GENOTYPE X ENVIRONMENT INTERACTIONS IN SORGHUM GROWN IN THE MEDIUM AGRICULTURAL POTENTIAL AREAS OF KENYA

BY

IQBAL R. KERMALI

A thesis submitted in partial fulfilment for the degree
of

MASTER OF SCIENCE
IN
PLANT BREEDING

UNIVERSITY OF NAIROBI
FACULTY OF AGRICULTURE
1981

DECLARATION

This thesis is my original work and has not been presented for a degree in any other University.

Date 7. 4 . 84 IKermali

(IQBAL RAMZANALI KERMALI)

This thesis has been submitted for examination with our approval as University Supervisors

Date 10. 4 . 84 R S Pathak

(DR. R.S. PATHAK)
FIRST SUPERVISOR

Date April 19 '84

(DR. D.N. NGUGI)
SECOND SUPERVISOR

TABLE OF CONTENTS

Page

CHAPTER II REVIEW OF LITERATURE

CHAPTER III MATERIALS AND METHODS

3.2. Methods

3.2.2. Statistical procedures

3.2.2.6.1. Finlay and Wilkinson

TABLE OF CONTENTS

Page

CHAPTER IV RESULTS

4.3. Variance components

TABLE OF CONTENTS

CHAPTER V DISCUSSIONS

LIST OF FIGURES

Figure Page

Figure Page

LIST OF TABLES

Table Page

LIST OF APPENDICES

ACKNOWLEDGEMENTS

I wish to express my deep gratitude to my supervisors, Dr. R.S. Pathak and Dr. D.N. Ngugi for their advice and supervision throughout the period of the field work and writing of this thesis. Without their cooperation and consideration, this work could not have been possible. I also wish to extend my appreciation to Dr. F.M. Onim, Department of Crop Science and Mr. S. Durrani, Kabete Library for the guidance and helpful suggestions.

During the period of this study, a good many people have helped me and I wish to thank them all. I would also like to express my appreciation to the Research Division, Ministry of Agriculture, Kenya, for the sponsorship support and for providing facilities which enabled this study to be completed. In this respect, I specially thank the former Director of Research, Mr. D.M. Thairu (at present the Coordinator, Dryland Farming Research and Development), the current Director of Research,Mr. Gitau, the Director, National Dryland Farming Research Station,Mr. Marimi, and the Team Leader,

Sorghum and Millet Development Project, Mr. F. Pinto. I also wish to thank the officers Incharge of Embu Agricultural Research Station and Coast Agricultural Research Stations for their cooperation. I owe many thanks to all my colleagues in the Ministry of Agriculture, especially, Mr. L. M'Ragwa, Mr. Ochienda and Mr. Rubui.

Finally, I extend special thanks to my loving mother, brother and sister and family of Karim Padamshi for giving me the moral support and encouragement. This work is dedicated to the memory of my beloved father, late Ramzanali Kermali.

GLOSSARY

EAAFRO	: East African Agricultural and Forestry Research Organization.
E	: Environment(s)
E_o	: Potential evapotranspiration
G	: Genotype(s)
G x E	: Genotype x environment (GE) interaction
G x Y	: Genotype x year (GY) interaction
G x S	: Genotype x season (GS) interaction
G x L	: Genotype x location (GL) interaction
G x S x L	: Genotype x season x location (GSL) interaction
ICRISAT	: International Crop Research Institute for Semi Arid Tropics.
L	: Location(s)
LR	: Long rain season (APRIL - AUG)
MS	: Mean squares
P	: Precipitation
P/E_o	: Ratio of P/E_o
S	: Season(s)
SR	: Short rainy season (NOV-MARCH)
F	: Variance ratio

ABSTRACT

Fourteen genotypes, (four hybrids, six varieties, and four random mating populations) were grown in a randomized complete block design and three replications in five locations for two seasons, i.e, 1979 long rains and 1979/80 short rains, in the medium agricultural potential areas of Kenya. Environment x Genotype interaction was studied for grain yield/plot, grain yield/head, days to 50% flowering and mean plant height.

The combined analysis of variance for each character indicated that genotype x location x season interaction (G x L x S) variance was highly significant and was also the most important component of genotype x environment (G x E) interaction. Both G x L and G x S interactions were not significant for any character except days to 50% flowering, although, the magnitude of G x S was higher than G x L interaction component in all cases.

The nature of G x E interactions were investigated by means of regression analysis techniques of Finlay and Wilkinson (1963), Eberhart and Russell (1966) and Perkins and Jinks (1968a and b).

It was concluded that a considerable portion of G x E interaction sum of squares (SS) could be attributed to the linear regressions in case of grain yield/plot (67%), grain yield/head (70%), plant height (83%) and days to 50% flowering (45%). For all characters, the pooled deviations from regressions were highly significant. In case of grain yield/plot and days to 50% flowering, G x E (linear) SS was not significant, showing more environmental effect on genotypes to express themselves in different environments. For grain yield/head and mean plant height, this variance was significant, showing that there are genetic differences among the genotypes for their regression on the environmental index. From the joint regression analysis, it was shown that for grain yield/plot, the predictions of GE interaction based on linear regression are difficult to make. While for grain yield/head and days to 50% flowering, reliable predictions can be made only for some genotypes. However, such predictions in case of plant height were more practical.

A number of adaptability and stability parameters were estimated. Adaptability was referred to the response of a particular genotype to environments and was determined by means of regression coefficient value (bi). Genotypes with bi = 1.00 were widely adapted, those with $bi < 1$, were adapted specifically to the unfavourable environments and those with $bi > 1$ were adapted specifically to the favourable environments. The stability was referred to as the ability to show minimum interaction with the environments. The stability parameters taken into consideration were 'Phenotypic stability factor' (PS), 'Ecovalence' (Wi), 'Coefficient of determination' (R_i^2), and 'deviations from the regression' (S_d^2). High correlation was found between the ranks of genotypes according to Wi, R_i^2 and S_d^2 parameters. The defects of PS parameter were pointed out. Hence, the stability of the genotypes was based on the value of S_d^2 alone. The genotypes with the lowest S_d^2 being the most stable and vice versa.

The hybrids gave the highest yield and were early at each environment, although they were slightly taller than the varieties. The hybrids, however, lacked stability and in general were more specific in adaptation. The populations tended to be taller, and their adaptability and stability were better.

The difference in adaptability and stability of the different genotype groups was attributed to their different buffering mechanisms. It was suggested that the adaptability and stability of populations be fully exploited to realise their full potential.

Considering the overall performance, the hybrids were the most desirable genotypes. HYBRID, which had wide adaptability, was most desirable together with HIJACK, which performed better in unfavourable enviroments and HIMIDI which performed better in the favourable environments. Among the varieties, MY 57 and 5D x 135/13/3/1, and among the populations, SERERE ELITE and RS/R appeared most promising.

A comparison of standard error of genotype means suggested that four locations, four seasons and three replications were optimum for such studies. The low intraclass correlations for all characters indicated that the location and seasons could be treated as random environments. Hence, seasons and locations can be used interchangeably when considering the allocation of plots for evaluating the genotypes.

CHAPTER 1

INTRODUCTION

Sorghum (Sorghum bicolor (L.) Moench.) is grown over a wide range of climatic conditions in the medium potential areaas of Western and Nyanza provinces, and to some extent in the Eastern and Coast provinces of Kenya. Sorghums are grown in combination with millets, maize, beans, cowpeas and rarely with cotton, cassava and sweet-potatoes. The estimated area under grain sorghum in 1979 was 210,000 hectares, which produced about 186,000 metric tons, giving a yield of 886 kg/ha (FAO production yearbook, 1979, Vol. 33). However, with the priority given by Kenya Government to develop agricultural production of the semi-arid medium potential areas, the production of drought resistant crops including sorghum is now receiving due emphasis under the Fourth Development Plan 1979-83.

Under the UNDP/FAO aided research project on sorghum and Millet development at the National

Dryland Farming Research Station, Katumani, a number of cultivars have been collected and are being evaluated at different locations. The yield potential of these cultivars under the medium potential areas of Kenya is not known.

In any crop evaluation programme, the ability of a genotype to perform well over a wide range of environmental conditions is always appreciated. This general adaptability is of particular importance because of edaphic variation between locations and seasons in any one locality. The results of a particular breeding programme are very easily influenced by genotype x environment (GE) interactions when dealing with quantitative trait such as grain yield. Hence, genotypic evaluation involving seasons and locations is required. It is possible to statistically analyse GE interaction by conducting yield trials over several locations and seasons.

This study, therefore, aims to:

1) Estimate the components of variance for GE interactions and consider the implications of these interactions in genotype evaluation procedures.

2) Determine the optimum number and allocations of locations and seasons that could be used to give a desired level of efficiency.

3) Estimate the stability parameters with respect to hybrids, varieties and random mating populations of sorghum and identify the most superior genotype(s).

CHAPTER 2

REVIEW OF LITERATURE

2.1. Procedures to estimate the GE interactions

Various methods have been proposed for the statistical analyses of GE interactions and have been discussed explicitly by Freeman (1973) and Hill (1975). Using the data from multilocational trials over a number of seasons, analyses of variance is conducted to calculate the variance due to GE interaction. If this variance is found significant, one of the various approaches known for measuring the stability of genotypes can be used and the varieties can be ranked accordingly. The models for estimating G, E and GE interaction variance components have been developed by Comstock and Moll (1963). Allard and Bradshaw (1964) have discussed the significance of GE interaction on the basis of these estimates of variance components. In the above models, data are analysed assuming that they represent a random sample of environments. But actually, they are collected in a non random fashion by taking a series of locations and seasons. Hanson (1964) devised a formula to compute intraclass correlations among seasons and locations, which could be used to decide whether the environments selected cause any bias on estimates of the genetic components.

Before the use of regression techniques for deriving stability parameters became popular, several other procedures were available. Lewis (1954) suggested the use of 'phenotypic stability factor' (PS) which took into consideration the mean values only in the highest and lowest yielding environments. The technique described by Plaisted and Peterson (1959), involved analysis for each pair of genotypes, making the procedure very cumbersome when many genotypes are to be analysed. Wrickle (1962, 1966) (cited by Jowett, 1972) developed a method to estimate a stability parameter which he named 'ecovalence' (Wi). This parameter has a limited use because it does not allow the prediction of performance of genotypes over environments.

Yates and Cochran (1938) had shown that the regression of yields of the separate genotypes on the mean yield of all genotypes accounted for a large part of GE interactions in a set of barley trials. This method was largely neglected untill Finlay and Wilkinson (1963) used it for testing the adaptability of some 277 barley genotypes in several environments. This regression technique was improved upon by Eberhart and Russell (1966) by adding another stability parameter i.e. deviation from regression. These regression techniques were further modified by Perkins and Jinks (1968a) who proposed a regression of GE interactions on the environmental index rather than the regression of mean performance on the latter as done in the Eberhart and Russell's (1966) model. Here, sum of squares (SS) due to environments (Joint regression) has the same value as SS due to environments (linear) of Eberhart and Russell (1966) model, while the GE interaction SS is further divided into (1) SS due to heterogeneity between regressions, which is the same as GE (linear) SS of Eberhart and Russell (1966) model, and (11) Remainder SS, which is the SS due to pooled deviations of Eberhart and Russell (1966) model.

Originally, Finlay and Wilkinson (1963) used the term 'Stability' to refer to the slope of the regression line (b_i). But now, it is considered to be a measure of the relative response of genotype to changes in the environment. According to Finlay and Wilkinson (1963) model, the average stability is indicated by b_i values approximating 1.0. Genotypes with b_i above 1.0 have below average stability i.e. are more sensitive to environmental changes. Similarly, regression values below 1.0 indicate above average stability i.e. are more resistant to environmental changes. On this criteria, an ideal genotype was defined as the one with maximum yield potential under the most favourable environment and with the maximum stability.

According to Eberhart and Russell (1966) model, a stable genotype is the one which has a high mean ($\bar{X}_i$), unit regression coefficient ($b_i = 1.0$) and the deviations from regressions as small as possible ($S_d^2 = 0$). Obilana and El-Rauby (1980) have considered an additional parameter, coefficient of determination (R_i^2). R_i^2 values near 1.0 indicated that the response of that genotype to environmental change was more stable. A stable genotype would thus have a very high R^2 value. The regression coefficient (b_i) corresponds to the b_i values of Finlay and Wilkinson (1963) and to ($1 + B_i$) values of Eberhart and Russell (1966), after subtracting 1.0, it corresponds with B_i values of Perkins and Jinks (1968 a and b).

Qualset (1968) working with wheat reported the absence of any correlation between W_i and both b_i and S_{di}^2. Jowett (1972) working with sorghum concluded that the W_i is considerably less informative than b_i and S_{di}^2. Prasad and Singh (1980) concluded that PS was as effective as S_{di}^2. They also reported the absence of any similarity between S_{di}^2 and W_i and also between PS and W_i.

2.2. GE Interaction in Sorghum

Liang and Walter (1966) evaluated 21 sorghum hybrids for grain yield at seven locations for two years in Kansas. GL and GY interactions were significant, but their components were relatively small compared with second order interactions and the genotype variance. Large second order interactions indicated diffential response of genotypes grown under different environmental conditions. The allocation of 3 replications, 10 locations and 2 years was recommended as the optimum.

Reich and Atkins (1970) tested eight parental lines, sixteen F_1 hybrids, sixteen two component blends of parental lines and sixteen two component blends of the F_1 hybrids in nine environments over two years in Iowa for grain yield, seeds/head, heads/plant and 100 seed weight. They found significant G, E and GE interaction sources of variation for all attributes. Data for grain yield and for the yield components indicated that the hybrid blends were the most productive and stable. In almost all environments, a hybrid was the highest yielding individual entry in each environment and it also had the highest mean yield among individual genotypes over all the environments.

Rao (1970) evaluated the performance of five hybrids and a local check at 18 locations in India for grain yield, fodder yield, days to 50% flowering and mean plant height. The combined analysis of variance showed that the second order G x L x Y interaction and the first order GL interaction were significant in all cases whereas GY interaction was not significant except for days to 50% flowering. The variance component for GL for almost all characters was of sizeable magnitude and statistically significant. Next to this was the GLY component. The GY component was of the lowest magnitude and statistically not significant.

Jowett (1972), planted eight single crosses, six three-way crosses and eight inbreds of sorghum at seven locations in Uganda and one location at Kampi-ya-mawe in Kenya. The hybrids uniformly outyielded the varieties. In terms of regression coefficients of yield on the environmental index, the hybrids were more stable and there was no difference between threeway and single crosses. In terms of S_{di}^2, weak evidence was presented that indicated that threeway crosses were more stable than single crosses. The varieties showed significantly smaller values of S_{di}^2 and of W_i.

Majisu and Doggett (1972) evaluated sorghum varieties and hybrids in East African lowlands over a period of five years. Combined analyses of variance showed significant differences for G, E and GE interaction mean squares each year. The genotypes usually differed significantly for their regression on environments. All but a few genotypes had large S_{di}^2. There was no evidence for superior stability of all hybrids over varieties, although hybrids were top yielders under favourable environments. They suggested the need to subdivide East Africa into portions with similar environments, especially with respect to rainfall, for which suitable sorghum varieties and hybrids could be developed.

Singhania and Rao (1976, a) studied the GE interaction of 21 male parents, the fertile counterparts of five female parents and their 105 hybrids in 3 different environments in a single season. Both parents and hybrids showed significant GE interaction. Both the linear and non-linear components of GE interaction were significant, but the linear component was greater in the parents. On the other hand, the F_1 hybrids showed greater non-linear components and a higher mean performance indicating that heterosis is generally associated with greater sensitivity to environment. In another study by Singhania and Rao (1976, b) involving the same materials, a study of GE interactions was made with respect to plant height, days to 50% bloom, panicle length, grain yield/panicle, hundred grain weight and number of grains/panicle. They showed that all characters except for days to 50% flowering, displayed considerable GE interaction. The relationship between performance of lines and the environmental values was essentially linear with respect to plant height, grain yield and number of grains per panicle. It was concluded that the homozygous lines could perform better than their hybrids in better environments while the hybrid superiority under less favourable conditions tended to be universal.

Kambal and Mahmoud (1978) obtained the estimates of GE interaction from a study involving 16 sorghum varieties grown at the same three locations over a three year period. They reported that while the GY interaction was small and not significant, the GL interaction was highly significant. They also indicated that a relatively more efficient testing procedure should involve at least two years, six locations and two replicates.

Obilana and El-Rouby (1980), obtained data of three to five genotypes evaluated in four locations each in four different ecological zones in West Africa for two-three years. LY, GL, and GLY interactions were most significant. GY interaction was significant only in one of the zones. The second order interaction variance components were larger than the first order interaction variance components. The environmental variance was the largest component in all zones. The ideal combinations of replicates, locations and years were computed as 4, 8 and 3 and 6, 8 and 4 respectively.

None of the above workers have determined the intraclass correlations. These have been reported by Hanson (1964) on soybeans, maize, tobacco and cotton. Such evaluations have also been reported by Gupton, *et al*. (1974) on burley tobacco. Both these reports concluded that years and locations taken in their respective experiments may be considered random environments and may be used interchangeably.

CHAPTER 3

MATERIALS AND METHODS

3.1. MATERIALS

The materials consisted of fourteen genotypes (four hybrids, six varieties and four random mating populations) as described below:

(i) Hijack (Code: HIJ): a hybrid of the cross CK60A x SB65, developed by EAAFRO, Serere Programme, produces light brown grains with floury endosperm. It is high yielding with fair disease resistance and good ratooning potential.

(2) Himidi (Code: HIM): a hybrid of the cross CK60A x Lulu Dwarf, developed by EAAFRO, Serere Programme, produces white grains with hard but not completely fainty endosperm. It has fairly good disease resistance and good ratooning potential.

(3) Hibrid (Code: HIB): a hybrid of the cross CK60A x Simila, developed by EAAFRO, Serere Programme, produces light brown grains with floury endosperm.

(4) Kafinum A x Lulu Dwarf (Code: KAF): a hybrid, developed at Katumani using Serere material, produces white grains. It is high yielding with fair disease resistance and good ratooning potential.

(5) 5D x 135/13/1/3/1 (Code: 5DX): a variety from EAAFRO, Serere Programme, produces brown grains with floury endosperm. It is widely adapted, high yielding and with fair resistance to leaf diseases.

(6) M-Y 57 (Code: MY5): a Machakos-Yatta selection, collected from Kampi-ya-mawe. It produces brown grains.

(7) 2K x 99 (Code: 2K9): a variety originating from EAAFRO, Serere Programme. It produces white grains.

(8) 9D x 5/F_5/41/1 (Code: 9DX): a variety originating from EAAFRO, Serere Programme. It produces white grains.

(9) 2K x 1/1 (Code: 2K1): a variety originating from EAAFRO, Serere Programme. It produces white grains.

(10) Kohomash (Code: KOB): an introduction from Ethiopia. It produces white grains.

(11) West African Early (Code: WAE): a random mating population obtained from ICRISAT. It is generally early, producing large white grains and has good ratooning potential. Early, short and disease free selections were made at Kampi-ya-mawe, in 1978 Short Rains to reconstitute the present population.

(12) Serere Elite (Code: SER): a random mating population obtained from ICRISAT. It originates from EAAFRO, Serere Programme, produces tall plants with brown grains. Selections were made at Ithookwe, in 1978 Short Rains to reconstitute the present population.

(13) US/R (Code: USR): a non restorer random mating population obtained from ICRISAT. It is generally late maturing, but has vigorous and uniform plants producing a mixture of white and brown grains.

(14) RS/R (Code: RSR): a restorer random mating population obtained from ICRISAT. Selections

were made at Katumani in 1978 short rains, biased towards dwarf, early white grain types to reconstitute the present population.

3.2. METHODS

3.2.1. Field Layout, Locations and Observations

The experiment was conducted at five locations, Katumani (KAT), Kampi-ya-mawe (KYM), Ithookwe (ITH), Murinduko (MUR) and Mtwapa (MTW), during 1979 long rains (LR, April to August) and 1979/80 short rains (SR, November to March). A brief outline of the environmental conditions of these locations is given in Appendix 1 and Appendix 2. These locations belong to the ecological (climatic) zone III and IV, which are of Medium Agricultural Potential and fall in between the very dry and very wet areas, where, the mean annual ratio of precipitation to potential evapotranspiration (P/Eo) is 53-67% in zone III and 38-52% in zone IV. Siderius and Muchena, 1977).

At each location the genotypes were grown in a randomized complete block design with three replicates for two seasons. A plot consisted of two rows, each three meters long and spaced at 75 cm apart. The plant spacing within the rows was 15 cm.

Fertilizer mixture (N-P-K = 11-52-0) at the rate of 100 kg/ha was applied at planting and a top dressing of CAN at 100 kg/ha at thinning was applied. A minimum of two hand weedings were done. D.D.T. and Furadhan were applied to protect from damage by stem borers,shootfly and other pests. Manual guarding was done at maturity to protect the heads from bird damage. Inspite of this, the damage from birds in some locations occured.

Within each environment, seasonal (5 months) climatic data was obtained with respect to mean maximum, mean minimum and mean temperatures, total precipitation and P/Eo% and is given in Appendix 2.

Data on the following plant characters were obtained:

Grain yield/plot: The grain yield was recorded in kg/4.5m^2 plot.

Grain yield/head: The grain yield in g per panicle (effective tiller) was obtained as under:

(grain yield kg/plot)/(number of heads harvested per plot).

Days to 50% flowering: The number of days from emergence to the day when 50% of the plants in the net plot were shedding pollen.

Mean plant height: The average length in cm from the ground level to the tip of the head of the plant.

3.2.2. Statistical Procedures

3.2.2.1. The Linear Model

Using means, the data was analysed following the linear model:

$$Y_{ijkm} = u + g_i + l_j + s_k + r_{jkm} + (gl)_{ij} + (ls)_{jk} + (gs)_{ik} + (gls)_{ijk} + e_{ijkm}$$

where

Y_{ijkm} is the measured value for the plot specified by the subscripts.

u is the population mean

g_i is the effect of ith genotype (G), where i = 1,2,3,....,14

l_j is the effect of jth location (L), where j = 1,2,3,4,5

s_k is the effect of kth season (S), where k = 1,2.

r_{jkm} is the effect of the mth block (RCBD) and jth location in the kth season, where m = 1,2,3.

e_{ijkm} is the composite of remaining effects (including the plot effects, error due to sampling among the plants of a plot and the error of measurement). Combination of symbols refer to the effects of interaction between factors indicated by single symbols. The first order interactions are represented by

$(gl)_{ij}$ or GL interaction
$(ls)_{jk}$ or LS interaction
$(gs)_{ik}$ or GS interaction

The second order interaction was represented by

$(gls)_{ijk}$ or GLS interaction

The population variances were symbolised by σ^2, and their subscripts indicate the source. It is assumed that g_i, $(gl)_{ij}$, $(gs)_{ik}$, $(gls)_{ijk}$ and e_{ijkm} are random factors normally and independently distributed (NID) with mean zero and variance as shown under, and that their effects are additive in contribution to the sum

$e_{ijkm} \sim$ NID $(0, \sigma^2_e)$
$(gls)_{ijk} \sim$ NID $(0, \sigma^2_{gls})$
$(gs(_{ik} \sim$ NID $(0, \sigma^2_{gs})$
$(gl)_{ij} \sim$ NID $(0, \sigma^2_{gl})$
$g_i \sim$ NID $(0, \sigma^2_g)$

3.2.2. Analysis of Variance (ANOVA)

The data from each individual trial was examined separately by ANOVA (Appendix 3). In the pooled ANOVA (Appendix 4), where data for all locations and seasons was combined, the sum of squares for replicates and for the experimental error are equal to the totals of these items in the individual analysis (Yates and Cochran, 1938).

The mean squares (MS) used for F tests of the variance ratio (VR) at 5% and 1% levels of significance were as under:
In case of ANOVA for each location per season, all the items were tested against error M.S. In case of combined ANOVA from all locations and seasons, the procedures described by Cochran and Cox (1957), Creech *et al.* (1968) and Bronius (1970) was followed as under:

SOURCE	MS
Season (S)	M_1
Location (L)	M_2
S x L	M_3
Replicates in S and L	M_4
Genotypes (G)	M_5
G x S	M_6
G x L	M_7
G x S x L	M_8
Error	M_9

Using the above layout, M_3 was used to test M_1 and M_2. M_9 was used to test M_8 and M_4. If M_8 was significant ($P = 0.05$), then M_8 was used to test M_3, M_6 and M_7. If either M_6 or M_7 was significant, then the significant interaction was used to test M_5. If both M_6 and M_7 were significant, then the significant interaction was used to test M_5. If both M_6 and M_7 were significant, then Scatterthwaite's approximation is followed as under for testing M_5, where n = no. of deg. of freedom.

$$VR = (M_5 + M_8)/(M_6 + M_7)$$

$$n'_1 = (M_5 + M_8)^2/[(M_5^2/n_g) + (M_8^2/n_{gls})]$$

$$n'_2 = (M_6 + M_7)^2/[M_6^2/n_{gs}) + M_7^2/n_{gl}]$$

If both M_6 and M_7 were not significant, then M_8 was used to test M_5. If M_8 was not significant, then M_9 was used to test M_5.

3.2.2.3. Variance Components Estimates

The estimates of the components of variance were obtained from the combined ANOVA following the procedures discussed by Miller *et al*. (1959) and Comstock *et al*. (1963). The form of ANOVA and the expected mean squares (MS) are given in Appendix 5.

Genotypes (G), seasons (S) and locations (L) were considered to be the representative samples of their respective populations and as random variables in the analysis.

Estimates were obtained for the following variance components: S(σ^2_s), L (σ^2_l), G (σ^2_g), G x S (σ^2_{gs}), G x L (σ^2_{gl}) and G x S x L (σ^2_{gsl}). The methods of determining these estimates are given in Appendix 6. Levels of significance of the variance components correspond to those of the respective MS from ANOVA.

3.2.2.4. Variances of Genotype Means

An estimate of the optimum number of replicates (R), S and L (which may be most efficient) in variety testing was obtained by determining their effect on the magnitude of the theoretical variance of genotype mean ($G_{\bar{x}}$), where

$G_{\bar{x}} = (\sigma^2_{gl})/L + (\sigma^2_{gs})/S + (\sigma^2_{gsl})/SL + (\sigma^2_e)/RLS$

By substituting the estimated values for variance components in the above formula, value of $G_{\bar{x}}$ may be predicted for any particular combination of R, S and L. Due to limitations of time and cost, it seemed desirable to investigate R = 3, S = 2, 4 and 6, and

L = 3, 6, 9, 12 and 15. Hence estimates of $G_{\bar{x}}$ for all possible allocations of R, S and L within these limits were obtained. These were then shown graphically relative to the conditions of the present trial i.e. R = 3, S = 2 and L = 5.

3.2. 2.5. Correlation among locations and among seasons

Location and season intraclass correlations as discussed by Hanson (1964) were calculated to test the hypothesis that the assumption of random effects of S and L did not lead to greatly biased estimates from testing in consecutive seasons at selected locations.

