phenotypic expression varied from partial dominance to over dominance under different

environments and the nature of the expression might take any sign.

Thus it may be concluded that no prediction as to the performance of a particular genotype can be made, because performances of a genotype varied from character to characters and from one environment to another environment. Both IRRI and local varieties showed wide range of genetic diversity. Most of the local varieties showed low responses to good environments while most of the IRRI varieties exhibited high responses to such environments. However, some of the IRRI varieties showed responses to the good environments even less than that of the local varieties with respect to some characters. The present findings indicate that strains better than the best parental lines may be expected from cross breeding and selection of rice. Some of the F_2S showed better performances than their parental lines.

SUMMARY

Genotype - environment interaction of eight parental lines for two seasons and five F_2s and their five parents of rice (Oryza sativa L.) under eight different nutritional treatments of presence and absence of N, P, K and their combinations were studied for yield and yield components and for some morphological and developmental characters.

Genotype-environment interactions were found to operate in both parental lines and F_2 generations. A significant portion of these interactions was accounted by the linear function of the environmental mean. In majority cases smaller but significant parts of interactions were non-linear and independent of the linear component. Both the linear and non-linear components of genotype-environment interactions were under the control of different gene systems.

A large proportion of significant remainder m. s. and fewer satisfactory linear regressions in some characters indicated the presence of great genetic diversity in the genotypes used. High and low genotypic as well as environmental variations were found in the characters investigated. Magnitude of the co-efficients of variability for genotype, GXE and environment varied from character to character.

There were real effects of different treatments of N, P, K and their combinations as well as of seasons. N alone had the largest single effect in most of the characters. K had no effect on yield performance.

The genotypes had varied responses to different environments. The range of responses among the F_2's exceeded the parental range in both the directions. The standard errors of responses (b_i) were heterogenous in most of the cases. Joint regression analysis and $\bar{S}_d^2$ also gave the same indication. Association of mean ($\bar{X}$), response (b_i) and stability ($\bar{S}_d^2$) was present in some and absent in others. And when the association existed, it had plus or minus sign. Responses (b_i) and $\bar{S}_d^2$ of one character was correlated in some characters and not correlated in others.

The characters under study were inherited quantitatively and were governed by both dominant and additive gene effects, the contribution of the former being more in all the cases. Both dominant and additive components of variation interacted with the environment and they were of different function of the environmental mean and were under different genetic systems. Potance ratios were usually high under poor environments and low under good environments in some characters while in other characters findings were reverse. Phenotypic expression varied from partial dominance to over dominance under different environments.

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