The G x E effect (n_{ijk}) was expressed as a linear model involving the interaction effects of G x S, G x L and G x S x L.

i.e. $n_{ijk} = (GS)_{ik} + (GL)_{ij} + (GLS)_{ijk}$

Thus, the intraclass correlations were expressed as:

among seasons $P_s = \sigma^2_{gs}/(\sigma^2_{gls} + \sigma^2_{gs} + \sigma^2_{gl})$

among locations $P_l = \sigma^2_{gl}/(\sigma^2_{gls} + \sigma^2_{gs} + \sigma^2_{gl})$

where, σ^2_{gls}, σ^2_{gs} and σ^2_{gl} were the estimated variance components such that

$$\sigma^2_n = \sigma^2_{gls} + \sigma^2_{gs} + \sigma^2 gl$$

The sum $D = (P_s + P_l)$ was thus used to test the hypothesis. Values of D in the range of 0.4 or less indicated that the L and/or S were to be treated as random environments.

3.2.2.6. Regression Analysis

The expectations of the sources of variation in the statistical analysis used by Yates and Cochran (1938) were calculated on basis of the standard model of genotype (G) and environmental (E) actions and interactions as under (Freeman, 1973): The performance Y_{ij} of the ith G in the jth E is regarded as

$$Y_{ij} = U + g_i + I_j + (gI)ij + (eij) \qquad (1)$$

where, $i = 1, 2, \ldots\ldots\ldots 14$

$j = 1, 2, \ldots\ldots\ldots 10$

u = the grand mean over all G and E.

g_i = the additive genetic contribution of ith G, calculated as departure from U of the mean of ith G averaged over all E, such that $\sum_j g_i = 0$.

$$g_i = (\sum_i y_{ij}/n) - (\sum_{ij}\sum y_{ij}/gn)$$

I_j = the additive environmental contribution of the jth E calculated as the

Environmental Index obtained as the difference between U and the mean of jth E averaged over all G, such that $\sum_j I_j = 0$

$$I_j = (\sum_j Y_{ij}/g) - (\sum_i \sum_j Y_{ij}/gn)$$

$(gI)_{ij}$ = the G x E interaction of ith G in jth E, such that $\sum_{ij} (gI)_{ij} = 0$

(e_{ij}) = the experimental error of ith G in jth E.

Since all the regressions were performed on mean values over all the replicates, σ_e^2/R was taken as representing σ_e^2 for R replications.

For each genotype and genotype group, the regression coefficient (b_i) on the I_j and the correlation coefficient (r_i) of the data was determined and their regression lines drawn after estimating the values of X and Y intercepts as under:

$$Y_{ij} = x_i + b_i I_j \tag{2}$$

where, Y_{ij} = genotype mean at jth E

x_i = genotype mean over all E

b_i = regression coefficient measuring the response of ith G to varying E.

I_j = environmental index

Y intercepts = $\bar{x}_i$

X intercepts = $-\bar{x}_i/b_i$

3.2.2.6.1. Finlay and Wilkinson Regression Model

The performance of the genotypes across environments was determined by the statistical procedure developed by Finlay and Wilkinson (1963). It was assumed that G x E of each genotype was a linear function of the environmental values. Hence, $(gI)_{ij}$ in the regression model (1) is regressed on I_j (Freeman, 1973)

i.e. $(gI)_{ij} = B_i I_j + \delta_{ij}$ (3)

where, B_i is the linear regression coefficient for the ith G and δ_{ij} is the deviations from regression line for the ith G in the jth E.

Thus the regression model (1) was rewritten as

$$Y_{ij} = U + g_i + I_j + B_i I_j + \delta_{ij} \qquad (4)$$

It can be shown mathematically that the regression slope B_i (obtained from regression of $(gI)_{ij}$ on I_j) is exactly one unit less than the stability parameter b_i (obtained from regression of Y_{ij} on I_j).

$$Y_{ij} = U + g_i + I_j (1 + B_i) + \delta_{ij} \qquad (5)$$

or $Y_{ij} = U + g_i + I_j b_i + \sigma_{ij}$ (6)

where, $b_i = (1 + B_i) = \sum_j Y_{ij} \, 1_j / \sum_j I_j^2$

or $b_i = 1 + B_i$, Phenotypic regression coefficient (Hill, 1975)

$B_i = b_i - 1$, Genotypic (linear) regression coefficient (Hill, 1975)

The b_i values of individual genotypes were used to compare their adaptability by plotting them against genotype means in a two dimensional scatter diagram. The ANOVA based on the mean performance of ith G in the jth E, as set out in Appendix 6 was used to test the contribution of linear regressions to the G x E variance component.

3.2.2.6.2. Eberhart and Russell Regression Model

The model developed by Eberhart and Russell (1966) can be stated as under:

$$Y_{ij} = U_i + B_i I_j + \delta_{ij} \qquad (7)$$

where, Y_{ij} = genotype mean of ith G at jth E.

U_i = mean of ith G over all E.

B_i = regression coefficient measuring the response of ith G to varying E.

δ_{ij} = deviation from regression of ith G in jth E.

I_j = environmental index obtained as mean of all G at the jth E minus the grand mean (U).

The appropriate regression analysis was performed as given in Appendix 7, where the sum of squares (SS) of E and G X E were added and partitioned into a linear component between environments, a linear component of G x E and deviations from regressions; the deviations being found separately for each genotype. The significance of differences among genotype means, i.e. $H_o = U_i = U_2 = ... = U_n$ was tested by F test of MS_1/MS_3. The significance of genetic differences among genotypes for their regression on environmental index, i.e. $H_o = b_i = b_2 = ... = b_n$ was tested by F test of MS_2/MS_3. The significance of the deviations from regressions for each genotype was tested by F test of their individual MS/error MS, averaged over all replicates.

The measures of stability parameters as described by Eberhart and Russell (1966), i.e. the phenotypic regression coefficient (b_i) and the genotypic regression coefficient (B_i) was obtained. The second measure, δ^2_{di} i.e. MS of deviations from regression was estimated as $s^2_{di} = [\sum_j \delta^2_{ij}/(n-2)] - s^2_e/r$, where s^2_e/r is the estimate of the pooled error (or the variance of a Genotype mean at jth L).

3.2.2.6.3. Perkins and Jinks Regression Model

In this analysis, also called the joint regression analysis, the G x E SS is partitioned into two parts, (1) the variation due to the response of the genotype to varying environmental indexes (Regression SS), measuring the differences between the slopes of the regression lines, and (2) the unexplained deviations from regressions on the environmental index (Remainder SS), measuring the scatter of the points about the regression line.

i.e. $\sum_j (Y_{ij} - \frac{Y_{i.}}{n})^2 = \left[(\sum_j Y_{ij} \; I_j^2)^2 / \sum_j (I_j)^2 \right] + \sum_j \delta_{ij}^2$

where $(\sum_j Y_{ij} I_j)^2 / \sum_j I_j^2 = (1 + B_i)^2 \sum_j I_j^2 = b_i^{\,2} \sum_j I_j^2$

In order to show that b_i MS accounts for a significantly larger portion of the total variation, it was compared with the remainder MS in the b_i analysis, as shown in Appendix 8. Here, the hypothesis being tested states that a significant portion of the variation of ith G over E is accounted by fitting a regression slope of b_i, which includes both the additive environmental variation and the portion of G x E SS that is a linear function of the environmental values.

The B_i analysis, as shown in Appendix 9 was

3.2.2.6.3. Perkins and Jinks Regression Model

In this analysis, also called the joint regression analysis, the G x E SS is partitioned into two parts, (1) the variation due to the response of the genotype to varying environmental indexes (Regression SS), measuring the differences between the slopes of the regression lines, and (2) the unexplained deviations from regressions on the environmental index (Remainder SS), measuring the scatter of the points about the regression line.

i.e. $\sum_j (Y_{ij} - \frac{Y_{i.}}{n})^2 = \left[(\sum_j Y_{ij} I_j^2)^2 / \sum_j (I_j)^2 \right] + \sum_j \delta_{ij}^2$

where $(\sum_j Y_{ij} I_j)^2 / \sum_j I_j^2 = (1 + B_i)^2 \sum_j I_j^2 = b_i^{\;2} \sum_j I_j^2$

In order to show that b_i MS accounts for a significantly larger portion of the total variation, it was compared with the remainder MS in the b_i analysis, as shown in Appendix 8. Here, the hypothesis being tested states that a significant portion of the variation of ith G over E is accounted by fitting a regression slope of b_i, which includes both the additive environmental variation and the portion of G x E SS that is a linear function of the environmental values.

The B_i analysis, as shown in Appendix 9 was against the remainder item.

3.2.2.7. Other Stability Parameters

In addition to the stability parameters based on the regression model, i.e. b_i, S^2_{di} and R^2, the following additional parameters were also determined:

3.2.2.7.1. Phenotypic Stability Parameter

The phenotypic stability factor (PS) suggested by Lewis (1954) is expressed as

$$PS = \bar{x}_{HE} / \bar{x}_{LE}$$

where, LE = Low yielding environment

HE = High yielding environment

$\bar{x}$ = Mean value.

The PS value for each genotype was derived as suggested above and its deviation from unity was calculated.

3.2.2.7.2. Wrickle's Stability Parameter

The ecological valence, or in short, ecovalence (W_i) of genotypes (g) grown under several environments (n), as developed by Wrickle (1962) was used to estimate the stability of their performance as under:

$$W_i = \sum_j \left[Y_{ij} - (Y_{i.}/n) - (Y_{.j}/g) + (Y_{..}/gn) \right]^2$$

where, Y_{ij} is the mean performance of ith G in jth E. As the W_i is the contribution of each G to G x E SS, it was expressed as its percentage. Since all the W_i were calculated from mean values over 3 replicates, (G x E SS)/3 was taken as representing the G x E SS for 3 replicates.

3.2.2.8. Rank Correlations

The spearman rank correlation measures the relationship between the rankings of individuals by two methods (Snedecor and Cochran, 1937). It is denoted by

$$r_s = 1 - (\sigma \sum_{i=1}^{n} d_i^2) / \left[n(n^2-1) \right]$$

where, r_s denotes the rank correlation coefficient, n is the number of pairs of observations and d_i is the difference in rankings of the ith individual.

The rank correlation was obtained for all combinations of mean performance ($\bar{x}$), Lewis' stability factor (PS), Wrickles' stability value (W_i), coefficient of determination (R_2), linear regression (b_i) and deviation from linear regression ($s^2 d_i$). The r_s values were tested for significance at 0.05

and 0.01 levels for (n-2) degrees of freedom from coefficient of correlation table.

CHAPTER IV

RESULTS

4.1. Mean Performance of Genotypes

4.1.1. Grain Yield (kg) per Plot

The grain yields per plot of each genotype and genotype groups in all environments are given in Table 1. Over all environments, the hybrids performed better (1.16 kg.) than the populations (1.00 kg) and varieties (0.95 kg). The hybrid, HIJ was found to be the best entry in KAT LR (1.40 kg), KAT SR (1.65 kg), ITH SR (1.66) MUR LR (0.80 kg) and MTW SR (1.93 kg). HIB and HIM, performed better than the others at KYM LR (1.70 kg) and MUR SR (1.00 kg) respectively. Among the environments, the yields at MUR LR (0.41 kg) and KAT LR (0.65 kg) were generally low. On the other hand, KYM SR, ITH SR, KYM LR and KAT SR gave better yields than the overall mean (1.02 kg).

4.1.2. Grain yield (g) per head

The mean grain yields (g) per head for each genotype in all the environments are given in Table 2.

Table 1. Grain yield (kg/plot) of 14 sorghum genotypes grown in ten environments in Kenya

Genotypes	KAT LR	KAT SR	KYM LR	KYM SR	ITH LR	ITH SR	MUR LR	MUR SR	MTW LR	MTW SR	Mean
Hybrids											
HIJ	1.40(1)	1.65(1)	1.52(4)	1.53(8)	0.98(11)	1.66(1)	0.80(1)	0.85(6)	0.71(12)	1.93(1)	1.30(1)
HIM	0.32(11)	1.47(3)	1.54(2)	1.60(5)	1.05(9)	1.49(4)	0.40(7)	1.00(1)	0.93(8)	1.47(2)	1.13(3)
HIB	1.17(2)	1.55(2)	1.70(1)	1.73(2)	1.07(7)	1.43(5)	0.65(2)	0.72(10)	0.98(6)	1.47(3)	1.25(2)
KAF	0.60(7)	1.44(4)	1.53(3)	1.01(14)	1.00(10)	1.27(7)	0.59(3)	0.97(2)	0.74(11)	0.57(12)	0.97(9)
Mean	0.87	1.53	1.57	1.47	1.03	1.46	0.61	0.89	0.84	1.36	1.16
Varieties											
5DX	0.29(12)	1.17(9)	0.96(12)	1.51(9)	1.46(1)	1.18(9)	0.48(5)	0.54(14)	0.91(9)	1.22(5)	0.97(10)
MY5	0.98(3)	1.39(5)	1.37(5)	1.72(3)	1.31(3)	1.13(11)	0.56(4)	0.81(7)	0.85(10)	0.68(11)	1.08(6)
2K9	0.35(10)	0.79(13)	1.01(11)	1.29(11)	0.55(14)	1.53(2)	0.24(11)	0.62(12)	1.05(4)	0.91(9)	0.83(13)
9DX	0.27(13)	1.12(10)	1.18(9)	2.16(1)	0.89(12)	1.02(14)	0.48(6)	0.77(9)	1.42(1)	0.45(13)	0.98(8)
2K1	0.25(14)	0.73(14)	0.72(14)	1.30(10)	1.41(2)	1.05(13)	0.21(13)	0.62(13)	1.38(2)	0.44(14)	0,81(14)
KOB	0.91(4)	1.07(11)	1.29(8)	1.20(13)	1.06(8)	1.15(10)	0.24(12)	0.78(8)	1.11(3)	1.17(6)	1,00(7)
Mean	0.51	1.05	1.09	1.53	1.11	1.18	0.37	0.69	1.12	0.81	0.95
Populations											
WAE	0.58(8)	0.84(12)	0.95(13)	1.57(6)	0.74(13)	1.10(12)	0.19(14)	0.91(4)	0.67(13)	1.14(7)	0.87(12)
SER	0.85(5)	1.31(7)	1.27(7)	1.54(7)	1.23(4)	1.22(8)	0.36(8)	0.92(3)	1.04(5)	1.45(4)	1.12(4)
USR	0.47(9)	1.36(6)	1.07(10)	1.23(12)	1.19(5)	1.30(6)	0.27(10)	0.68(11)	0.65(14)	0.91(10	0.91(11)
RSR	0.70(6)	1.24(8)	1.37(6)	1.72(4)	1.12(6)	1.50(3)	0.34(9)	0.90(5)	0.94(7)	1.14(8)	1.10(5)
Mean	0.65	1.19	1.17	1.52	1.07	1.28	0.29	0.85	0.83	1.16	1.00
Mean	0.65	1.22	1.25	1.51	1.08	1.29	0.41	0.79	0.96	1.07	1.02
C.V.%	34	32	23	28	38	26	57	33	49	36	34
LSD(P = 0.05)	0.37	0.66	0.47	0.70	0.69	0.55	0.40	0.44	0.78	0.64	0.19

Ranks are given in parenthesis.

Table 2. Grain yield (g/head) of 14 sorghum genotypes grown in ten environments in Kenya

Genotypes	KAT LR	KAT SR	KYM LR	KYM SR	ITH LR	ITH SR	MUR LR	MUR SR	MTW LR	MTW SR	Mean
Hybrids											
HIJ	278(1)	383(2)	340(4)	237(13)	298(7)	380(3)	377(1)	324(5)	497(4)	743(3)	386(2)
HIM	71(11)	348(4)	368(2)	383(3)	254(11)	368(4)	132(8)	427(2)	445(8)	630(4)	343(4)
HIB	234(3)	469(1)	324(5)	302(8)	304(5)	380(2)	261(2)	387(3)	429(9)	978(1)	407(1)
KAF	121(8)	350(3)	359(3)	280(10)	337(1)	567(1)	236(4)	513(1)	467(7)	458(10)	369(3)
Mean	176	388	348	301	299	424	251	413	459	702	369
Varieties											
5DX	70(12)	245(8)	237(10)	328(6)	316(2)	275(6)	194(5)	272(9)	322(14)	820(2)	308(5)
MY5	247(2)	220(11)	233(11)	311(7)	263(10)	149(13)	248(3)	221(13)	527(3)	365(12)	279(10)
2K9	93(10)	139(14)	264(8)	210(14)	174(13)	265(7)	103(12)	157(14)	346(12)	436(11)	219(14)
9DX	58(14)	244(9)	284(6)	460(1)	235(12)	174(11)	192(6)	226(12)	593(1)	228(13)	269(11)
2K1	70(13)	167(13)	269(7)	365(4)	278(9)	216(9)	107(11)	383(4)	388(10)	201(14)	244(13)
KOB	233(4)	273(6)	390(1)	300(9)	292(8)	148(14)	103(13)	313(6)	378(11)	590(6)	302(6)
Mean	128	215	280	329	260	204	158	262	426	440	270
Populations											
WAE	121(9)	155(7)	228(12)	329(5)	123(14)	172(12)	70(14)	262(11)	470(5)	594(5)	252(12)
SER	155(5)	222(10)	221(13)	277(12)	300(6)	178(10)	146(7)	265(10)	469(6)	558(7)	279(9)
USR	126(7)	313(5)	210(14)	369(3)	508(4)	315(5)	132(9)	278(8)	342(13)	482(9)	287(7)
RSR	145(6)	187(12)	240(9)	279(11)	308(3)	230(8)	130(10)	280(9)	539(2)	527(8)	287(8)
Mean	137	210	225	313	260	224	120	271	455	540	276
Mean	144	266	284	316	271	273	174	308	444	544	302
C.V.%	32	29	19	23	25	36	49	23	38	23	31
LSD(P = 0.05)	94	158	110	147	140	201	174	146	341	252	148

Ranks are given in parenthesis

Over all environments, the highest per head yield was obtained from HIB (407g) followed by HIJ (386 g), KAF (369 g) and HIM 343 g), HIB was the most superior entry at KAT SR (469 g) and MTW SR (978 g). HIJ was the best entry at KAT LR (278 g) and MUR LR (377 g), while KAF was the best entry at ITH SR (567 g), ITH LR (337 g) and MUR SR (513 g). At KYM LR, KYM SR and MTW LR, the highest yielding entries were KOB (390 g), 9DX (460 g) and 9DX (593 g) respectively, all of which are varieties. In general, the mean yields at MUR LR (120 g) and KAT LR (137 g) were poor.

4.1.3. Days to 50% Flowering

The mean number of days to 50% flowering for each genotype in all the environments are given in Table 3. On the average, the hybrids were early (60 days). HIJ was the earliest hybrid (57 days), followed by HIM (58 days) and HIB (59 days). All the populations, except USR (62 days) were also early. HIJ was the earliest entry at KAT LR (60 days), KAT SR (56 days), KYM (59 days), KYM SR (55 days), ITH SR (59 days) and MUR LR (55 days). 5DX was the earliest entry at ITH LR (54 days), MYS at MUR SR (55 days)

Table 3. Days to 50% flowering of 14 sorghum genotypes grown in ten environments in Kenya

Genotypes	KAT LR	KAT SR	KYM LR	KYM SR	ITH LR	ITH SR	MUR LR	MUR SR	MTW LR	MTW SR	Mean
Hybrids											
HIJ	60(1)	56(1)	57(1)	55(1)	59(8)	59(1)	55(1)	56(2)	55(5)	54(5)	57(1)
HIM	61(2)	59(4)	57(2)	57(4)	59(9)	60(2)	56(2)	58(4)	55(6)	62(9)	58(2)
HIB	65(5)	58(2)	61(3)	56(2)	61(13)	62(3)	56(3)	61(9)	53(3)	56(6)	59(3)
KAF	64(4)	62(9)	61(4)	58(7)	62(14)	65(9)	56(4)	63(12)	57(9)	65(11)	61(10)
Mean	62	59	59	57	60	62	56	59	55	59	60
Varieties											
5DX	66(6)	60(7)	63(8)	59(9)	54(1)	62(4)	58(10)	57(3)	56(7)	62(10)	60(7)
MY5	63(3)	59(5)	61(5)	56(3)	56(3)	63(6)	56(5)	55(1)	56(8)	75(12)	60(8)
2K9	71(13)	58(3)	68(13)	57(5)	58(6)	62(5)	61(13)	58(5)	63(13)	48(1)	60(9)
9DX	68(8)	63(11)	64(11)	61(12)	59(10)	73(14)	59(12)	61(10)	59(11)	78(13)	65(13)
2K1	68(9)	64(12)	67(12)	61(13)	54(2)	67(12)	57(8)	63(13)	62(12)	79(14)	64(12)
KOB	76(14)	64(13)	69(14)	60(11)	60(11)	68(13)	66(14)	63(14)	66(14)	57(7)	65(14)
Mean	69	61	65	59	57	66	59	59	60	67	62
Populations											
WAE	67(7)	59(6)	61(6)	58(8)	58(7)	64(7)	56(6)	60(7)	57(10)	52(4)	59(6)
SER	69(10)	64(14)	62(7)	59(10)	56(4)	65(10)	56(7)	59(6)	51(1)	49(3)	59(5)
USR	70(11)	62(10)	63(9)	62(14)	60(12)	66(11)	57(9)	61(11)	54(4)	60(8)	62(11)
RSR	70(12)	61(8)	63(10)	57(6)	57(5)	64(8)	58(11)	60(8)	51(2)	48(2)	59(4)
Mean	69	61	62	59	58	65	57	60	53	52	60
Mean	67	61	63	58	58	64	58	60	57	60	61
C.V. %	3	4	3	4	7	5	4	6	7	7	5
LSD(P = 0.05)	4	4	3	4	7	5	4	6	7	7	2

Ranks are given in parenthesis

and 2K9 at MTW SR (48 days). At MTW LR, SER was the earliest entry (51 days). In general, most genotypes were early at MTW LR (57 days), MUR LR (58 days), KYM SR (58 days) and ITH LR (58 days), but were late at KAT LR (67 days) and ITH SR (64 days).

4.1.4. Mean plant height (cm)

The mean plant heights (cm) at maturity for each genotype and genotype groups in all the environments are given in Table 4. In general, the hybrids grew taller (140 cm) than varieties (125 cm), but were shorter than the populations (145 cm). Among all the genotypes, 2K1 was the shortest (110 cm) followed by KOB (115 cm), MY5 (124 cm), 9D x (133 cm), 5D x (133 cm) and HIM (138 cm). 2K1 was the shortest at KAT LR (112 cm) KAT SR (108 cm), KYM LR (123 cm), MUR LR (78 cm), MUR SR (104 cm) and MTW SR (105 cm). KOB was the shortest at KYM SR (116 cm) and MTW LR (132 cm). 2K9 and HIM were shortest at ITH LR (88 cm) and ITH SR (111 cm) respectively. In general, all the genotypes were short at ITH LR (107 cm), ITH SR (107 cm) and MUR LR (108 cm) and were comparatively taller at MTW LR (143 cm), KYM LR (160 cm) and KAT LR (155 cm).

Table 4. Mean plant height (cm) at maturity of 14 sorghum genotypes grown in ten environments in Kenya

Genotypes	KAT LR	KAT SR	KYM LR	KYM SR	ITH LR	ITH SR	MUR LR	MUR SR	MTW LR	MTW SR	Mean
Hybrids											
HIJ	170(11)	142(10)	163(9)	157(11)	103(5)	109(8)	123(12)	137(10)	173(7)	109(2)	139(9)
HIM	164(10)	133(6)	162(8)	158(12)	110(11)	94(1)	113(9)	134(9)	164(6)	142(7)	138(6)
HIB	184(13)	137(8)	179(13)	141(7)	107(6)	112(12)	127(13)	131(8)	181(13)	134(4)	143(13)
KAF	166(9)	143(11)	160(7)	134(4)	97(2)	117(13)	112(8)	127(7)	182(14)	147(9)	139(8)
Mean	171	139	166	148	104	108	119	132	175	133	140
Varieties											
5DX	142(4)	134(7)	149(4)	137(5)	115(13)	125(14)	100(4)	116(4)	162(5)	154(1)	133(5)
MY5	129(3)	118(3)	154(5)	132(3)	108(9)	99(3)	90(3)	115(3)	153(4)	137(6)	124(3)
2K9	153(7)	138(9)	159(6)	140(6)	88(1)	111(9)	100(5)	145(13)	180(12)	164(12)	138(7)
9DX	145(6)	131(4)	148(3)	150(8)	120(14)	101(6)	107(7)	119(5)	174(8)	134(5)	133(4)
2K1	112(1)	108(1)	123(1)	118(2)	118(12)	99(4)	78(1)	104(1)	136(2)	105(1)	110(1)
KOB	122(2)	116(2)	131(2)	116(1)	102(3)	115(10)	78(2)	104(2)	132(1)	129(3)	115(2)
Mean	134	124	144	132	109	109	92	117	156	137	125
Populations											
WAE	145(5)	155(14)	174(11)	155(9)	107(7)	99(5)	102(6)	162(14)	151(6)	154(10)	140(10)
SER	192(14)	145(13)	193(14)	162(14)	108(8)	116(11)	145(14)	148(12)	177(11)	166(13)	155(14)
USR	163(8)	131(5)	171(10)	158(13)	110(10)	101(7)	117(11)	127(6)	176(9)	175(14)	143(11)
RSR	179(12)	143(12)	178(12)	155(10)	102(4)	94(2)	115(10)	143(11)	176(10)	146(8)	143(12)
Mean	170	135	179	158	107	103	120	145	170	160	145
Mean	155	134	160	144	107	107	108	129	166	143	135
C.V. %	4	8	8	10	19	18	12	11	5	14	11
LSD(P = 0.05)	13	21	25	30	41	38	27	30	17	41	23

Ranks are given in parenthesis

4.2. G x E Effects

The results of the combined analysis of variance involving all the seasons and locations are summarized in Table 5. The two factor interaction of G x S x L was highly significant in all traits. The one factor interactions, G x S and G x L, were not significant in case of grain yield/plot, grain yield/head and plant height, except in case of days to 50% flowering. The S x L was significant for days to 50% flowering, plant height, and grain yield/plot, but was not significant for grain yield/head.

For all the traits under consideration, the effect of G and E was highly significant (Table 6). When the components of environments were considered, S were not significant for days to 50% flowering and plant height, but were significant for grain yield/plot and grain yield/head. Similarly, L were not significant for days to 50% flowering, but were significant for plant height, grain yield/plot and grain yield/head.

4.3. Variance Components

4.3.1. Estimates of Variance Components

The estimates of variance components are given

Table 5. Mean squares from combined ANOVA including all locations in each season

Source of variation	df	Grain yield per plot	Grain yield per head (x 10^4)	Days to 50% flowering	Mean plant height (x 10^2
Reps./S/L	20	0.68**	5.12**	25**	4.2**
Seasons (S)	1	9.86*	63.66*	3	62.3
Locations (L)	4	7.03*	106.70*	387	412.2*
Genotypes (G)	13	0.65**	9.11**	182**	40.5**
S X L	4	0.66*	6.98	592**	41.9**
G X S	13	0.17	3.84	94**	5.4
G X L	52	0.15	1.99	52*	3.6
G X S X L	52	0.23**	2.86**	33**	5.7**
Pooled Error	260	0.04	0.27	3	0.7

* significant at P = 0.05

** significant at P = 0.01

Table 6. Mean squares from combined ANOVA including all environments as represented by each location in each season

Source of variation	df	Grain yield per plot	Grain yield per head $(\times 10^4)$	Days to 50% flowering	Mean plant height $(\times 10^2)$
Reps/E	20	0.68**	5.12**	26**	42**
Environments(E)	9	4.51**	57.60**	435**	208.7**
Genotypes (G)	13	0.65**	9.11**	182**	40.5**
E x G	117	0.19**	2.58**	26**	4.7**
Pooled error	260	0.04	0.27	3	0.7

* significant at P = 0.05

** significant at P = 0.01

in Table 7. The levels of significance of the variance components correspond to the respective mean squares from combined ANOVA (Table 5). Some components carry a negative sign and may be considered as estimates of zero or as small positive values of variance (Bronius, 1970). The relative magnitude of the variance component indicates its importance as a source of variation.

Among the main factors, L contributed maximum towards variance for all traits except for days to 50% flowering. The second order interaction G x S x L was highly significant for all characters. On the other hand, the first order interactions, viz. G x L and G x S, were not significant for any character except days to 50% flowering. In all cases, however, the magnitude of the second order interaction G x L x S was larger than those of the first order interactions G x S and G x L.

4.3.2. Allocation of Experiments

In addition to their usefullness in comparisons, the variance components were also used to find the ideal combination of replicates (R), L and S to be used for genotype evaluation by means

Table 7. Estimates of variance components

Variance components	Grain yield per plot	Grain yield per head (x 10^3)	Days to 50% flowering	Plant height
σ^2_s	0.04*(2)	2.65*(3)	-3.09(7)	10(5)
σ^2_l	0.08*(1)	11.98*(1)	-2.67(6)	444*(1)
σ^2_{sl}	0.01*(5)	0.98(5)	13.30**(1)	86**(4)
σ^2_g	0.02**(4)	2.05**(4)	2.32(5)	124**(2)
σ^2_{gl}	-0.01(6)	-1.45(7)	3.18*(4)	-36(7)
σ^2_{gs}	-0.004(7)	0.65(6)	4.03**(3)	-2(6)
σ^2_{gls}	0.04**(3)	6.68**(2)	7.70**(2)	20**(3)
σ^2_e	0.12	8.58	10.04	212
G^{-}_{x}	0.003	0.99	3.76	11

Ranks, according to their magnitudes are given in parenthesis.

* significant at P = 0.05

**significant at P = 0.01

of computing the standard errors of genotype mean ($G\bar{x}$). The calculated theoretical $G\bar{x}$ expected under different combinations of L and S when compared to the observed $G\bar{x}$ for 3R, 2S and 5L taken as equal to 100 are given in Table 8. These results are also shown graphically in Figures 1 to 4.

The smaller the $G\bar{x}$, the more precise is the estimate of genotype mean. It is obvious that increasing the number of plots results in the corresponding decrease in the standard error. This reduction depends on increase in the number of plots due to increase in the number of R, S or L. In each case, however, the reduction in the standard error differed.

For grain yield per plot (Figure 1), when the number of L were kept constant at five, a reduction of 52% in the standard error was realised when the number of S was increased from 2 to 4, and it was only 18% when the increase was from 4 to 6. Similarly, for grain yield/head (Figure 2), this reduction was 65% and 20% when the number of seasons was increased from 2 to 4 and 4 to 6 respectively. For days to 50% flowering (Figure 3) and mean plant

Table 8. Expected standard error of genotypic mean ($G\bar{x}$)

	Grain yield per plot ($\times 10^{-3}$)	Grain yield per head ($\times 10^{2}$)	Days to 50% flowering	Plant height
Observed $G\bar{x}$, when R,S,L = 3, 2, 5	2.7 (100)	9.9 (100)	3.8 (100)	10.8(100)
Expected $G\bar{x}$, when R,S,L = as under				
3, 2, 3	6.0(221)	14.3(145)	4.9(131)	18.7(173)
3, 2, 6	1.9(70)	8.8(89)	3.5(92)	8.9(82)
3, 2, 9	0.5(19)	7.0(70)	3.0(79)	5.6(51)
3, 2, 12	-0.2(-6)	6.0(61)	2.7(73)	3.9(36)
3, 2, 15	-0.6(-21)	5.6(55)	2.6(69)	2.9(27)
3, 4, 3	0.6(21)	4.7(48)	3.0(80)	3.4(31)
3, 4, 6	-0.3(-10)	3.2(32)	2.0(53)	1.4(13)
3, 4, 9	-0.6(-20)	2.7(27)	1.7(44)	0.8(7)
3, 4, 15	-0.8(-28)	2.3(23)	1.4(37)	0.3(2)
3, 6, 3	-1.2(-46)	1.5(16)	2.4(62)	-1.8(-16)
3, 6, 6	-1.0(-37)	1.3(13)	1.5(40)	-1.1(-10)
3, 6, 9	-0.9(-33)	1.2(13)	1.2(33)	-0.8(-8)
3, 6, 12	-0.9(-32)	1.2(12)	1.1(29)	-0.7(-7)
3, 6, 15	-0.8(-31)	1.2(12)	1.0(27)	-0.6(-6)

The expected $G\bar{x}$, when the observed $G\bar{x}$ is taken as equal to 100 are given in brackets.

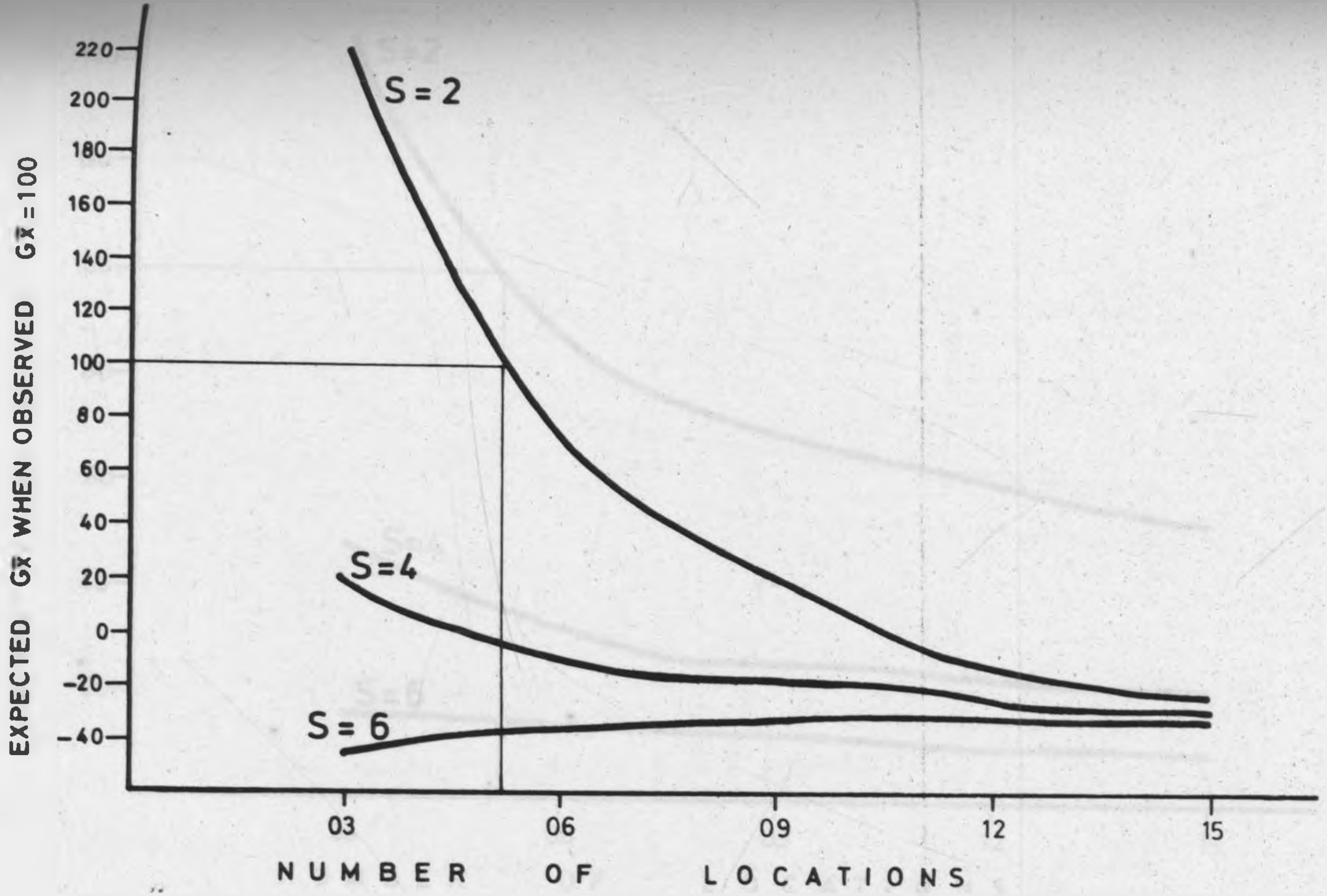


FIG. 1.

Theoretical expected variance of genotype mean (G$\bar{x}$) of grain yield (kg) per plot for various assumed values of R, L, S compared to observed standard error for 3R; 5L, 2S = 100.

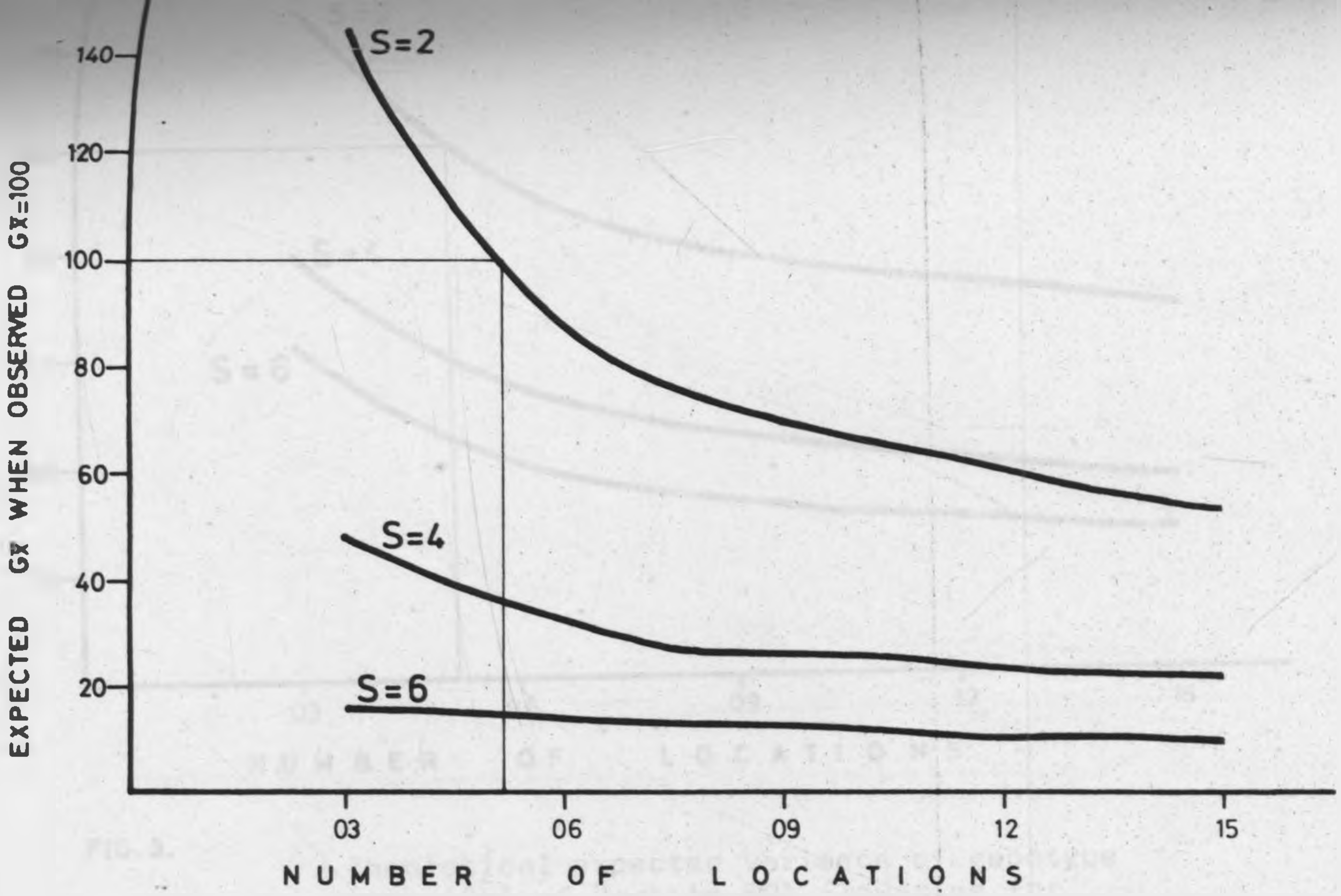


FIG. 2.

Theoretical expected variance of genotype mean (GX̄) of grain yield, (g) per head for various assumed values of R, L, S compared to observed standard error for 3R, 5L, 2S = 100.

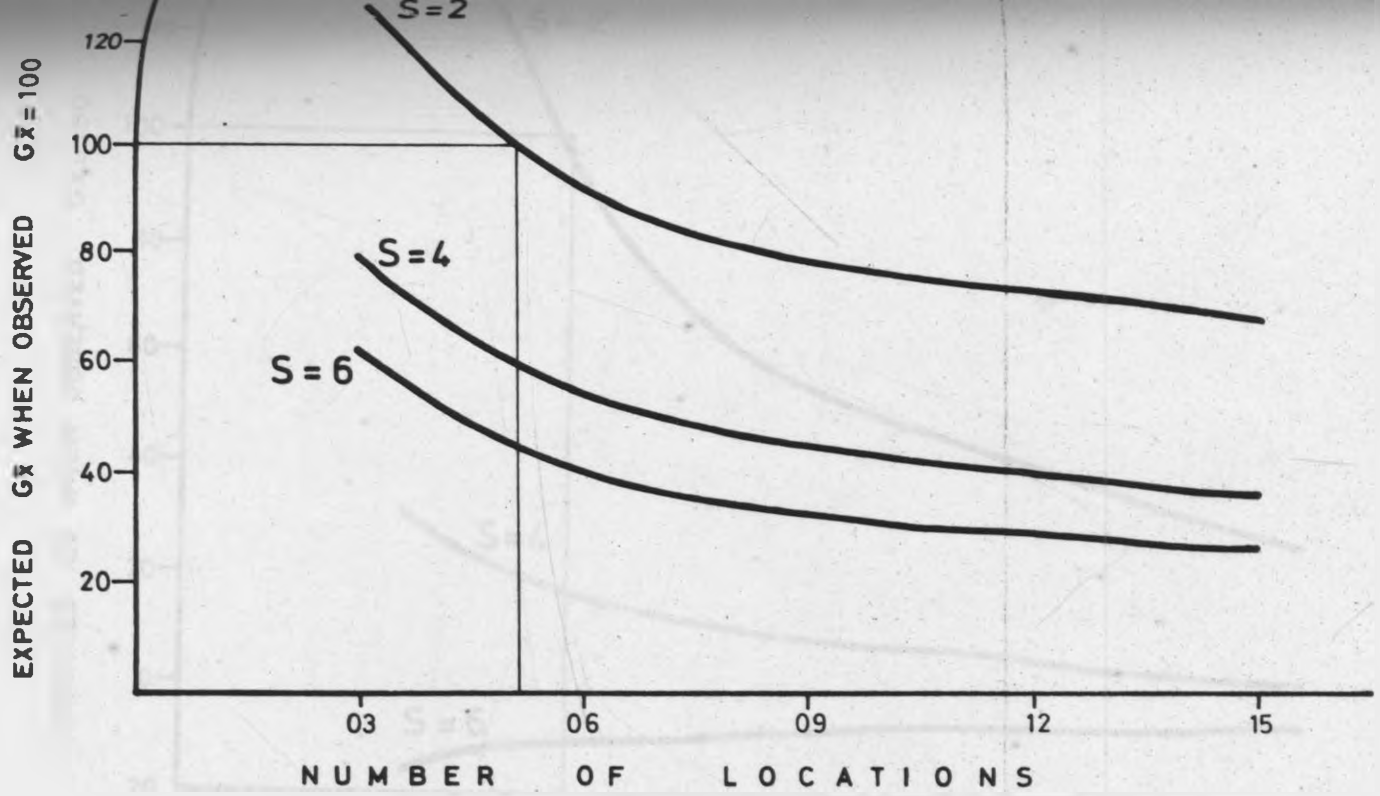


FIG. 3.

Theoretical expected variance of genotype mean ($G\bar{x}$) of days to 50% flowering for various assumed values of R, L, S compared to observed standard error for 3R, 5L, 2S = 100.

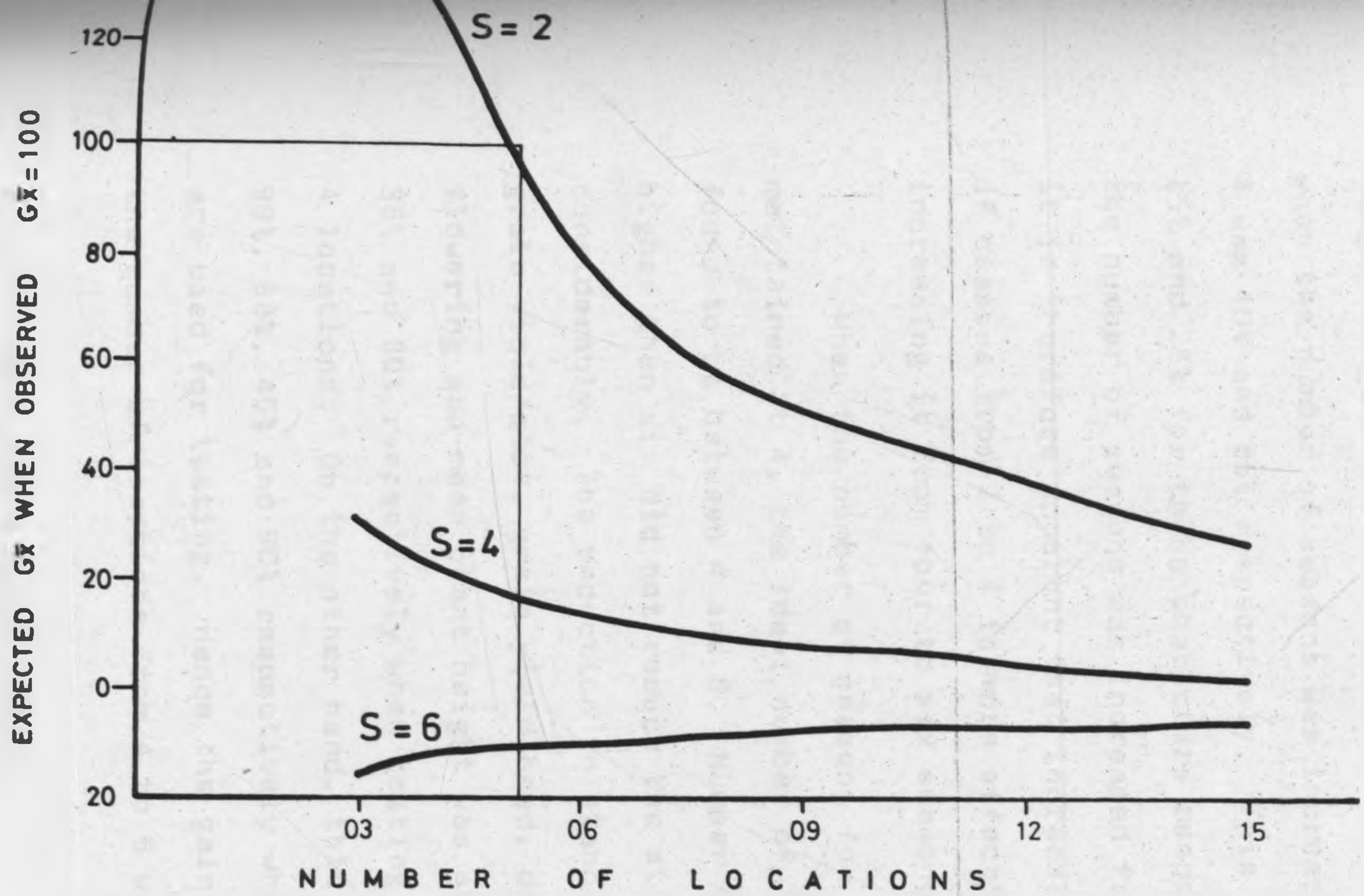


FIG. 4.

Theoretical expected variance of genotype mean ($G\bar{x}$) of mean plant height for various assumed values of R, L, S compared to observed standard error for 3R, 5L, 2S = 100.

height (Figure 4), the reduction in standard error when the number of seasons was increased from 2 to 4 was 40% and 85% respectively. This reduction was 15% and 25% for these characters respectively when the number of seasons was increased from 4 to 6. It is therefore apparent that increasing the number of seasons from 2 to 4 is more effective than increasing it from four to six seasons.

When the number of seasons for testing was maintained at 4, the ideal number of locations was found to be between 4 and 6. Number of locations higher than six did not reduce the standard error considerably. The reduction in standard error for grain yield/plot, grain yield/head, days to 50% flowering and mean plant height was about 90%, 60%, 35% and 80% respectively when testing was done at 4 locations. On the other hand, this reduction was 99%, 68%, 45% and 90% respectively when 6 locations are used for testing. Hence the gain by increasing the number of locations from 4 to 6 was insignificant.

4.3.3. Intraclass Correlations

For all traits the intraclass correlations among seasons were higher than the intraclass

Table 9. Locations and seasons intraclass correlations

Character	Variance component G x E σn^2	Intraclass correlations*		
		among seasons P_s	Among seasons P_l	D (P_s + P_l)
Grain yield/plot	0.02	-0.24	-0.79	-1.03
Grain yield/head	5878	0.11	-0.25	-0.14
Days to 50% flowering	14.91	0.27	0.21	0.48
Mean plant height	81.8	-0.02	-0.44	-0.47

*The negative values are to be considered as estimates of zero or small positive values.

correlations among locations (Table 9), but the sums of both the seasons and locations intraclass correlations (D) were less than 0.4 in case of all the characters. This shows that the seasons and locations used in the experiment could be considered as random environments. Hence testing in consecutive seasons at selected locations cannot be considered as a source of bias in these experiments.

4.4. Regression Analysis

Environmental index: The values of the environmental index obtained as the deviation from general mean from the mean of that specific environment averaged overall the genotypes is given in Table 10. The distribution of the values of environmental index in different traits is variable, highlighting the evident disadvantage of using the average yield of all genotypes in a particular environment to derive its value. But until an independent index based on the environmental factors can be obtained, it is the best available index. For all the analysis based on regression model presented here, the environmental index as obtained above has been utilised.

Table 10. Values of environmental index

Environment	Grain yield per plot	Grain yield per head	Days to 50% flowering	Mean plant height
1. KAT LR	-0.37	-158	6.5	20
2. KAT SR	0.20	-37	0.1	-1
3. KYM LR	0.23	-19	2.1	25
4. KYM SR	0.49	14	-2.3	9
5. ITH LR	0.05	-31	3.8	-28
6. ITH SR	0.27	-30	-2.5	-28
7. MUR LR	-0.61	-129	-2.9	-28
8. MUR SR	-0.23	5	-0.9	-6
9. MTW LR	-0.07	142	-3.8	30
10. MTW SR	0.05	241	-0.2	7

4.4.1. Finlay and Wilkinson (1963) Regression Model

The mean squares from ANOVA of each trait on natural scale are given in Table 11, together with the percentage of G x E SS which can be attributed to the linear regressions. This percentage was found to be 67%, 70%, 45% and 83% for grain yield/plot, grain yield/head, days to 50% flowering and mean plant height respectively. This was further confirmed by the highly significant effect due to regressions in all cases, showing that a significant portion of the G x E variance component was attributed to linear regressions. The deviations from regressions are also highly significant for all traits. This residual G x E variance (deviations from regressions) is in all cases higher than the experimental variance (error mean square). This implies that in addition to the experimental variability, there is an additional coefficient of variation due to deviations from regressions which are also highly significant.

4.4.2. Eberhart and Russel (1966) Regression Model

The mean squares from the regression analysis based on Eberhart and Russel (1966) model are given

Table 11. Mean squares from the regression analysis (Finlay and Wilkinson, 1963, model)

Source of variation	df	Grain yield per plot	Grain yield per head ($\times 10^4$)	Days to 50% flowering	Mean plant height ($\times 10^2$)
Genotypes (G)	13	0.22**	3.04**	62**	14.2**
Environments (E)	9	0.11**	1.37**	11**	5.0**
G x E	117	0.18**	2.34**	28**	6.9**
Regressions	13	1.07**	14.63**	112**	51.0**
(% of G x E)[1]		(67)	(70)	(45)	(83)
Deviation from regressions	104	0.07**	0.80**	17**	1.3**
Mean Error	260	0.04	0.27	3	0.7

[1] % of G x E SS which can be attributed to linear regressions.

** significant at P = 0.01

* significant at P = 0.05

in Table 12. For all characters, there was a highly significant difference among the genotype means. For grain yield/plot and days to 50% flowering, G x E (linear) MS was not significant, while it was significant for grain yield/head (at P = 0.05) and mean plant height (at P = 0.01). This shows that the relationship between the genotype performance and the environmental values is essentially linear with respect to grain yield/head and mean plant height. Hence for these traits, there are genotypic differences among the genotypes for their regression on environmental index, while such genetic differences for grain yield/plot and days to 50% flowering were not significant.

The mean squares for pooled deviations from regressions were highly significant for all characters, indicating that the major components for differences in regressions were due to the deviations from the linear function. From the tests of deviation from regression for each individual genotypes, with respect to grain yield/plot, significant differences occurred in HIJ, 9DX and 2K1 (all at P = 0.01) and KAF (at P = 0.05). Similarly, with respect to grain yield/head, HIJ, HIB, KAF, 5DX, 9DX, 2K1 (all at

Table 12. Mean squares from the regression analysis (Eberhart and Russel, 1966, model)

Source of variation	df	Grain yield per plot	Grain yield per head 9x 10^4)	Days to 50% flowering	Mean plant height (x 10^2)
G	13	0.22**	3.04**	61.73**	14.20**
E + (G x E)	126	0.17**	2.17	25.67	6.36
E (linear)	1	13.52**	172.80	1325.50	626.53
G x E (linear)	13	0.03	1.34*	10.19	2.80**
Pooled Deviations	112	0.06**	0.74**	15.86	1.24**
HIJ	8	0.14**	0.85**	2.57	2.31**
HIM	8	0.04	0.39	3.33	0.54
HIB	8	0.05	1.54**	5.38	1.47*
KAF	8	0.08*	1.31**	6.31	0.82
5DX	8	0.06	0.94**	3.42	1.06
MY5	8	0.05	0.70*	33.34**	0.58
2K9	8	0.06	0.21*	32.96**	1.34
9DX	8	0.15**	1.83**	31.53**	0.84
2K1	8	0.15**	1.06**	39.30**	1.38*
KOB	8	0.03	0.59*	17.16**	1.10
WAE	8	0.04	0.28	7.55*	2.59**
SER	8	0.02	0.17	17.44**	1.60*
USR	8	0.03	0.30	3.22	1.10
RSR	8	0.01	0.25	18.55**	0.57
Mean Error	260	0.04	0.29	3.35	0.71

** significant at P = 0.01
* significant at P = 0.05

P = 0.01) and KAF (at 0.01). Similarly, with respect to grain yielc/head, HIJ, HIB, KAF, 5DX, 2K1 (all at P = 0.05), MYS and KOB (both at P = 0.01), the deviation from regression was significant. For both these traits, all the populations did not differ significantly. On the other hand, for Days to 50% flowering, all the hybrids were not significant, while all the varieties except 5DX were highly significant in addition to SER and RSR (all at P = 0.05) and WAE (at P = 0.01). With respect to plant height, the entries which showed significant deviation from regression included HIJ and WAE (both at P = 0.01) and 2K1 HIB and SER all at P = 0.05).

4.4.3. Joint Regression Analysis (Perkins and Jinks, 1968a, Model)

Phenotypic Regression Coefficient (b_i)

Analysis: For all the traits under consideration, the mean squares from b_i analysis of each genotype are given in Table 13. In general, most of the genotypes have significant b_i MS, except for grain yield/plot, HIJ was not significant, while for grain yield/head, KAF, 9DX and 2K1 were not significant.

Table 13. Mean squares of phenotypic regression coefficient (b_i) analysis of individual genotypes

Genotypes	Grain yield per plot	Grain yield per head (x 10^5)	Days to 50% flowering	Mean plant height x 10^3)
Hybrides				
HIJ	0.58	1.20**	17.8*	4.48**
HIM	1.70**	1.98**	17.8*	5.25**
HIB	0.99**	2.88**	77.9**	6.10**
KAF	0.49*	0.61	45.6*	5.66**
Varieties				
5DX	1.13**	2.69**	90.8**	2.55**
MY5	0.80**	0.42*	67.3	3.67**
2K9	1.04**	0.92**	98.7	6.70**
9DX	1.52*	0.60	132.3	3.75
2K1	0.76*	0.29	107.2	1.06*
KOB	0.61**	1.19**	129.6*	1.54**
Populations				
WAE	0.92**	2.31**	97.2**	4.57**
SER	0.91**	1.50**	212.5**	6.22**
USR	1.08**	0.81**	150.8**	6.63**
RSR	1.41**	1.62**	212.5**	8.12**

** significant at P = 0.01
* significant at P = 0.05

MY5, 2K9, 9DX and 2K1 were not significant in case of days to 50% flowering. All the entries were significant for plant height. The genotypes that were significant indicated, that in their cases, a significant portion of G x E could be explained by b_i, which accounts for both the additive environmental variation and that part of G x E SS that is a linear function of the environmental values.

Genotypic (linear) Regression Coefficient (B_i)

Analysis: Table 14 gives the MS of each genotype from the B_i analysis. In general, most of the genotypes did not show significant B_i MS. However, in case of grain yield/plot, RSR was significant (at $P = 0.05$), while in case of grain yield/head, WAE was significant (at $P = 0.05$). HIJ (at $P = 0.01$) and HIM (at $P = 0.05$) were significant for days to 50% flowering. For mean plant height, 2K1, KOB and RSR (all at $P = 0.01$) were significant. In these genotypes, a significant portion of G x E SS was accounted by B_i, which represents the component of G x E which is a linear function of the environmental values.

Table 14. Mean squares of genotypic (linear) regression coefficient (B_i) analysis of individual genotypes

Genotypes	Grain yield per plot	Grain yield per head (10^4)	Days to 50% flowering	Mean plant height
Hybrides				
HIJ	0.049	0.003	30.33**	0
HIM	0.103	0.867	30.44*	30
HIB	0.0001	3.441	0.82	126
KAF	0.081	1.074	8.87	70
Varieties				
5DX	0.006	2.785	0.06	269
MY5	0.008	2.116	2.33	40
2K9	0.001	0.228	0.04	225
5DX	0.063	1.118	3.14	32
2K1	0.012	3.286	0.39	1182**
KOB	0.041	0.005	2.74	767**
Populations				
WAE	0.001	1.672*	0.02	1
SER	0.001	0.134	23.48	143
USR	0.003	0.441	6.50	211
RSR	0.041*	0.267	23.48	539**

** significant at P = 0.01
* significant at P = 0.05

Joint Regression Analysis: The joint regression analysis of the data for all the four characters is summarized in Table 15. In case of each trait, the additive environmental item (joint regression SS) is highly significant indicating that some of the B_i are significantly positive, while others are significantly negative. For all the traits, G x E MS was highly significant, as further indicated by either heterogeneity between regression MS, the remainder M.S., or both being significant. In case of grain yield/plot, remainder MS alone was significant, indicating that there is no relationship or no simple relationship between G x E and the environmental values, hence predictions of G x E for each genotype from the linear regressions are difficult to make. For grain yield/head and days to 50% flowering, the heterogeneity between regressions MS was significant when compared with error MS, but was not significant when tested against the remainder MS, hence reliable predictions can only be made for those individual genotypes whose b_i is highly significant. On the other hand, for mean plant height, heterogeneity between regression MS is significant against both the remainder and error MS,

Table 15. Mean squares from joint regression analysis (Perkins and Jinks, 1968a, model)

Source of variation	df	Grain yield per plot	Grain yield per head (x 10^4)	Days to 50% flowering	Mean plant height
Genotypes (G)	13	0.217**	3.04**	62	14.20**
Environments (E)	9	1.503**	19.20**	147	69.62**
(Joint regression)					
G x E	117	0.063**	0.86**	16**	1.50**
Heterogeneity between regressions	13	0.032	1.34**[1]	10**[1]	2.80**[1]**[2]
Remainder	104	0.066**	0.80**	17**	1.33**
Mean error	260	0.041	0.29	3	0.71

[1] variance ratio 1

[2] variance ratio 2

** significant at 0.01

* significant at 0.05

indicating that the predictions of G x E based on b_i have a considerable practical value.

4.4.4. Adaptability and Stability Parameters

The term 'adaptability' refers to the response of a particular genotype to varying environments as defined by its mean performance over all the environments where it was tested ($\bar{x}_i$) and slope of its regression line (b_i) measuring the response of the genotype to all the environments quantified by the environmental index. On the other hand, the 'stability' of this performance, refers to the ability of the genotype to show a minimum of interaction with environments, which may be gauged from the squared deviations from regression coefficient (S_d^2). The additional stability parameters also considered included the phenotypic stability factor (SF), ecovalence (W_i) and coefficient of determination (R_i^2). Two of these factors, SF and W_i are not based on the regression model and will thus be treated separately.

The relationship of the stability of each genotype and genotype group in different environments is shown by means of regression lines for grain yield/

plot (Figure 5), grain yield/head (Figure 7), days to 50% flowering (Figure 9) and mean plant height (Figure 11). The regression lines show the sensitivity of the genotypes to environmental changes and can also be used to predict their performance in general. The relationship between the genotypes and environmental changes was further explained by means of the scatter diagrams given in Figures 6, 8, 10 and 12, showing the adaptability of the genotypes and genotypes groups. Lines were drawn around all the genotypes belonging to specific genotype groups, and the position of the enclosed area showed the type of adaptation of that genotype group. The generalised interpretation of these scatter diagrams is given by Finlay and Wilkinson (1963) and reproduced in Appendix 11.

The values of mean ($\bar{x}_i$) and regression coefficient (b_i) for each genotype have been given in Tables 16 and 19, together with the stability parameters S^2_{di} and R^2_i. The $\bar{X}_i$ have been ranked according to their magnitude, while the b_i for each genotype have been ranked according to their deviation from unity in the assending order. For convenience of comparison of b_i, the B_i have also been included. Genotypes with b_i approximating 1.0 have average adaptability, while those above and below 1.0 are adapted specifically to the favourable and unfavourable environments respectively. Similarly, all the genotypes have been ranked separately with respect to stability factors S^2_{di} and R^2_i, according to their magnitude. For S^2_{di}, the genotypes with the lowest values are most stable and vice versa. On the other hand, for R^2_i, the genotypes with the highest values are more stable and vice versa.

Grain Yield/Plot

The genotypes which performed above mean (1.02 kg/plot) are HIJ (1.30), HIB (1.25), HIM (1.13), SER (1.12), RSR (1.10) and MY5 (1.08). The first three genotypes are hybrids, while SER and RSR are populations and MY5 is a variety. Among these genotypes, the b_i of HIB and SER showed minimum deviation from unity (i.e. B_i = 0.01 and - 0.03 respectively) and hence were well adapted to all environments. HIJ and MY5 with deviation of b_i from unity being - 0.23 and - 0.09, respectively

Table 16. Mean and stability parameters estimates from the regression model for grain yield/plot

Genotypes (G)	Mean $\bar{x}$	Coef. of Det. R^2_i	Regression coefficient Phenotypic b_i	Regression coefficient Genotypic b_i	Deviation from reg. $s^2_{d_i}$
Hybrides (H)					
1. HIJ	1.30(1)	0.35(14)	0.78(11)	-0.23	1.08**(12)
2. HIM	1.13(3)	0.85**	1.33**(14)	0.33	0.30(5)
3. HIB	1.25(2)	0.73**	1.01**(1)	0.01	0.37*(7)
4. KAF	0.97(9)	0.44*(12)	0.71*(13)	-0.29	0.63**(11)
mean	1.16	0.80**	0.96	-0.04	
*Varieties (V)					
5. 5DX	0.97(10)	0.72**(8)	1.08**(6)	0.08	0.44*(9)
6. MY5	1.08(6)	0.66**(10)	0.91**(7)	-0.09	0.42(8)
7. 2K9	0.83(13)	0.69**(9)	1.04**(4)	0.04	0.46(10)
8. 9DX	0.98(8)	0.56*(11)	1.26*(12)	0.26	1.21**(14)
9. 2K1	0.81(14)	0.41*(13)	0.89*(8)	-0.11	1.08**(13)
10. KOB	1.00(7)	0.73**(6)	0.79**(9)	-0.21	0.22**(4)
mean	0.95	0.88**	0.99	-0.01	
Populations (P)					
11. WAE	0.87(12)	0.75**(5)	0.98**(2)	-0.02	0.31(6)
12. SER	1.12(4)	0.85**(2)	0.97**(3)	-0.03	0.16(2)
13. USR	0.91(11)	0.84**(4)	1.06**(5)	0.06	0.20(3)
14. RSR	1.10(5)	0.98**(1)	1.21**(10)	0.21*	0.03(1)
mean	1.00	0.96**	1.06	0.06	
Mean	1.02				

Ranks are given in parenthesis
**significant at P = 0.01
*significant at P = 0.05

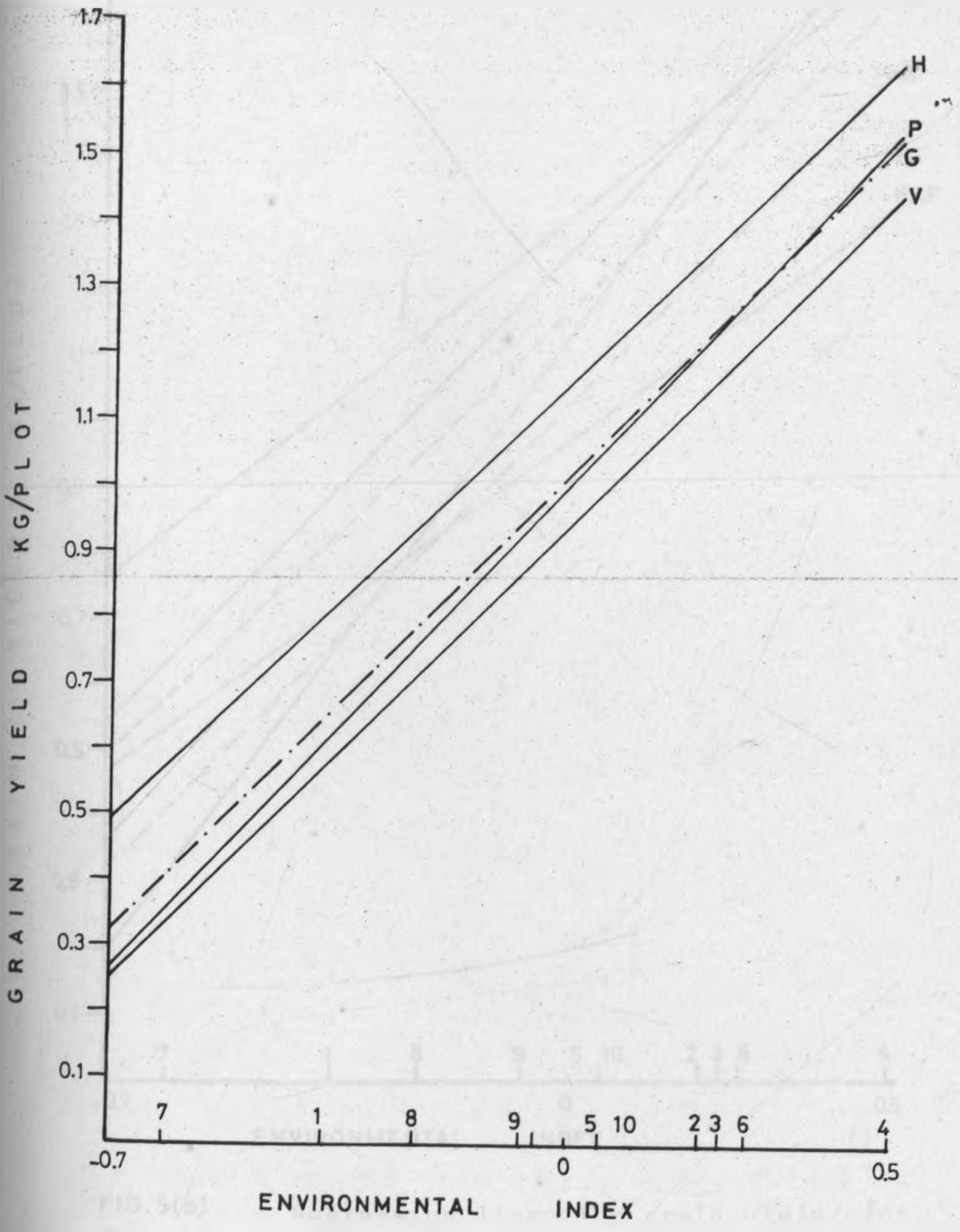


FIG. 5(a)

Regression lines for grain yield/plot showing the relationship of means of Hybrids (H); Varieties (V) and Populations (P) and mean of all genotypes (G). The environments 1 to 10 on the X axis correspond to those in Table 10.

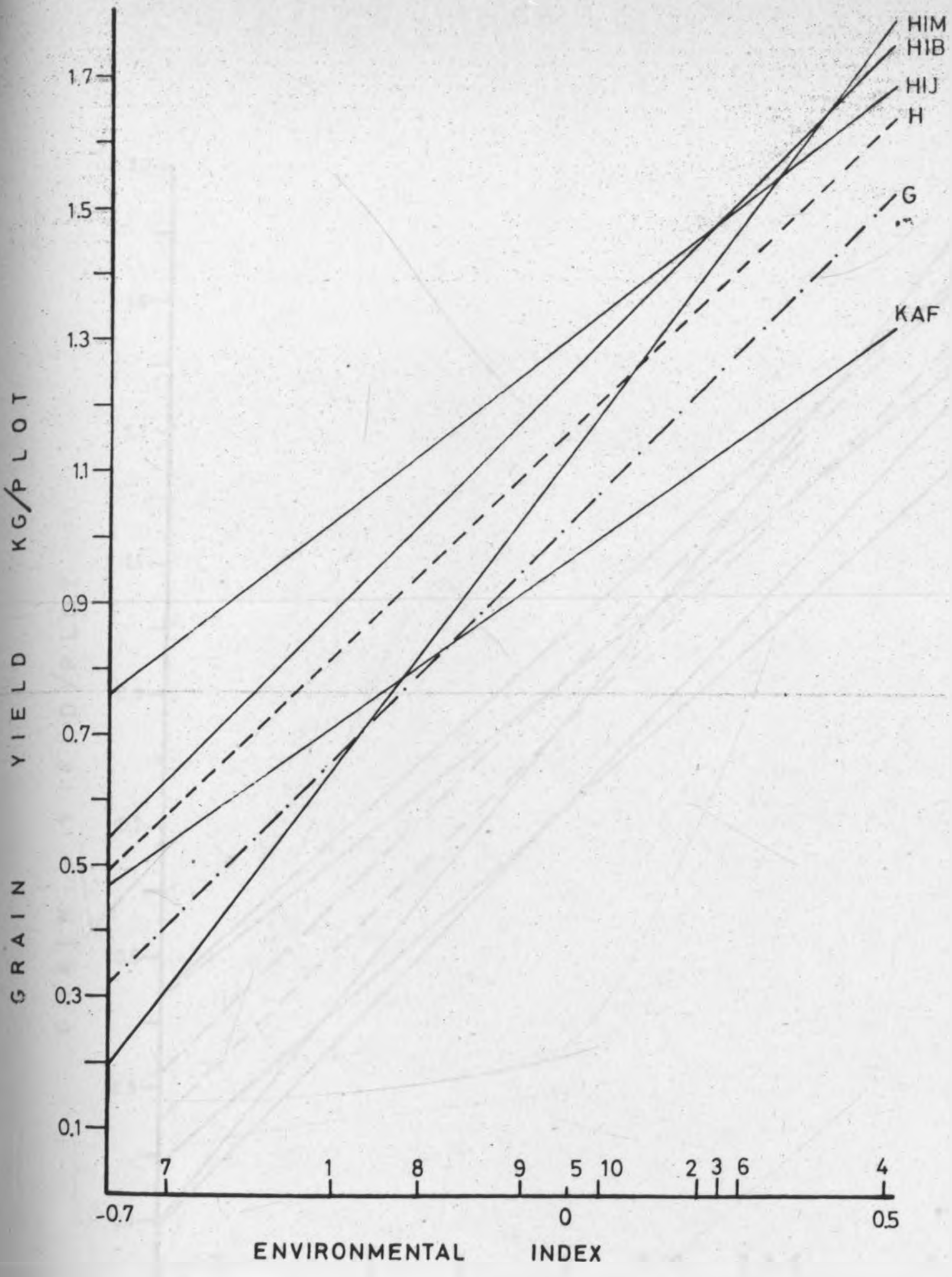


FIG. 5(b) Regression lines for grain yield/plot showing the relationship of the individual hybrids, mean of all hybrids (H) and mean of all genotypes (G). The environments 1 to 10 on the X axis correspond to those in Table 10.

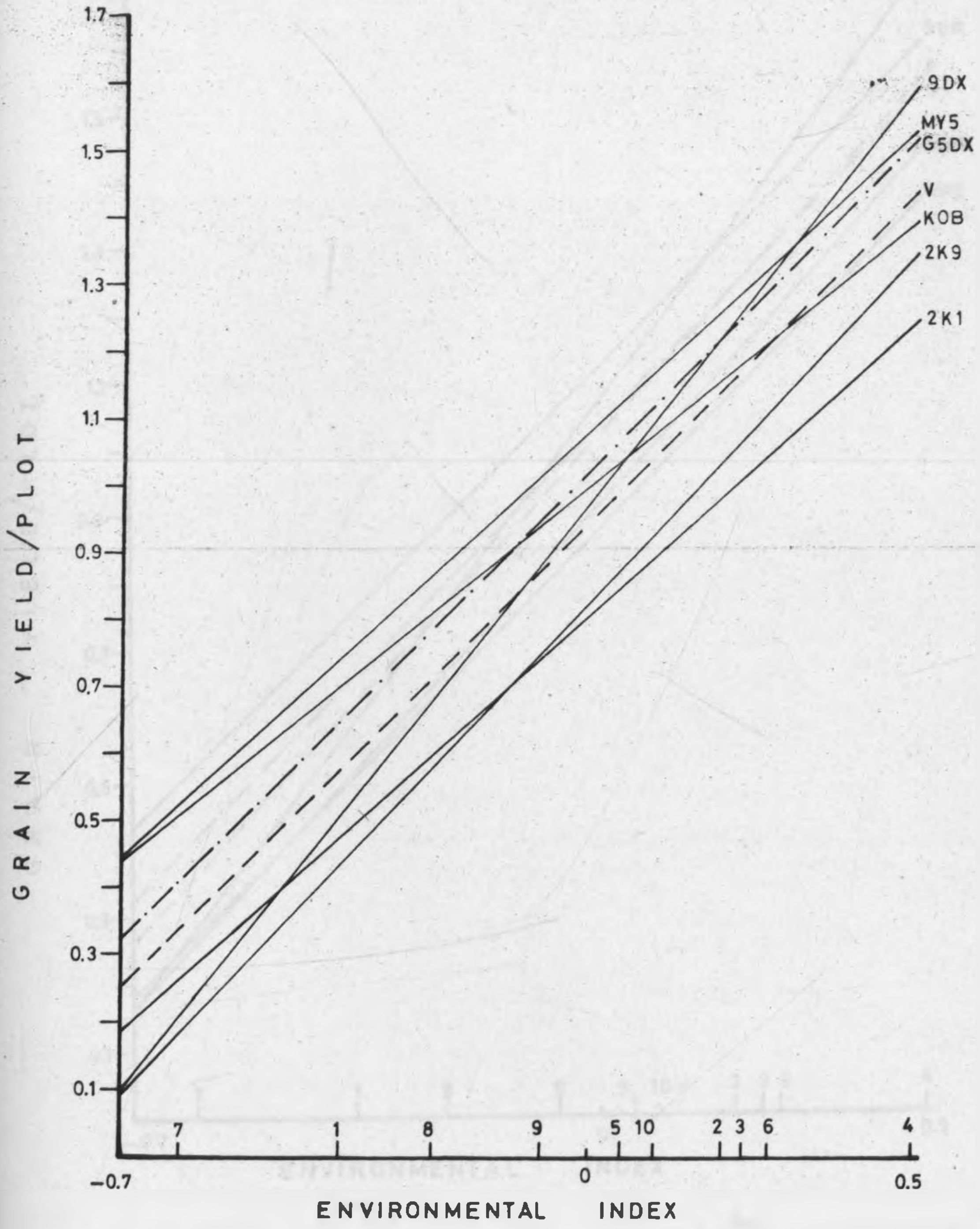


FIG. 5(c) Regression lines for grain yield/plot showing the relationship of the individual varieties, mean of all varieties (V) and mean of all genotypes (G). The environments 1 to 10 on the X axis correspond to those in Table 10.

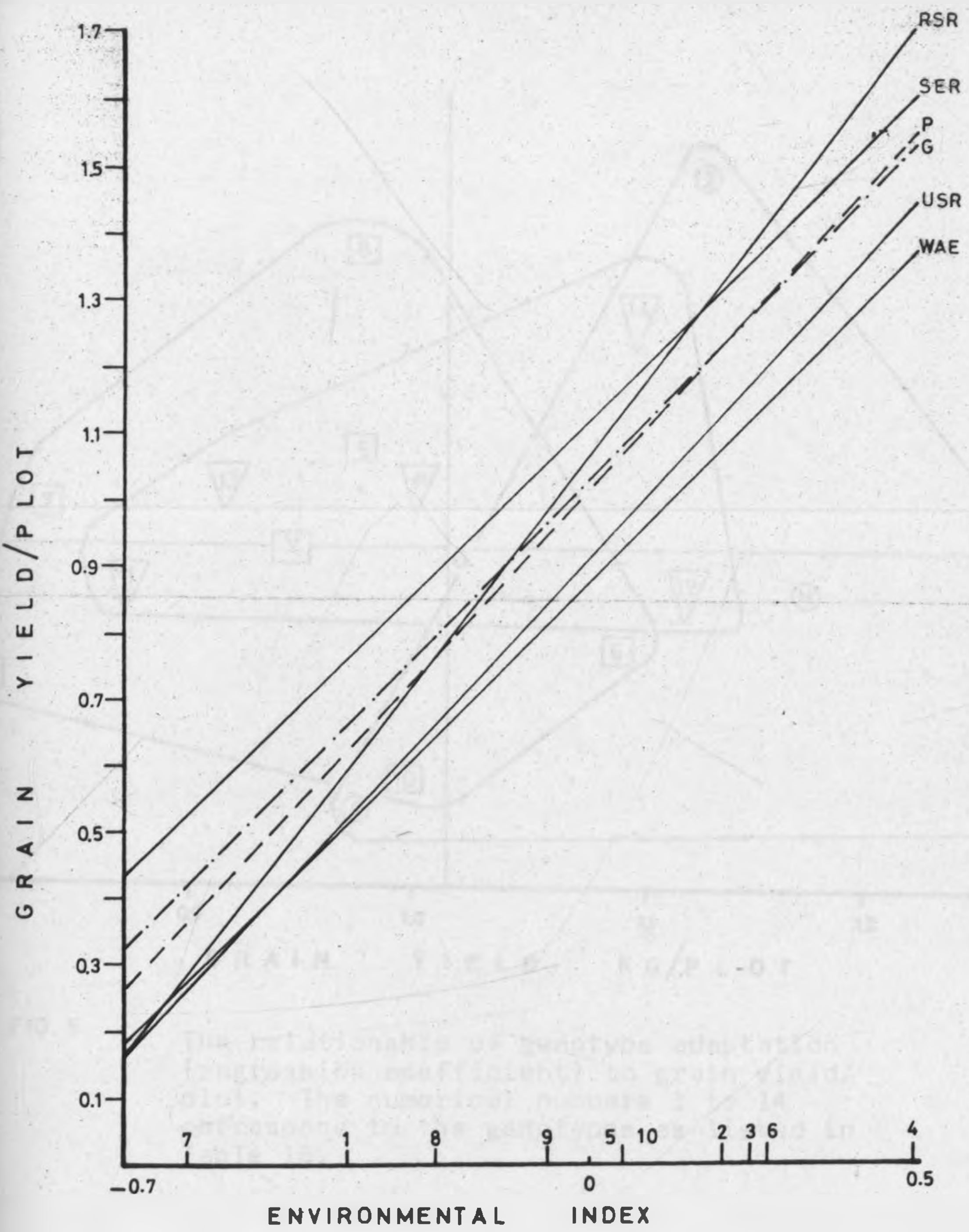


FIG. 5(d) Regression lines for grain yield/plot showing the relationship of the individual populations, mean of all populations (P) and mean of all genotypes (G). The environments 1 to 10 on the X axis correspond to those in Table 10.

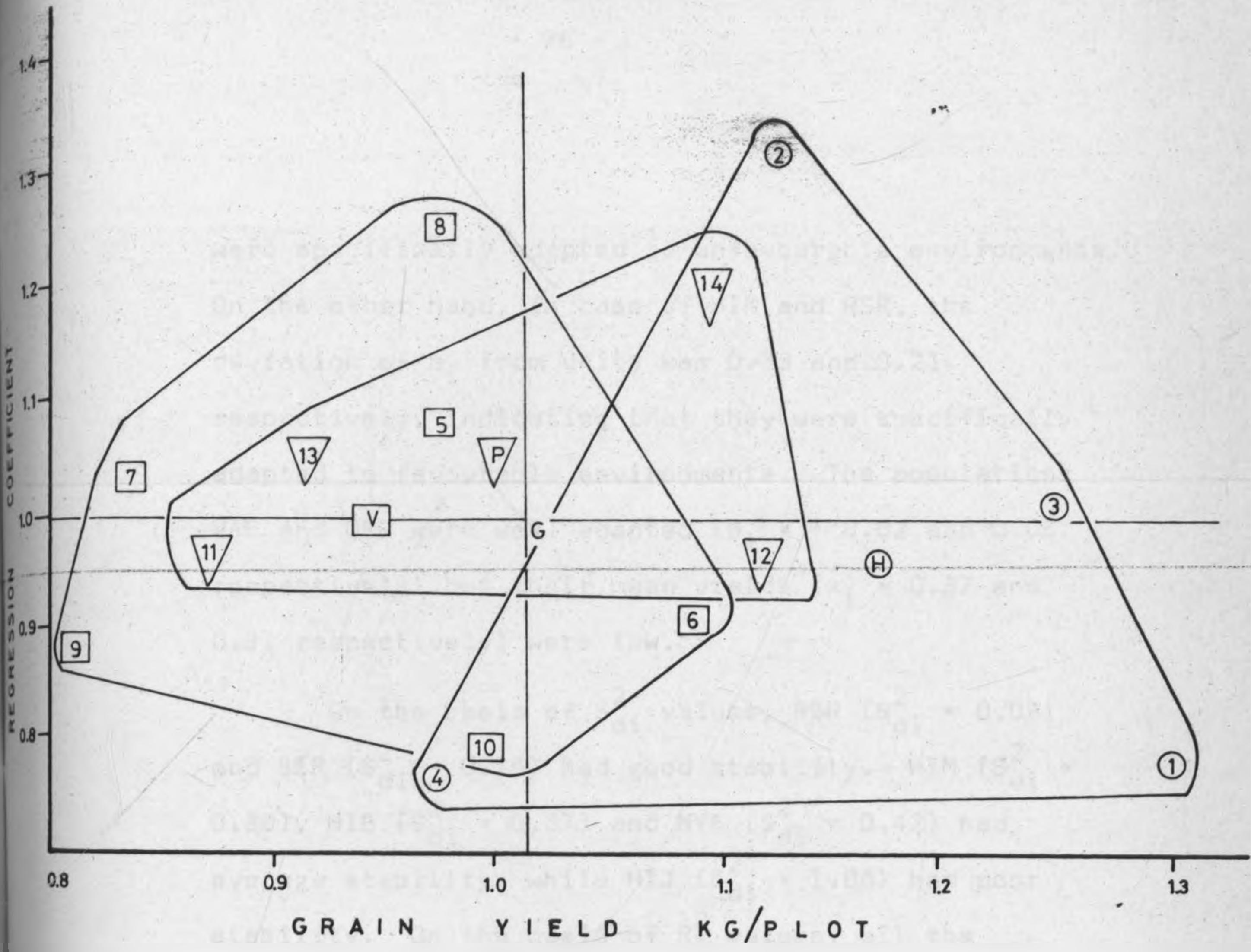


FIG. 6. The relationship of genotype adaptation (regression coefficient) to grain yield/ plot. The numerical numbers 1 to 14 correspond to the genotypes as listed in Table 16.

were specifically adapted to unfavourable environments. On the other hand, in case of HIM and RSR, the deviation of b_i from unity was 0.33 and 0.21 respectively, indicating that they were specifically adapted to favourable environments. The populations WAE and USR were well adapted (B_i = - 0.02 and 0.06 respectively) but their mean yields ($\bar{x}_i$ = 0.87 and 0.91 respectively) were low.

On the basis of S^2_{di} values, RSR (S^2_{di} = 0.03) and SER (S^2_{di} = 0.16) had good stability. HIM (S^2_{di} = 0.30), HIB (S^2_{di} = 0.37) and MY5 (S^2_{di} = 0.42) had average stability, while HIJ (S^2_{di} = 1.08) had poor stability. On the basis of R^2_i values, all the populations together with HIM had good stability (R^2_i = above 0.75). HIB (R^2_i = 0.73) and MY5 (R^2_i = 0.66) had average stability while HIJ (R^2_i = 0.35) had the poorest stability.

Based on the above parameters it was found that in general HIB ($\bar{x}$ = 1.25, b_i 1.01, S^2_{di} = 0.37, R^2_i = 0.73) and SER ($\bar{x}$ = 1.12, b_i = 0.97, S^2_{di} = 0.16, R^2_i = 0.85) were the most desirable genotypes for grain yield and were well adapted. HIM ($\bar{x}$ = 1.13, b_i = 1.33, S^2_{di} = 0.30, R^2_i = 0.85) and RSR ($\bar{x}$ = 1.10,

$b_i = 1.21$, $S^2_{di} = 0.03$, $R^2_i = 0.98$) were found to have very good stability, but they were more adapted to the favourable environments. HIJ($\bar{x}_i = 1.30$, $b_i = 0.78$, $S^2_{di} = 1.08$, $R^2_i = 0.35$) was found to be more adapted to the poorer environments, although its stability was poor.

Grain yield/head

The entries which yielded above average ($\bar{x} = 302$ g/head) included all the four hybrids, HIB (407 g), HIJ (386 g), KAF (369 g) and HIM (343 g), together with 5DX (308 g) and KOB (302 g). Next to these, the yields of USR (287 g), RSR (287 g), SER (279 g) and MY5 (279 g) were also encouraging. HIJ, KOB and SER were well adapted to all environments ($B_i = -0.02$, -0.02 and 0.10 respectively), HIB, HIM, 5DX and RSR are adapted to the more favourable environments ($B_i = 0.53$, 0.27, 0.48 and 0.15 respectively), while KAF, USR and MY5 are adapted specifically to the unfavourable environments ($B_i = -0.30$, -0.19 and -0.42 respectively).

For stability based on S^2_{di} and R^2_i values, most hybrids, especially KAF did not have good

Table 17. Mean stability parameters estimates from the regression model for grain yield/head

Genotypes (G)		Mean $\bar{x}$	Coef. of Det. R_i^2	Regression coefficient		Deviation from Reg. S^2_{di} ($\times 10^4$)
				Phenotypic b_i	Genotypic B_i	
Hybrides (H)						
1.	HIJ	386(2)	0.64**(10)	0.98**(1)	-0.02	6.8**(9)
2.	HIM	343(4)	0.86**(4)	1.27**(7)	0.27	3.2(6)
3.	HIB	407(1)	0.70**(9)	1.53**	0.53	12.3**(13)
4.	KAF	369(3)	0.37(12)	0.71(8)	-0.30	10.5**(12)
	mean	376	0.84**	1.12	0.12	
Varieties (V)						
5.	5DX	308(5)	0.78**(6)	1.48**(12)	0.48	7.5**(10)
6.	MY5	279(10)	0.43*(11)	0.59*(11)	-0.41	5.6*(8)
7.	2K9	219(14)	0.85**(5)	0.86**(4)	-0.14	1.7*(2)
8.	9DX	269(11)	0.29(13)	0.70(9)	-0.30	14.6**(14)
9.	2K1	244(13)	0.25(14)	0.48(13)	-0.52	8.5**(11)
10.	KOB	302(6)	0.72**(8)	0.98**(2)	-0.02	4.7**(7)
	mean	270	0.92**	0.85	-0.15	
Populations (P)						
11.	WAE	252(12)	0.91**(2)	1.37**(10)	0.37*	2.2(4)
12.	SER	279(9)	0.91**(1)	1.10**(3)	0.10	1.4(1)
13.	USR	287(7)	0.77**(7)	0.81**(6)	-0.19	2.4(5)
14.	RSR	287(8)	0.89**(3)	1.15**(5)	0.15	2.0(3)
	mean	276	0.97**	1.11	0.11	
Mean		302				

Ranks are given in parenthesis
**significant at P = 0.01
*significant at P = 0.05

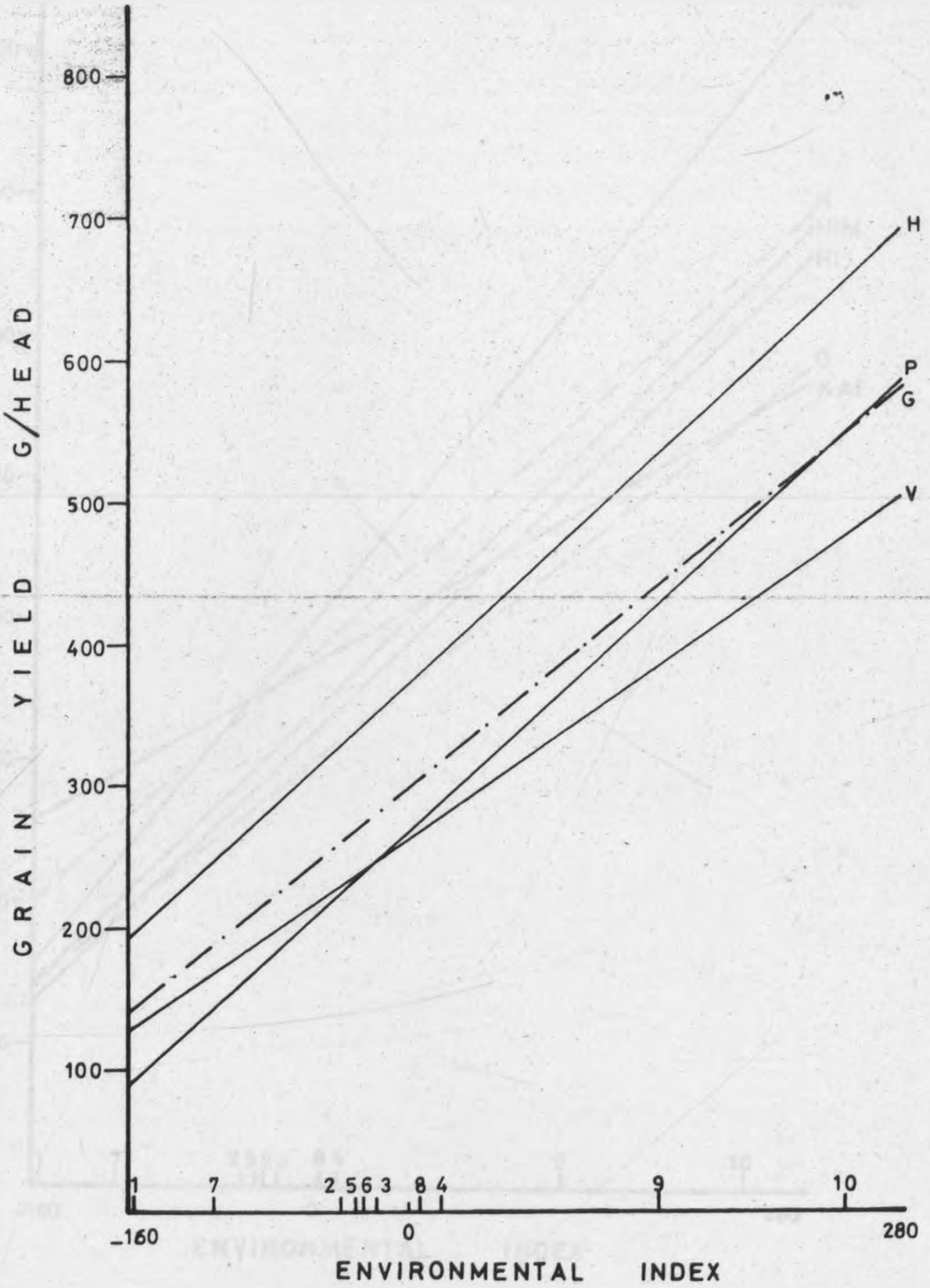


FIG 7(a)

Regression lines for grain yield/head showing the relationship of means of hybrids (H), varieties (V) and Populations (P) and the mean of all genotypes (G). The environments 1 to 10 on the x axis correspond to those in Table 10.

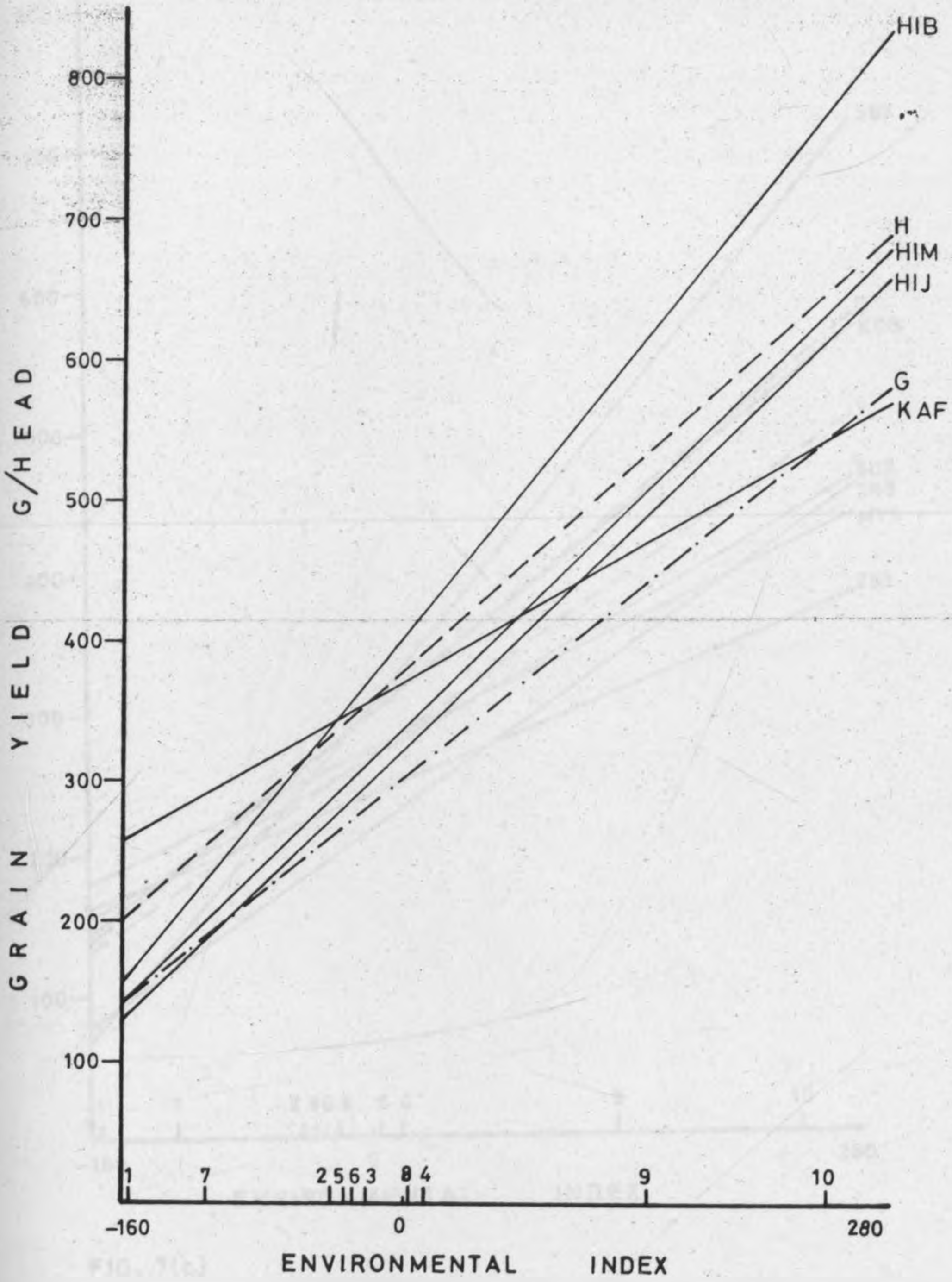


FIG.7(b) Regression lines for grain yield/head showing the relationship of the individual hybrids, mean of all hybrids (H) and mean of all genotypes (G). The environments 1 to 10 correspond to those in Table 10.

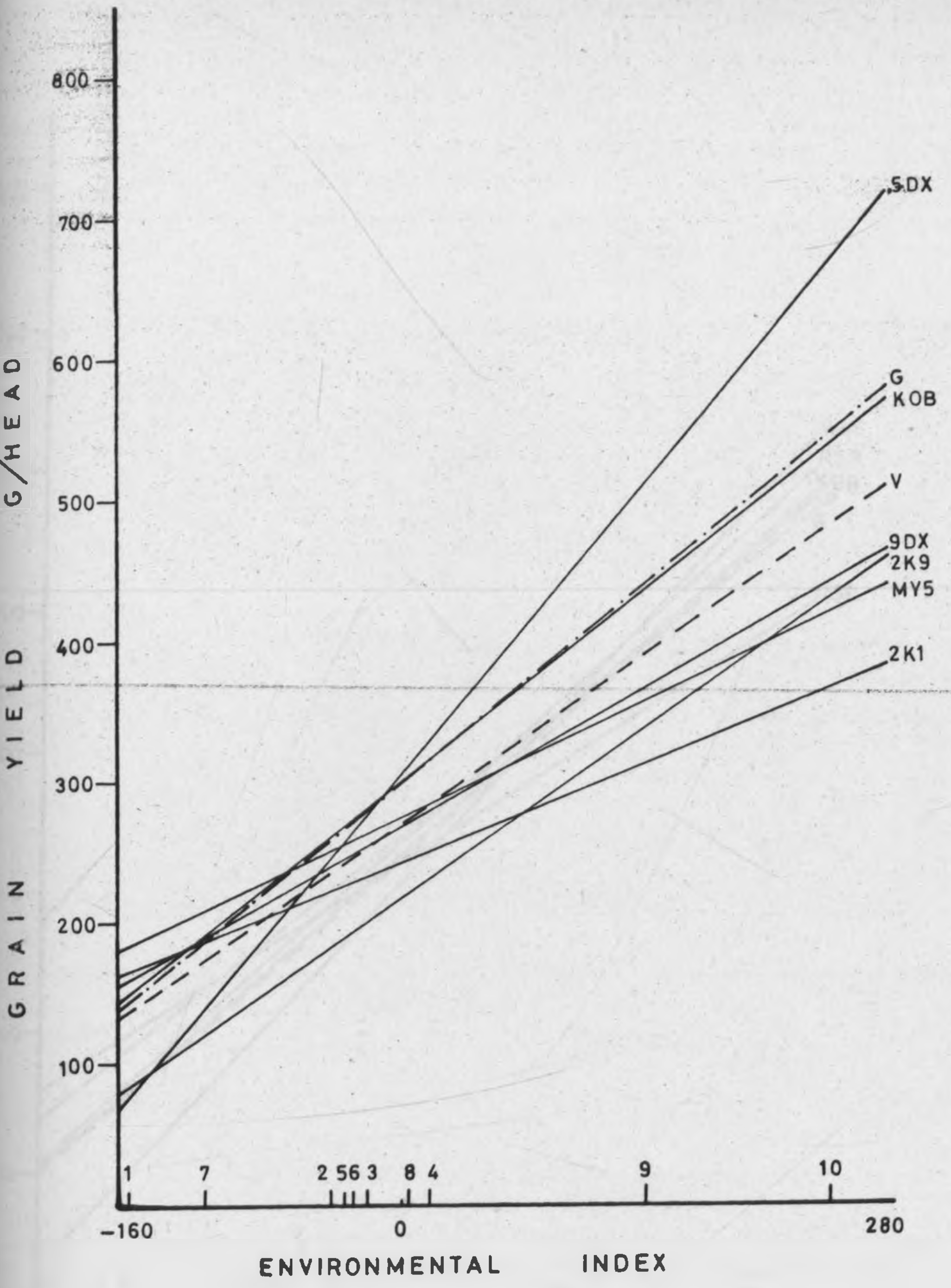


FIG. 7(c)

Regression lines for grain yield/head showing the relationship of the individual varieties, mean of all varieties (V) and mean of all genotypes (G). The environments 1 to 10 on the X axis correspond to those in Table 10.

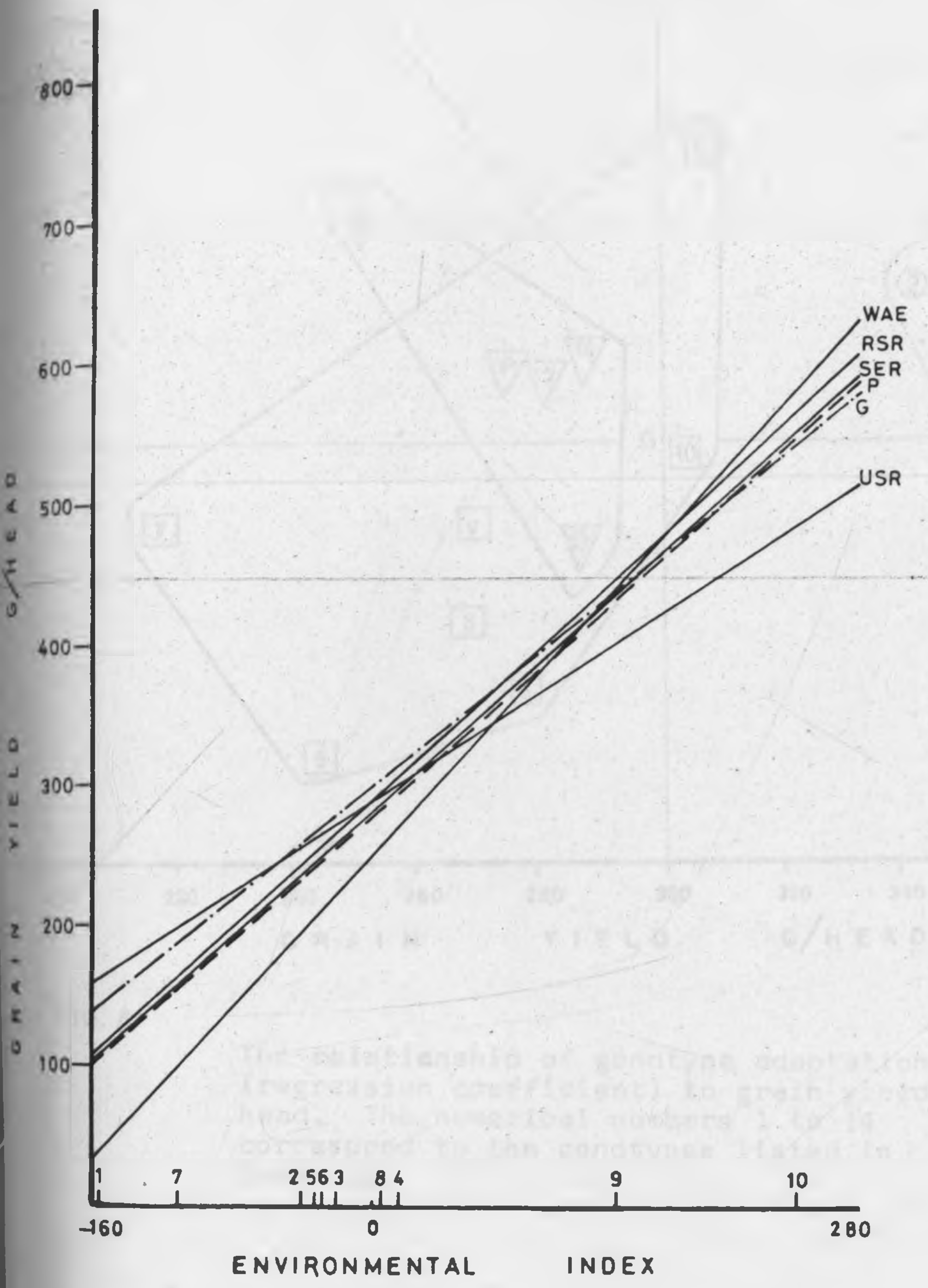


FIG. 7(d)

Regression lines for grain yield/head showing the relationship of the individual populations, mean of all population (P), and mean of all genotypes (G). The environments 1 to 10 on the X axis correspond to those in Table 10.

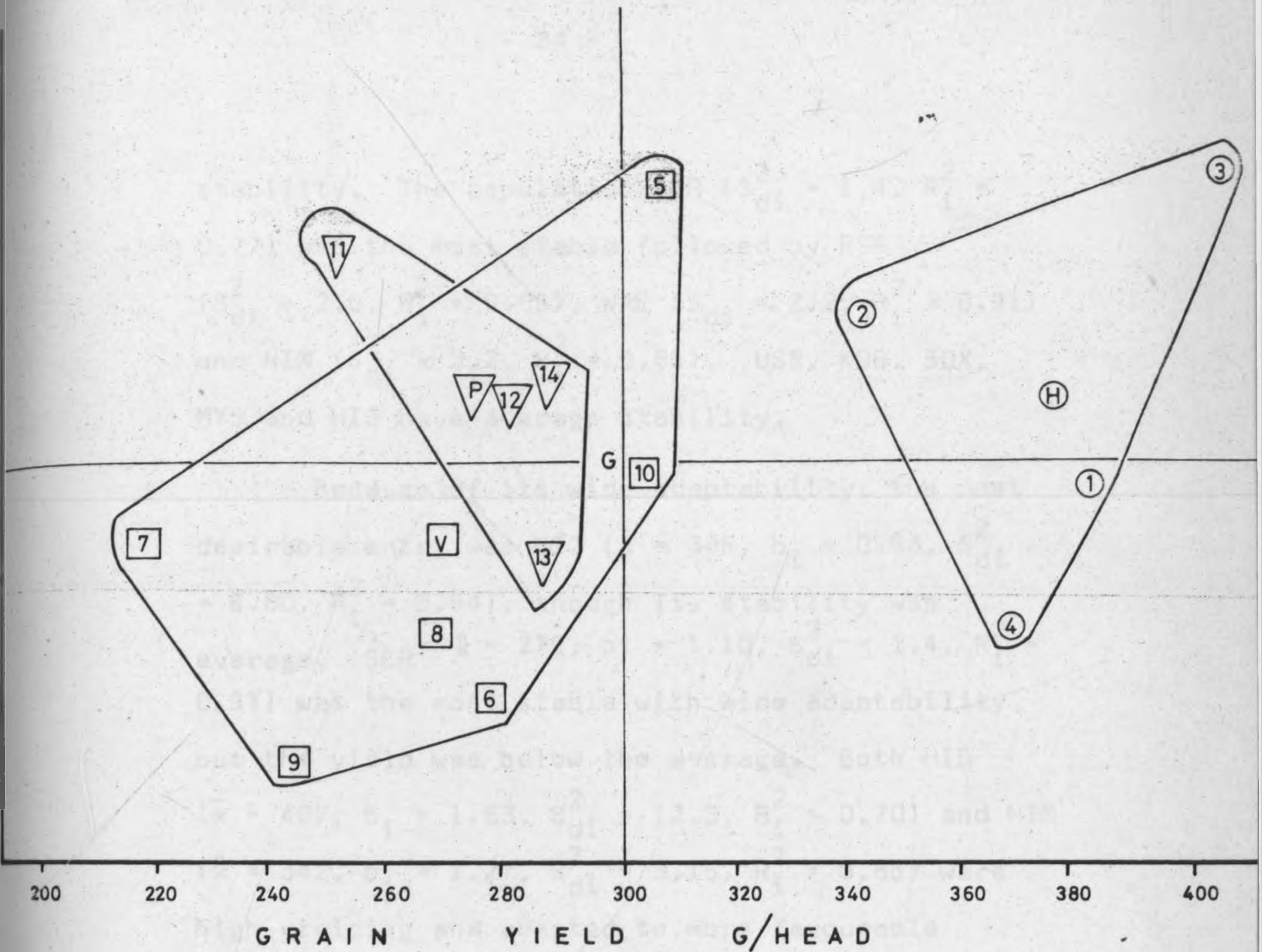


FIG. 8.

The relationship of genotype adaptation (regression coefficient) to grain yield/ head. The numerical numbers 1 to 14 correspond to the genotypes listed in Table 17.

stability. The population SER (S^2_{di} = 1.4, R^2_i = 0.77) was the most stable followed by RSR (S^2_{di} = 2.0, R^2_i = 0.89), WAE (S^2_{di} = 2.2, R^2_i = 0.91) and HIM (S^2_{di} = 3.2, R^2_i = 0.86). USR, KOB, 5DX, MY5 and HIJ have average stability.

Because of its wide adaptability, the most desirable entry was HIJ ($\bar{x}$ = 386, b_i = 0.98, S^2_{di} = 6.80, R^2_i = 0.64), though its stability was average. SER $\bar{x}$ = 279, bi = 1.10, S^2_{di} = 1.4, R^2_i = 0.91) was the most stable with wide adaptability, but the yield was below the average. Both HIB ($\bar{x}$ = 407, b_i = 1.53, S^2_{di} = 12.3, R^2_i = 0.70) and HIM ($\bar{x}$ = 342, b_i = 1.27, S^2_{di} = 3.15, R^2_i = 0.86) were high yielding and adapted to more favourable environments, but their stability, particularly of HIB, was poor.

<u>Days to 50% flowering</u>

Two hybrids, HIJ and HIM were found to be well adapted to unfavourable environments (b_i = 0.43 in both cases) and were early flowering ($\bar{x}$ = 56.6 and 58.4 respectively), while the two populations RSR and SER were more adapted to the favourable environments (b_i = 1.50 in both cases) and were also early ($\bar{x}$ = 58.9 and 59.0 respectively). On the other

Table 18. Mean and stability parameters estimates from the regression model for days to 50% flowering

Genotypes (G)		Mean	Coef. of Det.	Regression coefficient		Deviation from
		$\bar{x}$	R_i^2	Phenotypic b_i	Genotypic B_i	reg. S^2_{di}
Hybrids (H)						
1.	HIJ	56.6(1)	0.47*(9)	0.43*(13)	-0.57**	21(1)
2.	HIM	58.4(2)	0.40*(10)	0.43*(14)	-0.57*	27(3)
3.	HIB	60.0(7)	0.64**(3)	0.91**(5)	-0.09	43(5)
4.	KAF	61.3(10)	0.47*(8)	0.69*(10)	-0.31	51(6)
	mean	58.8	0.68**	0.61	-0.39	
Varieties (V)						
5.	5DX	59.7(6)	0.77**(2)	0.98**(3)	-0.02	27(4)
6.	MY5	60.0(8)	0.20(14)	0.84(6)	-0.16	267(13)
7.	2K9	60.4(9)	0.27(12)	1.02(2)	0.02	264**(12)
8.	9DX	64.5(13)	0.34(11)	1.18(8)	0.18	252**(11)
9.	2K1	64.2(12)	0.25(13)	1.06(4)	0.06	314**(14)
10.	KOB	64.9(14)	0.49*(7)	1.17*(7)	0.17	137**(8)
	mean	64.2	0.72**	1.04	0.04	
Populations (P)						
11.	WAE	59.2(5)	0.62**(4)	1.01**(1)	0.01	60*(7)
12.	SER	59.0(4)	0.60**(5)	1.50**(11)	0.50	140**(9)
13.	USR	61.5(11)	0.85**(1)	1.26**(9)	0.26	26(2)
14.	RSR	58.9(3)	0.59**(6)	1.50**(12)	0.50	148**(10)
	mean	59.7	0.71**	1.31	0.31	
Mean		60.5				

Ranks are given in parenthesis

** significant at P = 0.01

* significant at P = 0.05

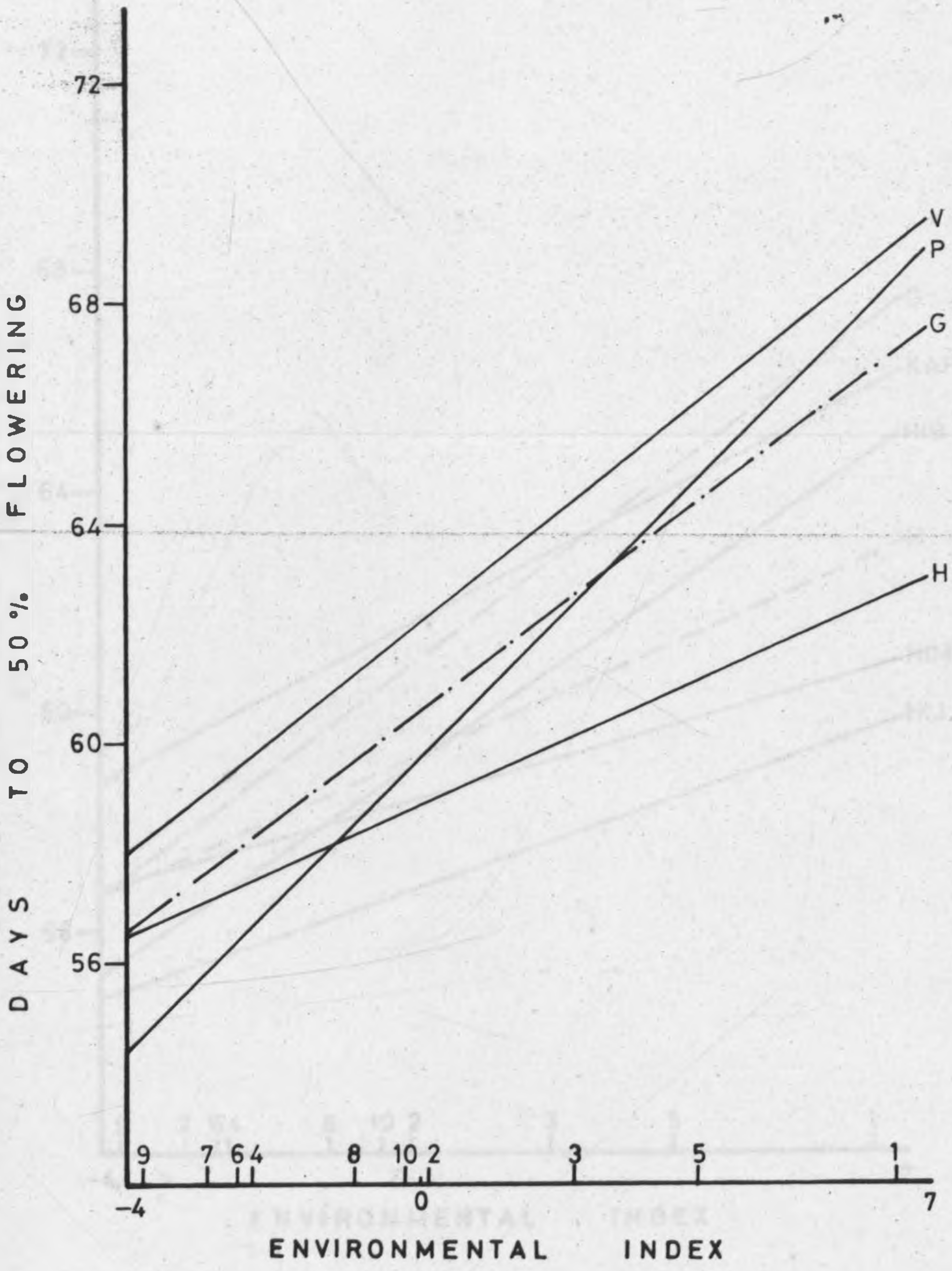


FIG. 9(a) Regression lines for mean number of days to 50 flowering showing the relationship of means of hybrids (H), Varieties (V) and Population (P) and mean of all genotypes (G). The environments 1 to 10 on the X axis correspond to those in Table 10.

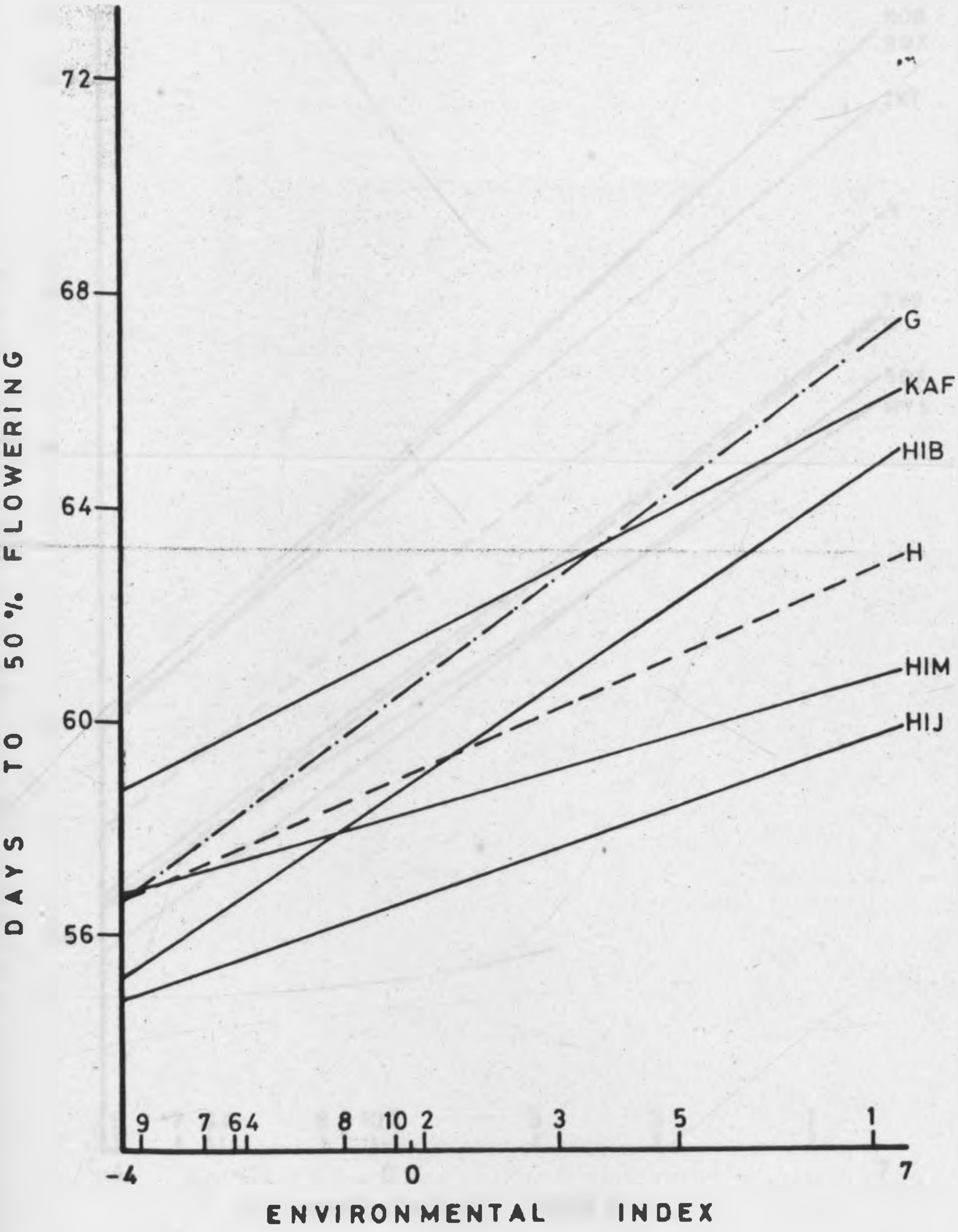


FIG. 9(b)

Regression lines for mean number of days to 50% flowering showing the relationship of individual hybrids, mean of all hybrids (H) and mean of all genotypes (G). The environments 1 to 10 on the x axis correspond to those in Table 10.

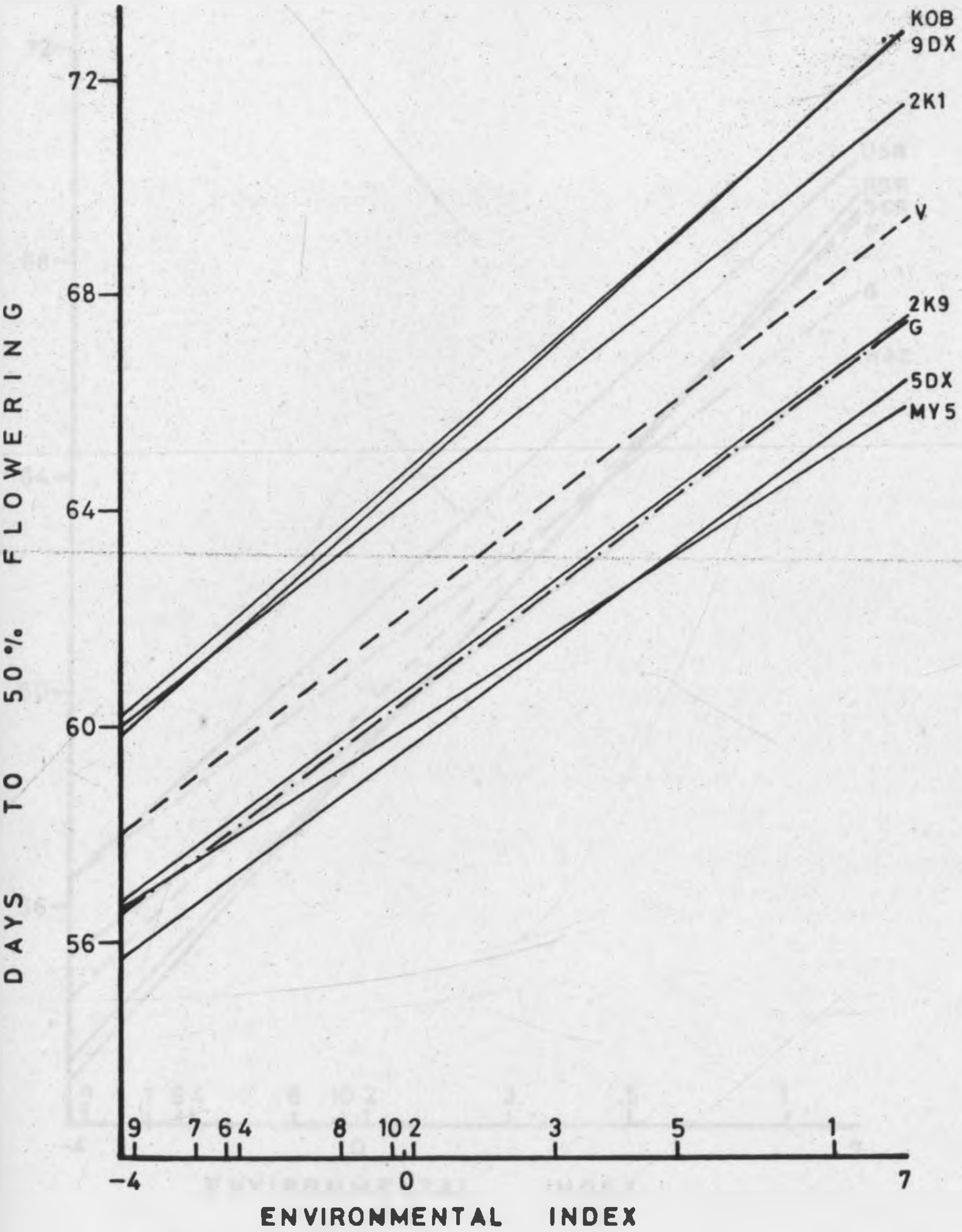


FIG. 9(c)

Regression lines for mean number of days to 50% flowering showing the relationship of individual varieties, mean of all varieties (V) and mean of all genotypes (G). The environments 1 to 10 on the X axis correspond to those in Table 10.

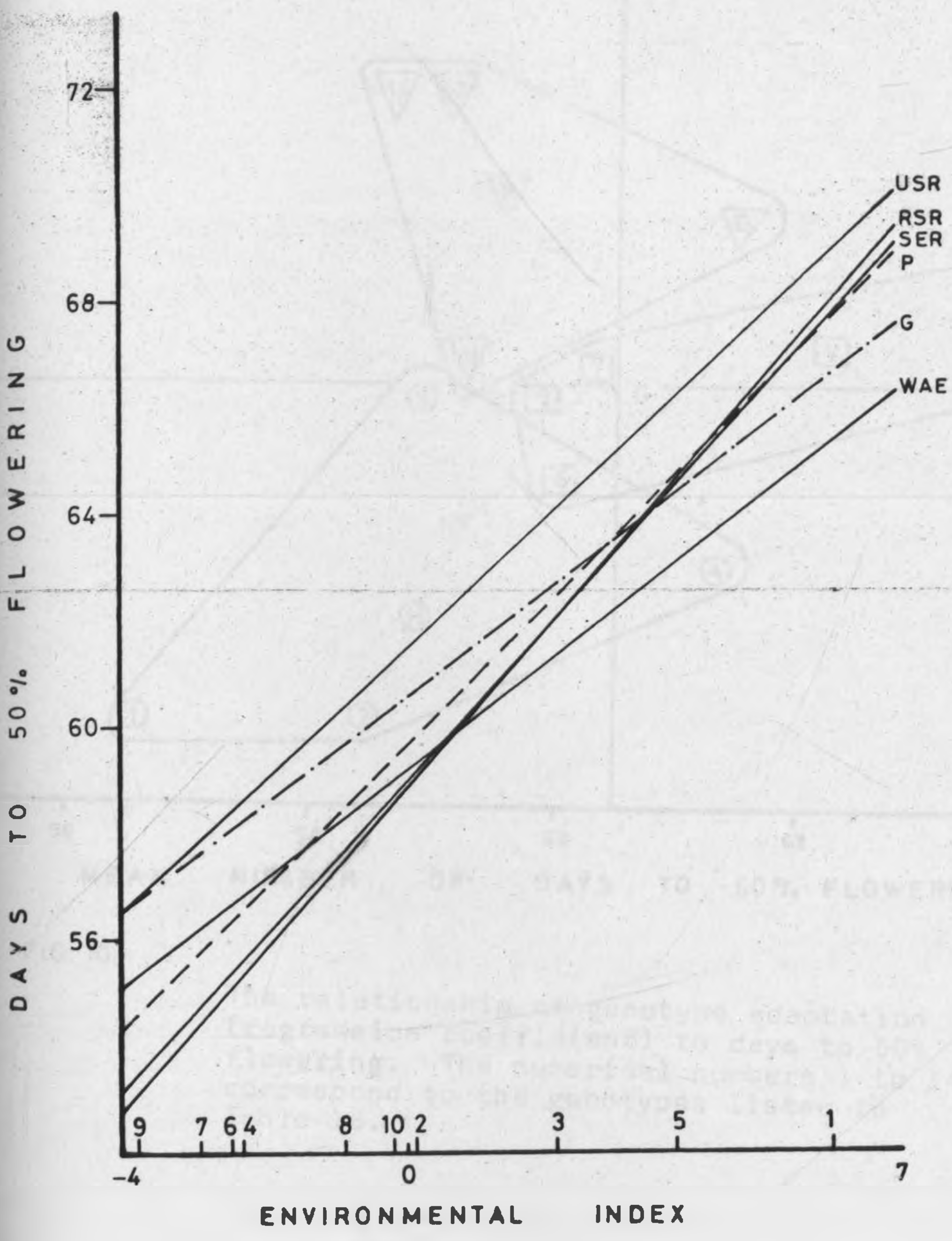


FIG. 9(d)

Regression lines for mean number of days to 50% flowering showing the relationship of individual populations, mean of all populations (P) and mean of all genotypes (G). The environments 1 to 10 on the X axis correspond to those in Table 10.

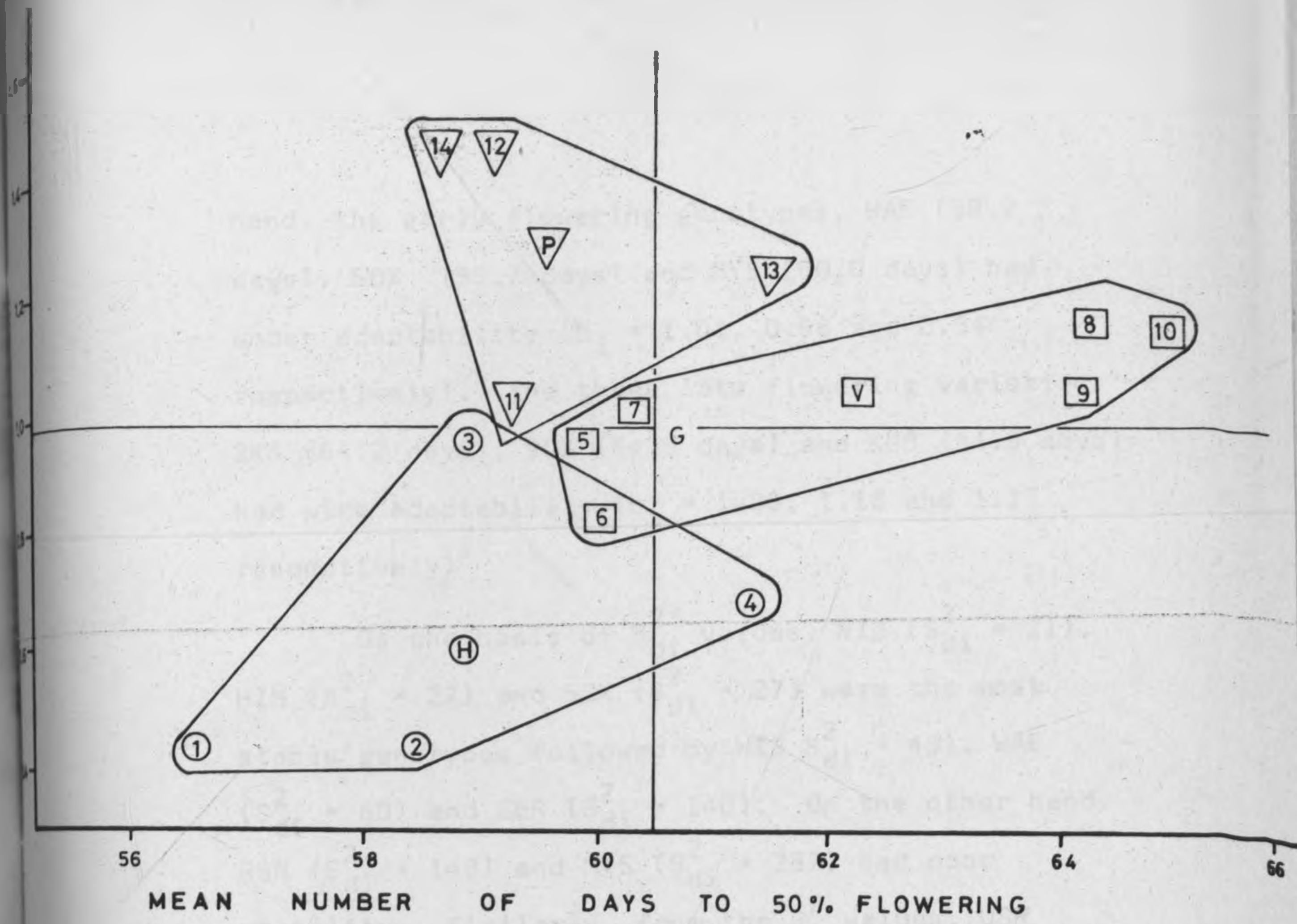


FIG. 10.

The relationship of genotype adaptation (regression coefficient) to days to 50% flowering. The numerical numbers 1 to 14 correspond to the genotypes listed in Table 18.

hand, the early flowering genotypes, WAE (59.2 days), 5DX (59.7 days) and MY5 (60.0 days) had under adaptability (b_i = 1.01, 0.98 and 0.84 respectively). The three late flowering varieties, 2K1 (64.2 days), 9DX (64.5 days) and KOB (64.9 days) had wide adaptability (b_i = 1.06, 1.18 and 1.17 respectively)

On the basis of S_{di}^2 values, HIJ (S_{di}^2 = 21), HIM (S_{di}^2 = 27) and 5DX (S_{di}^2 = 27) were the most stable genotypes followed by HIB S_{di}^2 = 43), WAE (S_{di}^2 = 60) and SER (S_{di}^2 = 140). On the other hand, RSR (S_{di}^2 = 148) and MY5 (S_{di}^2 = 267) had poor stability. Similarly, from the R_i^2 values, USR (R_i^2 = 0.85) was the most stable genotype followed by 5DX, HIB, WAE, SER and RSR (R_i^2 = 0.77, 0.64, 0.62, 0.60 and 0.59 respectively). HIJ, HIM and MY5 had poor stability (R_i^2 = 0.47, 0.40 and 0.20 respectively).

Based on the adaptability and stability parameters, the early flowering hybrids, HIJ ($\bar{x}$ = 56.6, b_i = 0.43, S_{di}^2 = 20.6, R_i^2 = 0.47) and HIM ($\bar{x}$ = 58.4, b_i = 0.43, S_{di}^2 = 26.7, R_i^2 = 0.40) were found to be adapted to the more unfavourable environments i.e. where the minimum temperatures are lower. This indicates that these hybrids have cold tolerance, and moreover, they are quite stable. The other desirable genotypes which have wider adaptability are 5DX ($\bar{x}$ = 59.7, b_i = 0.98, S^2_{di} = 27.34, R^2_i = 0.20), WAE ($\bar{x}$ = 59.2, b_i = 1.01, S^2_{di} = 60.43, R^2_i = 0.62) and HIB ($\bar{x}$ = 59.9, b_i = 0.91, S^2_{di} = 43.00, R^2_i = 0.64).

Mean Plant Height

In terms of deviation of b_i from unity, it was minimum in HIJ (B_i = 0.01), WAE (B_i = 0.01), HIM (B_i = 0.08) and MY5 (B_i = -0.10), showing that these genotypes had wide adaptability. 2K1 (B_i = -0.51), KOB (B_i = -0.41) and 5DX (B_i = -0.25) were more adapted to the unfavourable environments. The heights of HIM, RSR, RSR, MY5 and KAF showed very good stability as compared to others, while 2K1, KOB, HIJ, HIB, WAE and SER had poor stability.

Two genotypes, MY5 ($\bar{x}_i$ = 123.5, b_i = 0.91, S^2_{di} = 468, R^2_i = 0.89) and HIM ($\bar{x}_i$ = 137.5, b_i = 1.08, S^2_{di} = 431, R^2_i = 0.93) had the best stability and were well adapted, though both are slightly taller. Inspite of being tall, HIJ ($\bar{x}_i$ = 138.7, b_i = 1.00, S^2_{di} = 1849, R^2_i = 0.71) and WAE ($\bar{x}_i$ = 140.3, b_i = 1.01, S^2_{di} = 2071, R^2_i = 0.69) had very wide

Table 19. Mean and stability parameters estimates from the regression model for mean plant height

Genotypes (G)		Mean $\bar{x}$	Coef. of Det. R_i^2	Regression coefficiient		Deviation from Reg. S^2_{di} ($\times 10^2$)
				Phenotypic b_i	Genotypic B_i	
Hybrids (H)						
1.	HIJ	138.7(9)	0.71**(11)	1.00**(1)	0.001	1.85**(13)
2.	HIM	137.5(6)	0.93**(2)	1.08**(3)	0.08	0.43 (1)
3.	HIB	143.3(13)	0.84**(8)	1.17**(7)	0.17	1.18*(11)
4.	KAF	138.5(8)	0.90**(3)	1.13**(6)	0.13	0.66(4)
	mean	139.5	0.93**	1.09	0.09	
Varieties (V)						
5.	SDX	133.3(5)	0.75**(10)	0.76**(11)	-0.25	0.86(6)
6.	MY5	123.5(3)	0.89**(4)	0.91**(5)	-0.10	0.47(3)
7.	2K9	137.9(7)	0.86**(6)	1.22**(10)	0.22	1.07(9)
8.	9DX	133.0(4)	0.85**(7)	0.92**(4)	-0.09	0.67(5)
9.	2K1	110.3(1)	0.49*(14)	0.49*(14)	-0.51**	1.11*(10)
10.	KOB	114.5(2)	0.63**(13)	0.59*(13)	-0.41**	0.89(8)
	mean	125.4	0.90**	0.81	-0.19	
Populations (P)						
11.	WAE	140.3(10)	0.69**(12)	1.01**(2)	0.01	2.07**(14)
12.	SER	155.2(14)	0.83**(9)	1.18**(8)	0.18	1.28*(12)
13.	USR	142.9(11)	0.88**(5)	1.22**(9)	0.22	0.89(7)
14.	RSR	143.3(12)	0.95**(1)	1.35**(12)	0.35**	0.46(2)
	mean	144.6	0.93**	1.19	0.19	
Mean		135.2				

Ranks are given in parenthesis
**significant at P = 0.01
*significant at P = 0.05

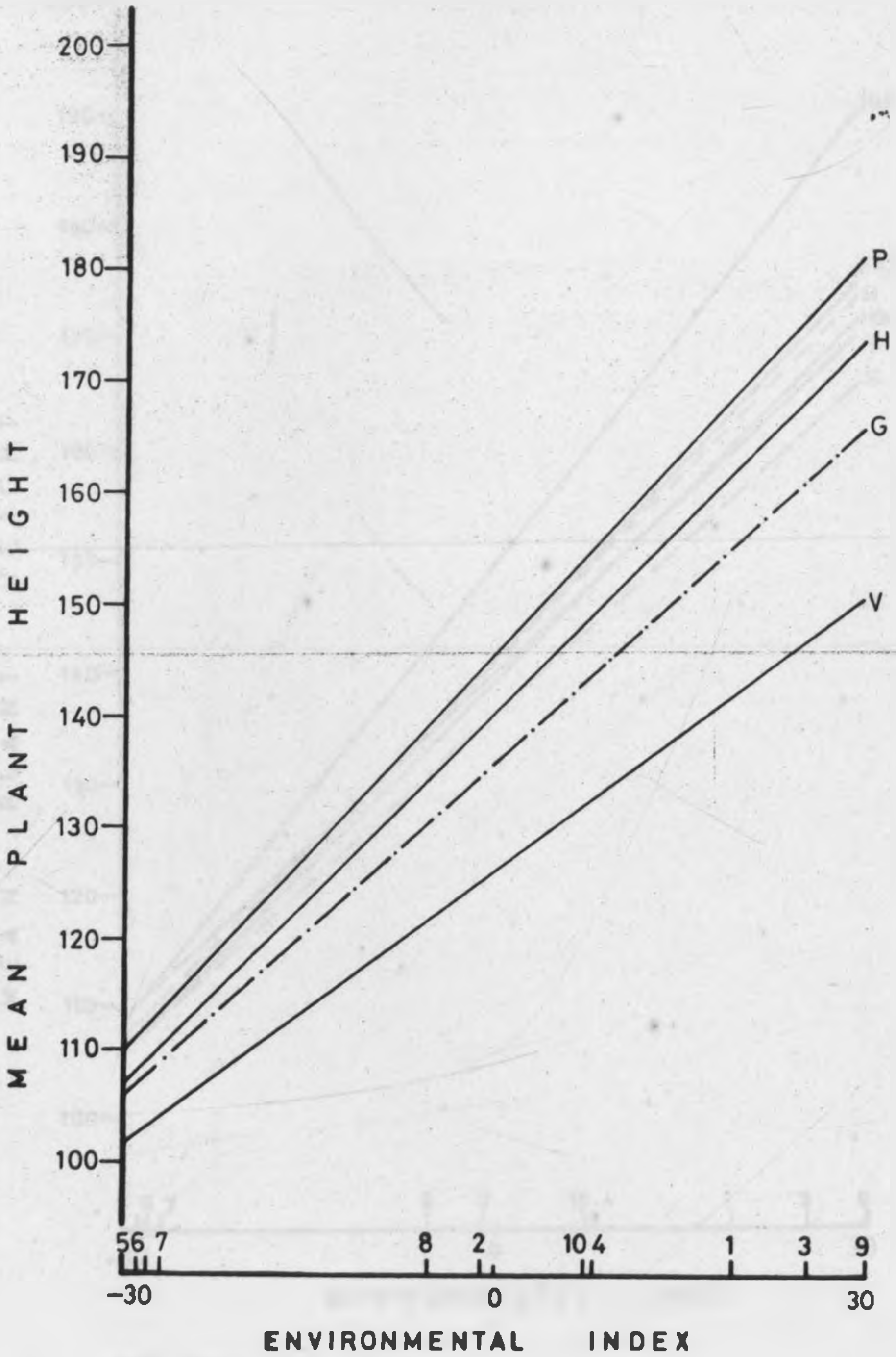


FIG. 11(a)

Regression lines for mean plant height showing the relationship of means of hybrids (H), varieties (V) and populations (P) and mean of all genotypes (G). The environments 1 to 10 on the X axis correspond to those in Table 10.

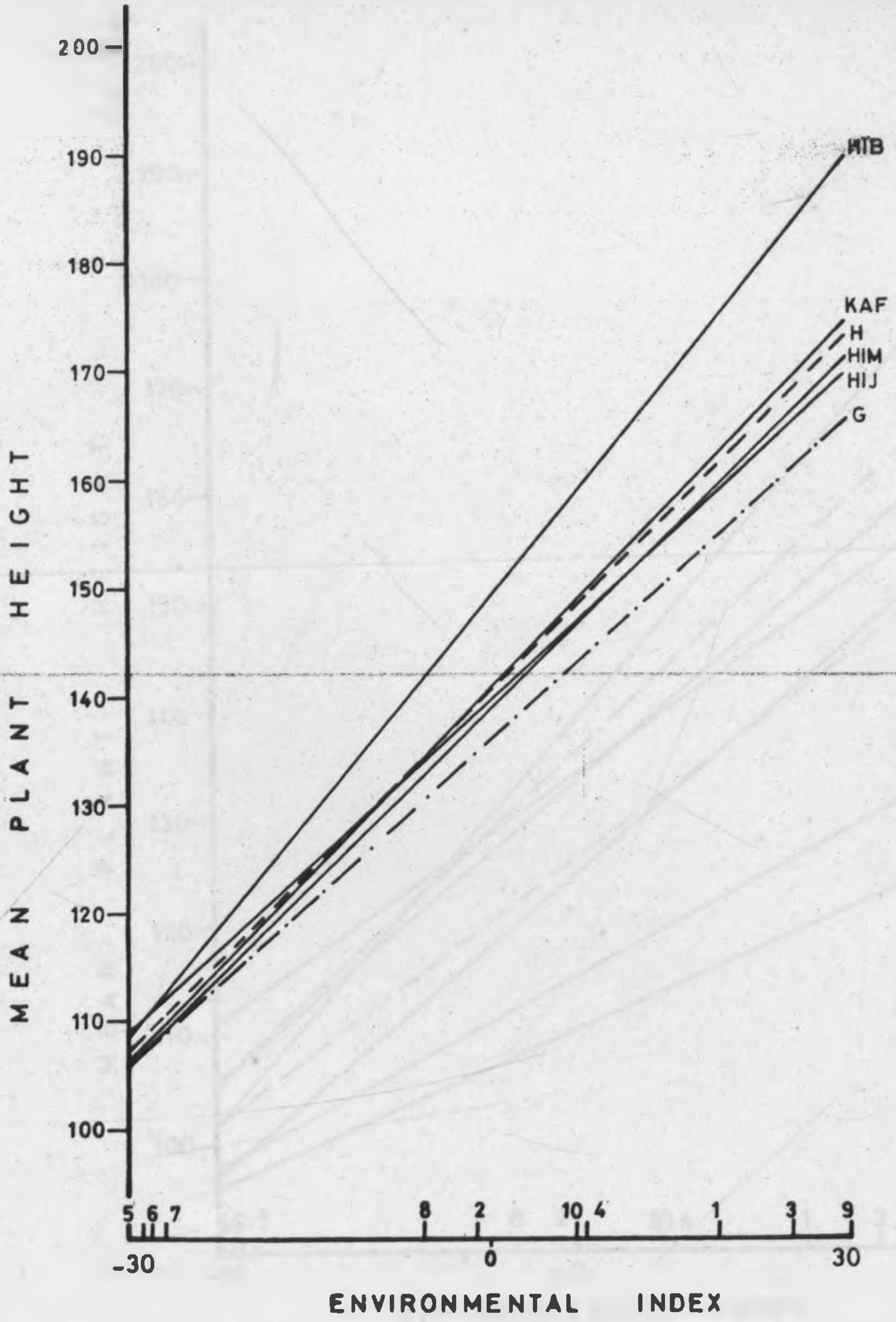


FIG. 11(b)

Regression lines for mean plant height showing the relationship of individual hybrids, mean of all hybrids (H) and mean of all genotypes (G). The environment 1 to 10 on the X axis correspond to those in Table 10.

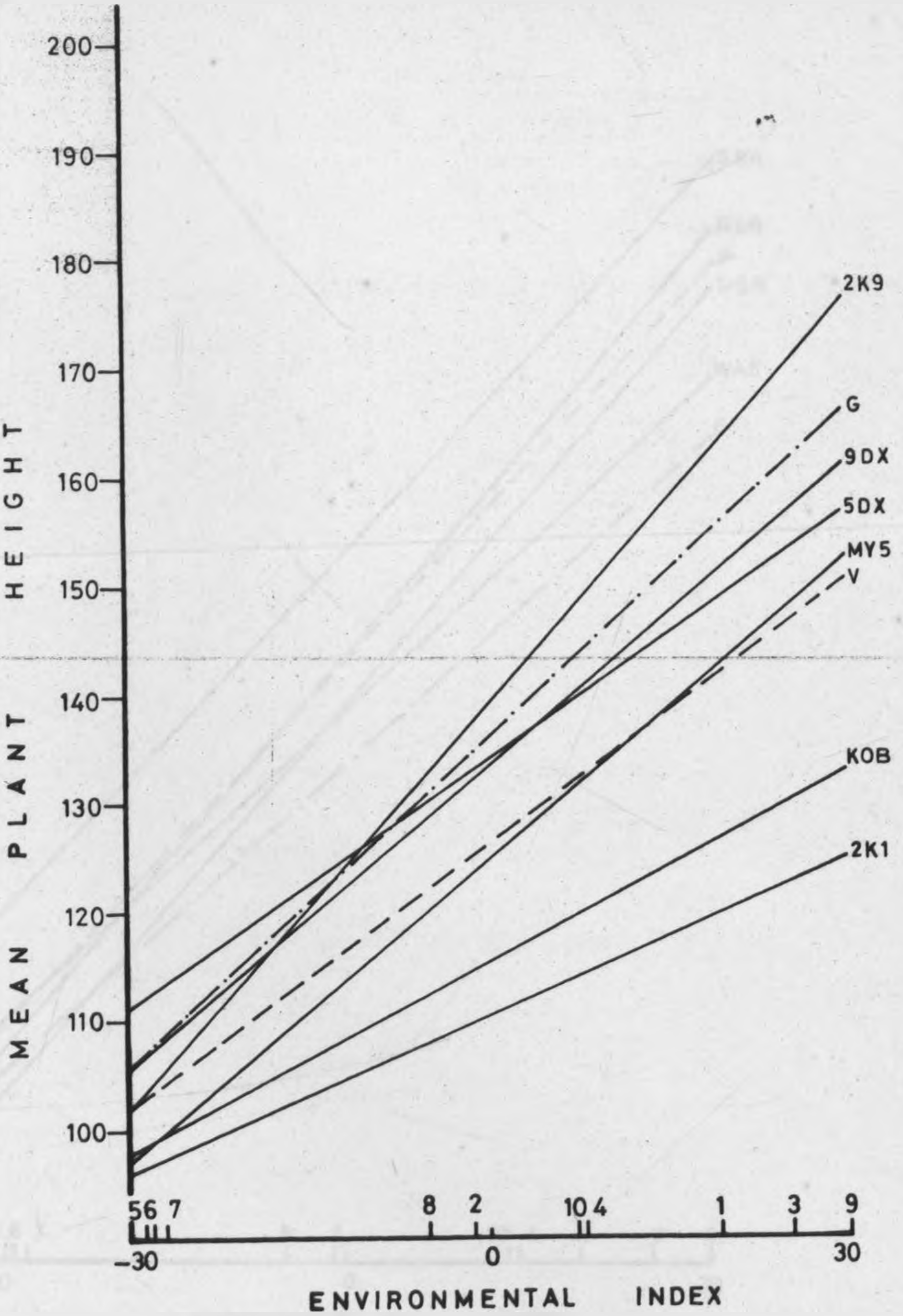


FIG. 11(c)

Regression lines for mean plant height showing the relationship of individual varieties, mean of all varieties (V) and mean of all genotypes (G). The environments 1 to 10 on the X axis correspo to those in Table 10.

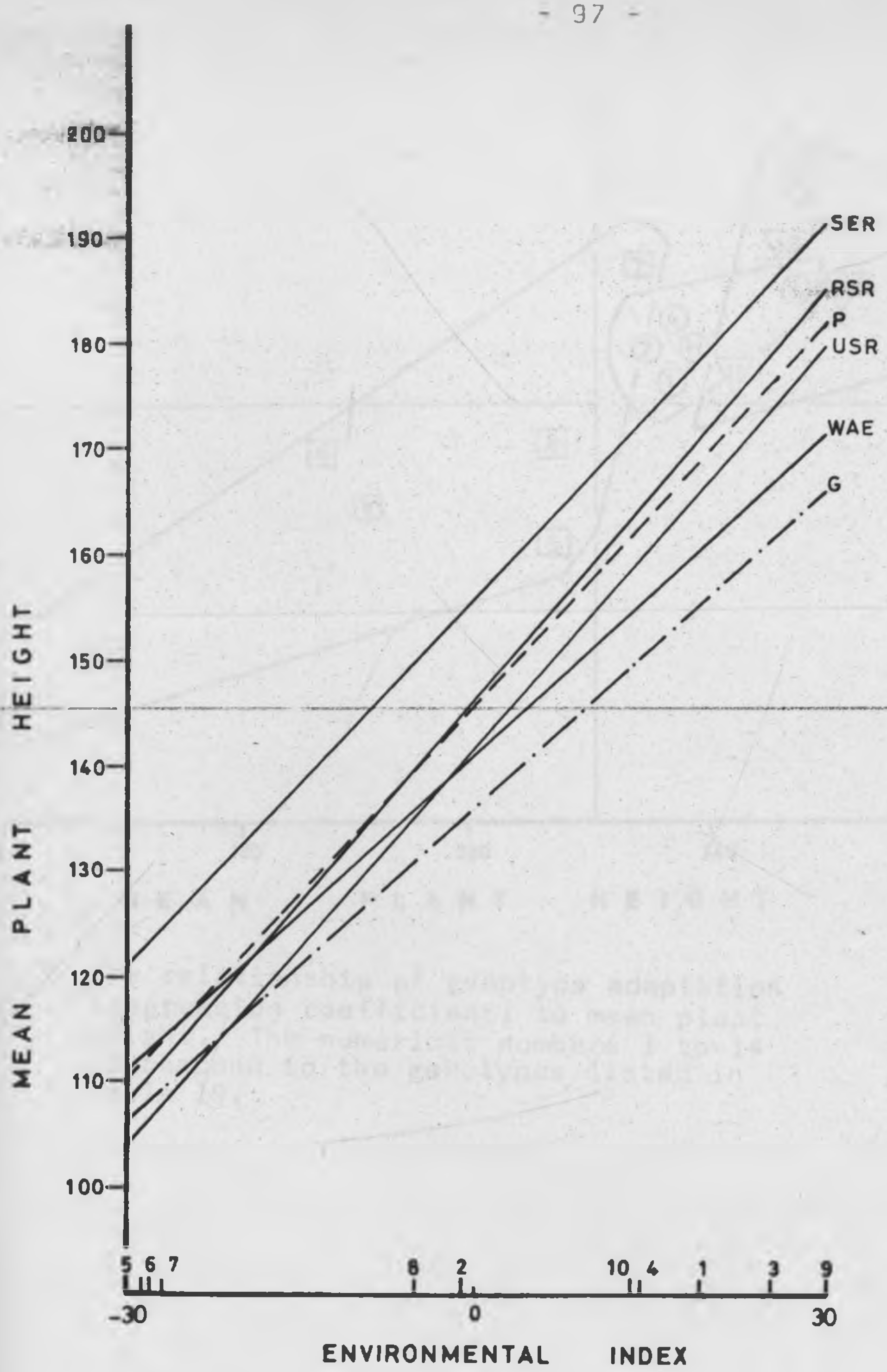


FIG. 11(d) Regression lines for mean plant height showing the relationship of individual populations, mean of all populations (P) and mean of all genotypes (G). The environments 1 to 10 on the X axis correspond to those in Table 10.

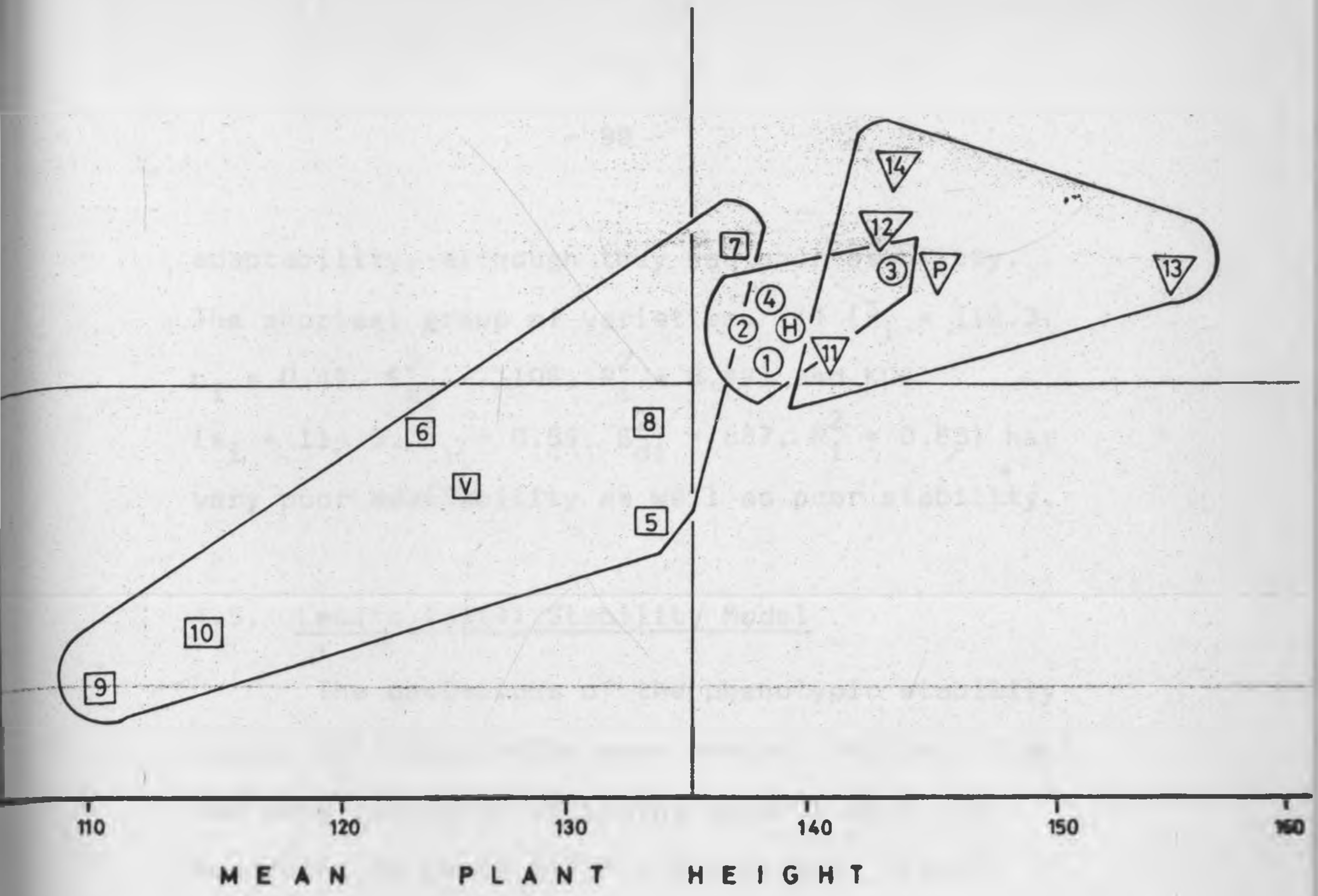


FIG. 12. The relationship of genotype adaptation (regression coefficient) to mean plant height. The numerical numbers 1 to 14 correspond to the genotypes listed in Table 19.

adaptability, although they had poor stability. The shortest group of varieties, 2K1 ($\bar{x}_i$ = 110.3, b_i = 0.49, S^2_{di} = 1106, R^2_i = 0.49) and KOB ($\bar{x}_i$ = 114.5, b_i = 0.59, S^2_{di} = 887, R^2_i = 0.63) had very poor adaptability as well as poor stability.

4.5. Lewi's (1954) Stability Model

The deviations of the phenotypic stability factor (SF) from unity were derived for each trait and were ranked in ascending order (Table 20). According to Lewis (1954), the greater the SF deviates from unity, the less stable is the phenotype.

For yield/plot, HIB was the most stable (deviation of SF from unity = 1.62) followed by KAF (1.68), HIJ (1.72) and MY5 (2.07). On the other hand, for grain yield/head, HIJ was most stable (2.14) followed by MY5 (2.54). KAF (3.73) and HIM (7.87) had poor stability. Similarly, in case of days to 50% flowering, HIJ (0.11) was the most stable followed by HIM (0.13) and KAF (0.16). MY5 had poor stability (0.36). For mean plant height, 2K1 (0.37), 5DX (0.62) and HIJ (0.67) were most stable, while KAF (0.89), HIM (0.74) and HIB (0.73) had poorer stability. Overall, HIJ was the most stable followed

Table 20. Deviation of phenotypic stability factor from unity

Genotype	Grain yield per plot	Grain yield per head	Days to 50% flowering	Mean plant height
Hybrids				
HIJ	1.72(3)	2.14(1)	0.11(1)	0.67(3)
HIM	4.00(6)	7.87(12)	0.13(2)	0.74(9)
HIB	1.62(1)	2.18(6)	0.23(5)	0.73(8)
KAF	1.68(2)	3.73(8)	0.16(3)	0.89(13)
Varieties				
5DX	4.24(9)	10.7(14)	0.22(4)	0.62(2)
MY5	2.07(4)	2.54(2)	0.36(10)	0.71(6)
2K9	5.38(11)	3.69(7)	0.48(14)	0.80(12)
9DX	6.89(13)	9.22(13)	0.32(8)	0.72(7)
2KT	5.86(12)	4.53(9)	0.46(13)	0.37(1)
KOB	4.39(10)	4.73(10)	0.33(9)	0.69(5)
Populations				
WAE	7.26(14)	7.49(11)	0.29(6)	0.76(11)
SER	3.28(5)	2.82(4)	0.41(11)	0.67(4)
USR	4.04(7)	2.65(3)	0.30(7)	0.74(10)
RSR	4.06(8)	3.15(5)	0.46(12)	0.90(14)

Ranks according to magnitude in assending order are given in parenthesis.

by HIB and MY5.

4.6. Wrickle's Stability Model

The values of ecovalence (W_i) were calculated for each genotype with respect to all the characters and are given in Table 21. These values were further used to calculate the percentage of G x E that they represent in each genotype and are given in Table 22. Lower the W_i, the smaller are its fluctuations from the experimental mean under different environments and thus have a smaller share in the interaction SS. Hence, the genotype with minimum W_i (or W_i as a percentage of G x E SS) is more stable, while those with higher values have poor stability. The stability factors of genotypes have been ranked in ascending order according to their magnitude.

In general, for grain yield/plot and grain yield/head, all the populations were more stable (representing between 4.2 and 1.0% of G x E) as compared to varieties (17.3 to 1.9% of G x E), while the hybrids had moderate stability (15.6 to 4.0% of G x E). HIJ showed very poor stability with respect to grain yield/plot and represented about

Table 21. Wrickle's stability parameter (W_i)

Genotypes		Grain yield per plot	Grain yield per head (x 10^5)	Days to 50% flowering	Mean plant height (x 10^2)
Hybrids					
HIJ		1.13	0.68	51.0	1.85
HIM		0.40	0.40	57.1	0.46
HIB		0.37	1.57	43.8	1.30
KAF		0.71	1.15	59.3	0.73
	mean	0.65	0.95	52.8	1.08
Varieties					
5DX		0.44	1.03	27.3	1.12
MY5		0.42	0.77	269	0.51
2K9		0.46	0.19	264	1.30
9DX		1.27	1.58	255	0.71
2K1		1.09	1.18	315	2.29
KOB		0.26	0.47	140	1.66
	mean	0.66	0.87	212	1.26
Populations					
WAE		0.31	0.39	60.4	2.07
SER		0.16	0.15	163	1.43
USR		0.21	0.29	32.3	1.10
RSR		0.08	0.22	172	1.00
	mean	0.19	0.26	107	1.40
Mean		0.52	0.72	136	1.25

Table 22. Wrickle's value as % of G x E SS

Genotypes		Grain yield per plot	Grain yield per head	Days to 50% flowering	Mean plant height
Hybrids					
HIJ		15.4(13)	6.7(8)	2.7(4)	10.6(12)
HIM		5.5(7)	4.0(6)	3.0(5)	2.6(1)
HIB		5.0(6)	15.6(13)	2.3(3)	7.4(8)
KAF		9.7(11)	11.5(11)	3.1(6)	4.1(4)
	mean	8.9	9.4	2.8	6.2
Varieties					
5DX		6.0(9)	10.2(10)	1.4(1)	6.4(7)
MY5		5.8(8)	7.6(9)	14.1(13)	2.9(3)
2K9		6.2(10)	1.9(2)	13.8(12)	7.4(9)
9DX		17.3(14)	15.6(14)	13.4(11)	4.0(3)
2K1		14.8(12)	11.7(12)	16.5(14)	13.1(14)
KDB		3.6(4)	4.7(7)	7.3(8)	9.5(11)
	mean	9.0	8.6	11.1	7.2
Populations					
WAE		4.2(5)	3.9(5)	3.2(7)	11.8(13)
SER		2.1(2)	1.5(1)	8.5(9)	8.1(10)
USR		2.8(3)	2.8(4)	1.7(2)	6.3(6)
RSR		1.0(1)	2.2(3)	9.0(10)	5.7(5)
	mean	2.5	2.6	5.6	8.0

Ranks according to magnitude in assending order are given in parenthesis.

15.4% of G x E, as compared to populations, each of which represented 1.0 to 4.2% only. For grain yield/plot, the best hybrid, HIB and the best variety, KOB represented 5.0% and 3.6% of G x E respectively. Similarly, with respect to grain yield/head, HIB had very poor stability (15.6% of G x E) compared to the populations (between 1.5 and 3.9% of G x E) and the best variety, 2K9 (1.9% of G x E). HIJ represented 6.7% of G x E.

On the other hand, for days to 50% flowering, all hybrids showed good stability (representing 2.3 to 3.1% of G x E). The most stable entry was a variety, 5DX (1.4% of G x E)followed by USR (1.7% of G x E). With respect to mean plant height, the entries with good stability are HIM, MY5 and 9DX (% of G x E = 2.6%, 2.9% and 4.0% respectively), while HIB and HIJ did not have the desired stability (% of G x E = 7.4% and 10.6% respectively).

4.7. Rank Correlations

The ranked correlation coefficients between the different stability parameters (Table 23), indicates that for all the characters under consideration, there is a highly significant correlation between the ranks of W_i and R_i^2

Table 23. Rank correlation coefficients between different stability parameters

Parameters			Grain yield per plot	Grain yield per head	Days to 50% flowering	Mean plant height
$\bar{X}_i$	VS	SF	0.69**	0.13	0.38	0.42
$\bar{X}_i$	VS	W_i	0.17	-0.27	0.31	0.05
$\bar{X}_i$	VS	R^2_i	0.19	-0.08	0.18	-0.28
$\bar{X}_i$	VS	b_i	-0.22	0.07	-0.41	-0.22
$\bar{X}$	VS	S^2_i	0.27	-0.37	0.42	0.30
SF	VS	W_i	0.09	0.34	0.78**	-0.39
SF	VS	R^2_i	-0.05	-0.01	0.33	-0.69*
SF	VS	b_i	-0.08	0.36	-0.35	-0.14
SF	VS	S^2_i	0.14	0.29	0.85**	-0.03
W_i	VS	R^2_i	0.91**	0.83**	0.78**	0.86**
W_i	VS	b_i	0.41	0.65*	-0.18	0.24
W_i	VS	S^2_{di}	0.98**	0.99*	0.94**	0.88**
R^2_i	VS	b_i	0.27	0.35	0.03	0.17
R^2_i	VS	S^2_{di}	0.93**	0.84**	0.63*	0.77**
b_i	VS	S^2_{di}	0.29	0.56*	-0.39	0.11

**significant at P = 0.01

*significant at P = 0.05

(r = 0.78 to 0.91) and R_i^2 and S_{di}^2 (r = 0.63 to 0.93). In case of grain yield/head, the ranks of W_i and b_i (r = 0.65*) and b_i and S_{di}^2 (r = 0.56*) were significant. For days to 50% flowering, the ranks of SF were significantly correlated with the ranks of both W_i (r = 0.78**) and S_{di}^2 (r = 0.85**). Similarly, for plant height, there was a significant negative correlation between the ranks of SF and R_i^2 (r = -0.69*). There was a highly significant correlation between the ranks of $\bar{X}_i$ and SF for grain yield/plot (r = 0.69**).

Taking into consideration the general trend of rank correlations, there was a highly significant positive correlation between the ranks of W_i, R_i^2 and S_{di}^2, indicating that these three parameters are equally effective in estimating the genotype stability.

CHAPTER V

DISCUSSIONS

5.1. Mean Performance of Genotypes

The major objective of sorghum breeding in the medium agricultural potential areas of Kenya is to develop high yielding, early maturing and short to medium statured stable genotypes. Since rainfall is the limiting factor in these areas, it is desirable to select genotypes which can flower within 60 days from emergence and escape moisture stress. This would also help to reduce the exposure period to diseases and pests. For plant height, emphasis should be given on short to medium heights, to prevent lodging, allow for better management and higher populations and are also easier for bird scaring.

For grain yield/plot, over all environments, hybrids ranked first followed by populations and varieties. Infact, in each environment except ITH LR, KYM SR and MTW LR, the highest yielding entry was a hybrid. Among the hybrids, HIJ and HIB performed the best; among the varieties, MY5 was the best; while among the populations, SER and RSR were the best. When comparing the best hybrid with the genotype mean, in each environment, the difference ranged from 115% in case of KAT LR to 2% in case of MTW LR. Only in case of ITH LR, the difference was almost nil. On the average, the best hybrid (HIJ) yielded 27% above the genotype mean. On comparing the best hybrid with the best variety (MY5), the hybrid yielded 20% above the variety mean overall the environments. This difference ranged from 58% at MTW SR to 8% at ITH SR. Only at KYM SR, ITH LR and MTW LR, the performance of the hybrid was 20%, 24% and 31% respectively below the best variety.

Over all the environments, the hybrids were earliest, followed by populations and varieties. HIJ was the earliest among all the hybrids. Only KAF was late among all the hybrids and only USR was late among all the populations. Within the varieties, 5DX, MY5 and 2K9 were early. Among the genotypes included in this trial, the varieties were shortest followed by hybrids and populations. On basis of mean over all environments, the varieties 2K1, KOB and MY5 are shortest. Within hybrids, HIM is the shortest and WAE is shortest among populations.

The genotypes were tested in the medium agricultural potential areas where the main limiting factor is the available soil moisture during the cropping season. From the data presented above, it appears that these hybrids are more efficient in utilizing the available soil moisture than the populations and varieties. It may also be because of early flowering and medium plant height, as these traits may help to enhance the grain productivity of the plant under such conditions.

5.2. G x E Effects

For all traits, the G x S x L was highly significant and also the most important variance component of G x E. This indicates that the genotypes responded differently when grown under different environments. On taking into consideration the pattern of climatic distribution, management of trials and pests, especially bird, damage in each environment, they were found not to be consistent at any location for both seasons or for all locations in any season. Hence, consistent location and season effects are absent. In all previous studies in sorghum G x E has been reported to be highly significant. A major role of G x S x L variance component has been reported by Liang and Walter (1966), Kambal and Mahmoud (1978) and Obilana and El-Rouby (1980). Although, Rao (1970) reported that for grain yield/plot, days to 50% flowering and mean plant height, the G x L component was more important than G x S x L component.

The lack of significant G x S for all traits except days to 50% flowering in this study indicates that the relative performance of the genotypes was essentially similar in both seasons of testing. Similar results were reported by Liang and Walter (1966) and Obilana and El-Rouby (1980) for grain yield, while Kambal and Mahmoud (1978) and Rao (1970) reported it as not significant. A significant G x L interaction for sorghum grain yield has been reported by Liang and Walter (1966), Rao (1970), Jowett (1972), Kambal and Mahmoud (1978) and Obilana and El-Rouby (1980). In contrast to their findings, the lack of significant G x L for all traits except days to 50% flowering in the present study could be attributed to the similarity of locations at which the experiments were conducted. Hence there would be little advantage to divide the region comprising these locations for breeding and testing purposes. However, for all traits, G x S was found to be of a higher magnitude than G x L indicating that G x S was more important. This is in agreement with Liang and Walter (1966). Although Rao (1970), Kambal and Mahmoud (1978) and Obiliana and El-Rouby (1980) reported that for grain yield/plot, G x L was more important than G x Y component.

As indicated earlier, G x S for days to 50% flowering was highly significant. This indicated that with respect to flowering, the genotypes are influenced by the seasons of long rains (LR) and short rains (SR). G x S appears due to difference in temperatures of the two seasons as indicated by the highly significant negative correlation ($r = -0.83^{**}$) between mean number of days to 50% flowering and mean minimum seasonal temperatures. Similarly, different minimum temperatures of locations appear to be contributing to the significant G x L for days to 50% flowering. Rao (1970) also reported significant G x Y for days to 50% flowering in sorghum.

5.3. Regression Analysis

After the importance of G x E in the present study was established, it was desired to assess the nature of this interaction by means of regression analyses. From the results of the various regression analyses, the following points were deduced.

1) Estimates based on Finlay and Wilkinson's (1963) model, showed that in case of grain yield/plot, about 67% of G x E SS could be attributed to the linear regressions. For other characters it was 70% (for grain yield/head), 83% (for mean plant height) and 45% (for days to 50% flowering).

2) The residual G x E variance component was highly significant in case of all characters. Moreover, its magnitude was higher than the experimental variance (mean error). This implied, that in addition to the experimental variability, there is an additional coefficient of variation in the genotype responses which could be attributed to the deviations from linear regression. The results in this study agree with Majisu and

Doggett (1972), Reich and Atkins (1970) and Jowett (1978) for grain yield/plot. Similar observations have been made by Singhania and Rao (1976 a & b) for grain yield/head, days to 50% flowering, mean plant height and grain yield/plot in case of hybrids only. However, in their studies they found that the pooled deviations were significant for grain yield/plot (hybrids only) and plant height, but were not significant for grain yield/plot (parents only), grain yield/head and days to 50% flowering.

3) The comparison of the linear component of interaction against deviation from regressions as in case of Eberhart and Russell (1966) model and Perkins and Jinks (1968 a & b) model are identical and more valid than comparisons with mean error in case of Finlay and Wilkinson (1963) model. It was shown that with respect to grain yield/plot, the environment played greater role than the genotype. This does not agree with the results of Reich and Atkins (1970), Jowett (1978) and

Majisu and Doggett (1972). This does not however mean that there were no genetically controlled responses in the genotypes used in this study to the different environments for grain yield/plot. This could probably be due to the number of environments in which these genotypes were tested were not adequate to detect the statistical differences. For days to 50% flowering the G x E (linear) SS was not significant, while it is significant for grain yield/head and plant height. This indicates that there are genetic differences among genotypes for their regression on environmental index for plant height and grain yield/head, but not for days to 50% flowering. These results are in agreement with those of Singhania and Rao (1976 b).

4. The significant remainder item (not the heterogeneity between regression item) for grain/plot in the present study indicates that the predictions of G x E based on linear regression cannot be made (Perkins and Jinks, 1968) In case of grain yield/head and days

to 50% flowering, reliable predictions can be made only for some genotypes. However, for plant height, the predictions of G x E based on linear regression will have considerable practical value.

5.4. Adaptability and Stability Parameters

The adaptability, or response of a particular genotype to environments was determined conjointly from its mean performance over all environments ($\bar{x}_i$) and the slope of its regression line (b_i). The stability of this performance, or the ability to show a minimum of interaction with environments was determined as the squared deviations from the regression coefficient (S^2_{di}). The additional stability parameters such as the phenotypic stability factor (SF), ecovalence (W_i) and coefficient of determination (R^2_i) were also estimated.

The rank correlation coefficients between these parameters indicated that the values of W_i, R^2_i and S^2_{di} are equally effective in ranking the stability of genotypes. There was no correlation between b_i and S^2_{di}, and also between S^2_{di} and SF. These results agree partly with the finding of other workers. Jowett (1972) indicated that W_i is less informative than S_{di}^2, while Qualset (1968) reported the absence of any correlation between W_i and S_{di}^2. Prasada and Singh (1980) reported the absence of correlation between W_i and b_i, and between the SF and W_i. Qualset (1968) also found the absence of any correlation between W_i and b_i. The present study does not agree with Prasada and Singh (1980) on similarity between SF and b_i. The SF has some very obvious defects as it does not consider the intermediate environments. The bias introduced as a result of considering only the highest and least performing environments does not warrant the use of this parameter in estabilishing the stability of that genotype. Hence, in the following discussions, in addition to the mean performance $(\bar{x}_i)$, linear regression coefficient (b_i) will be regarded as a measure of adaptability, whereas, only the summed deviations from regressions (S_{di}^2) will be considered as a measure of stability, and the other stability measures will be ignored. The estimates of these parameters have been discussed with respect to the following traits.

Grain Yield/plot

The highest yielding genotype HIJ is specifically adapted to unfavourable environments. On yield basis, this is followed by HIB, SER and MY5 which are well adapted to all environments HIM and RSR are also high yielding, but they are specifically adapted to the favourable environments. Considering the stability of these entries, RSR ranks first followed by SER, HIM and HIB. The stability of MY5 and HIJ is poor. Although the stability of USR, KOB and WAE is good, the adaptability and/or mean yield of these entries is poor. The most desirable entry on the basis of adaptability and stability is HIB followed by SER, RSR, HIM, HIJ and then MY5.

Grain Yield/head

HIJ and KOB are well adapted to all environments. KAF is specifically adapted to unfavourable environments, while HIM, HIB and 5DX are adapted more specifically to the favourable environments. The adaptability of HIB and 5DX is relatively poor. Among these genotypes, USR is most stable followed by HIM, KOB and HIJ. The stability of 5DX, KAF and HIB is poor. SER is well adapted with high stability, but its yield is poor. In general, the most desirable entry is HIJ, followed by KOB, HIM, USR, KAF and then HIB.

Days to 50% Flowering

The hybrids HIJ and HIM are early flowering and are adapted to more unfavourable environments. HIB and WAE are early entries with good adaptation to all environments. The populations RSR and SER are also early and are adapted to more favourable environments. The varieties in general have a good adaptability, but except for 5DX and MY5, they are late. Among the early entries with wide adaptability, HIB is the most stable followed by 5DX, HIM, HIJ and WAE are also very stable. From general point of view, the most desirable entries are HIJ, HIM, 5DX, WAE and HIB. Although HIJ and HIM are more adapted to flower early in unfavourable environments i.e. where minimum temperatures are low, this factor may be considered as an additional attribute.

Mean Plant Height

The hybrids, although of medium height, are well adapted to all environments. All the populations tend to be very tall and except for WAE are poorly adapted. The varieties with the exception of 2K9 are short. 2K1 and KOB are the shortest and, with 5DX are adapted to the unfavourable environments. MY5 and 9DX are also short and are well adapted to all environments. From the entries with wide adaptability and also adaptability specifically to unfavourable environments, those which are stable include HIM, MY5, KAF, 9DX and 5DX. Among these, the most desirable is HIM followed by MY5, 9DX, KAF and 5DX. HIM has got very good stability inspite of it being slightly taller.

When the overall performance of the genotypes was considered, the hybrids were the most superior. The superior performance of the hybrids has also been demonstrated, among others, by Doggett and Jowett, (1966), Jowett (1972) and Majisu and Doggett (1972). HIB had wider adaptability to all environments, while HIM was specifically adapted to the favourable environments and HIJ was specifically adapted to the unfavourable environments.

probably due to its earliness.

Among the genotypes evaluated, some of the varieties and populations have better stability and adaptability than the hybrids. Most of the hybrids and varieties considered in this study were originally released for East African lowlands, mostly in Uganda, where the rainfall distribution is more reliable. Hence the poor stability of the hybrids as compared to varieties and populations under the unreliable, low rainfall areas of medium agricultural potential areas of Kenya is not unexpected. These results are in agreement with those of Majisu and Doggett (1972) who also found that the hybrids had no superior stability over varieties considered broadly as genotype groups. This suggests that varieties and populations with better buffering capacities have wider adaptability as compared to the hybrids. This can be explained by the different buffering mechanisms operating in these genotypes. Allard and Bradshaw (1964) have distinguished between a number of buffering mechanisms which promote the genotype stability. A hybrid may be considered a homogenous mixture of heterozygous genotypes with individual buffering mechanisms. Similarly, a variety is a homogenous mixture of homozygous genotypes with individual buffering mechanism. Individual buffering refers to the situation where each member of a population is well adapted to a range of environments. On the other hand, the random mating population, is made up of heterogeneous mixture of heterozygous genotypes, with population buffering, in which each genotype may be adapted to a somewhat different range of environments. In this connection, it may be mentioned that the random mating population is able to maintain a high level of heterogeneity and heterozygosity. This was apparently evident in this study. Inspite of the fact that the populations in this study had undergone only one cycle of random mating, their stability was better than those of the hybrids and varieties.

The four populations studied, hence, have a lot of potential for improvement in one or more characters. All these populations are tall growing and can hence be selected for short plant height. The population USR needs to be improved for earliness. The most appropriate selection procedure to effect these improvements together with high grain yield can be the use of recurrent selection. This would provide the opportunity to fully exploit the adaptability and stability of these populations.

5.5. Allocation of Experiments

By increasing the number of seasons, locations and replicates, there is a corresponding decrease in the standard error and hence an increase in the efficiency of the experiment. Increasing the number of seasons was found to be more effective than increasing the number of locations. From the estimates of the standard error, it was established that in order to obtain a fair estimate of G x E, the minimum number of environments should be 4 locations and 4 seasons, with 3 replicates at each environment. The use of four seasons would cover two short rains and two long rains and would thus be more effective for this zone. Similar computations on sorghum by Liang and Walter (1966), Kambal and Mahmoud (1978) and Obilana and El-Rouby (1980) have recommended the allocation of 10 locations over 2 years with 3 replicates; 6 locations over 2 years with 2 replicates and 6 locations over 2-3 years with 4 replications respectively.

In order to find out if the selection of consecutive seasons and selection of sites to represent a wide range of environment would bias the estimates of G x E component, Hanson's (1964) intraclass correlations were computed. The low intraclass correlation values in the present study indicated that the locations and years may be treated as random environments. These results agree with those of Hanson (1964) and Gupton et al. (1974).

CONCLUSIONS

1. The hybrids gave the highest grain yield and were the earliest in maturity at each environment, although they were slightly taller than the varieties. Their adaptability was more specific and they had poor stability as compared to populations and varieties. Of the genotypes tested in this experiments, the most desirable genotypes were the hybrids; HIBRID - which had comparatively wide adaptability, HIJACK - which was adapted to the unfavourable environments, and HIMIDI - which was adapted to more favourable environments.

2. Genotypes x season x location interaction MS was highly significant for all traits. The first order interactions, genotype x season and genotype x location were not significant for all traits except days to 50% flowering.

3. Genotype x season x location variance was the most important of the genotype x environment components in case of all traits and genotype x season interaction was of a

higher magnitude than genotype x location interaction component.

4. A considerable proportion of Genotype x environment interaction sum of squares could be attributed to the linear regressions in case of grain yield/plot (67%), grain yield/head (70%), mean plant height (83%) and days to 50% flowering (45%).

5. The pooled deviations from regressions were highly significant in case of all the traits under consideration. Genetic differences among the genotypes for their regression on environmental index were identified for mean plant height and grain yield/head, but non could be identified for grain yield/plot and days to 50% flowering. From joint regression analyses, it was concluded that for grain yield/plot, the predictions of genotype x environment interactions based on linear regression cannot be made, while such predictions could be made for only some genotypes in case of grain yield/head and days to 50%

flowering. For plant height, such predictions could be made reliably. The rank correlations of different stability parameters showed that the summed deviations from regression (S^2_{di}), Ecovalence (W_i) and coefficient of determination (R^2_i) gave similar rankings of the genotypes.

6. The random mating populations, due to population buffering, were most stable and widely adapted. It was recommended that the full potential of these populations be further utilized.

7. The ideal allocation of four locations, four seasons and three replications was recommended. Seasons and locations could be considered random environments and could be used interchangeably.

REFERENCES

Allard, R.W., and A.D. Bradshaw. 1964. Implications of Genotype-Environmental interactions in applied plant breeding. Crop Sci. 4: 503-507.

Bronius Povilaitis. 1970. Variance components in tobacco cultivar trials. Can. J. Genet. Cytol. 12: 331-339.

Cochran, W.G., and G.M. Cox. 1957. Experimental Designs. John Wiley and Sons, Inc. New York.

Comstock, R.E., and R.H. Moll. 1963. Genotype-environment interactions. Symposium on statistical genetics and plant breeding, NAS-NRC Publ. 982, pp. 164-196 Washington, D.C.

Creech, R.G., R.J. Snyder, E.V. Wann, and W.H. Lachman. 1968. Genotype-environmental interactions for sweet corn hybrids produced by the conventional and cytoplasmic-genetic male sterile methods. Crop. Sci. 8: 380-383.

Doggett, H., and D. Jowett. 1966. Yields of maize, sorghum varieties and sorghum hybrids in the East African lowlands. J. Agric. Sci. 67: 31-39.

Eberhart, S.A., and W.A. Russell. 1966. Stability parameters for comparing varieties. Crop Sci. 6: 36-40.

Finlay, K.W., and G.N. Wilkinson. 1963. The analysis of adaptation in a plant-breeding programme. Aust. J. Agric. Res. 14: 742-754.

Freeman, G.H. 1973. Statistical methods for the analysis of genotype-environment interactions. Heredity 31: 355-366.

Gupton, C.L., P.D. Legg, L.A. Link, and H.F. Ross. 1974. Genotype x environment interactions in Burley tobacco variety tests. Crop Sci. 14: 811-814.

Hanson, W.D. 1964. Genotype-environment interaction concepts for field experimentation. Biometics 20: 540-553.

Hill, J. 1975. Genotype-environment interactions - a challenge for plant breeding. J. Agric. Sci., Camb. 35: 477-493.

Jowett, D. 1972. Yield stability parameters for sorghum in East Africa. Crop Sci. 12: 314-317.

Kambal, A.E., and M.A. Mahmoud. 1978. Genotype x environment interactions in sorghum tests in the Sudan central rainlands. Expl. Agric. 14: 41-48.

Lewis, D. 1954. Gene environment interaction. A relationship between dominance, heterosis, phenotypic stability and variability. Heredity, Lond. 8: 333-356.

Liang, George H.L., and T.L. Walter. 1966. Genotype x environment interactions from yield tests and their application to sorghum breeding programs. Can. J. Genet. Cytol. 8: 306-311.

Majisu, B.N., and H. Doggett. 1972. The yield stability of sorghum varieties and hybrids in East African environments. E. Afr. agric. For. J. 38: 179-192.

Miller, P.A., J.C. Williams, and H.F. Robinson. 1959. Variety-environment interactions and their implications on testing methods. Agron. J. 51: 132-135.

Obilana, A.T., and M.M. El-Rouby. 1980. Cultivar x environments interactions in sorghum, *Sorghum bicolor* (L.) Moench. Theor. Appl. Genet. 56: 81-84.

Perkins, J.M., and J.L. Jinks. 1968 (a). Environmental and genotype-environmental components of variability. III. Multiple lines and crosses. Heredity 23: 339-356.

Perkins, J.M., and J.L. Jinks. 1968 (b). Environmental and genotype-environmental components of variability. IV. Non-linear interactions for multiple inbred lines. Heredity 23: 525-535.

Plaisted, R.L., and L.C. Peterson. 1959. A technique for evaluating the ability of selections to yield consistently in different locations or seasons. American Potato J. 36: 381-385.

Prasad, S.K., and T.P. Singh. 1980. A comparison of different methods for determining the stability of maize varieties. Indian J. agric. Sci. 50 (10): 731-733.

Qualset, C.O. 1968. Population and performance in wheat. Proc. 3rd int. Wheat Genet. Symp., Canberra (Aust. Acad. Sci., Canberra), pp. 397-402. (Cited in Prasad and Singh, 1980).

Rao, N.G.P. 1970. Genotype x environment interaction in grain sorghum hybrids. Indian J. Genet. 30: 75-80.

Reich, V.H., and R.E. Atkins. 1970. Yield stability of four population types of grain sorghum, Sorghum bicolor (L.) Moench, in different environments. Crop Sci. 10: 511-517.

Siderius, W., and F.N. Muchena. 1977. Soils and environmental conditions of agricultural research stations in Kenya. Kenya Soil Survey. Misc. soil paper No. 5.

Singhania, D.L., and N.G.P. Rao. 1976 (a). Genetic analysis of some exotic x Indian crosses in sorghum. XIII. Environmental and genotype-environmental components of variability for grain yield in hybrids and their parents. Indian J. Genet. 36: 111-117.

Singhania, D.L., and N.G.P. Rao. 1976 (b). Genetic analysis of some exotic x indian crosses in sorghum. XIV. Stability of hybrids and parents. Indian J. Genet. 36: 118-124.

Snedecor, G.W.., and W.G. Cochran. 1937. Statistical methods. The Iowa State University Press, Ames, Iowa, U.S.A.

Wrickle, G., 1962. Uber eine Methode Zur Erfassung der Ecologischen Streubreite in Freldversuchen. Z.F. Planzenuchfung 47: 92-96. (Cited in Jowett, 1972)

Wrickle, G., 1966. Uber eine Biometrishe Methode Zur Erfassung der Okologishen Anpassung. Acta Agric. Scand. (Suppl.) 16: 98-101 (Cited in Jowett, 1972)

Yates, F., and W.G. Cochran. 1938. The analysis of groups of experiments. J. agric. Sci. 28: 556-582.

Appendix 1: Environmental conditions of the five locations in Kenya (Source: Siderium and Muchena, 1977)

Location	Centre cordinates	Altitude	Physiography and ecological zone
1. Katumani (Machakos) Eastern Prov.	01°35'S 37°14'E	1575	Undulating upland zone IV, P/Eo = 40%, Med. Low Agri. Potential
2. Kampi ya Mawe (Makueni) Eastern Prov.	01°50'S 37°40'E	1125	Gently undulating upland, zone IV, P/Eo = 35%, Med. Low Agri. Potential
3. Ithookwe (Kitui) Eastern Prov.	01°22'S 38°01'E	1130	Gently undulating upland, zone III, P/Eo = 50%, Med. High Agri. Potential
4. Murinduko (EmbU) Eastern Prov.	00°35'S 37°22'E	1380	Undulating volcanic upland, zone III, P/Eo = 53%, Med. High Agri. Potential
5. Mtwapa (Kikambala) Coast Prov.	03°56'S 39°44'E	21	Very gently undulating Coastal plain, zone III, P/Eo = 58% Med. High Agri. Potential

Appendix 2. Climatic data of the ten environments

Environment			Mean temperature	Precipitation		Seasonal P/Eo %
				Mean	1979/80	
1.	KAT	LR	17.6(23-13)	228	340	35
2.	KAT	SR	20.0(26-14)	449	351	55
3.	KYM	LR	20.3(26-15)	210	301	27
4.	KYM	SR	22.8(29-17)	455	574	52
5.	ITH	LR	20.8(25-17)	308	711	39
6.	ITH	SR	22.4(28-17)	661	414	73
7.	MUR	LR	20.6	506	484	53
8.	MUR	SR	21.9	421	306	53
9.	MTW	LR	25.2(29-22)	826	889	105
10.	MTW	SR	26.8(31-22)	267	187	26

Appendix 3: Analysis of variance table when genotypes are tested at each environment

Source of variation	df	ms	Expected MS	VR
Replicates	(r-1)	M_1		M_1/M_3
Genotypes	(g-1)	M_2	$\sigma_e^2 + r\sigma_g^2$	M_2/M_3
Error	(r-1)(g-1)	M_3	σ_e^2	

Appendix 4: Analysis of variance table when Genotypes (G) are tested at different locations (L) for a number of seasons(S)

Source of variation	df	MS[*1]	Expected MS
Replicates/L/S[*2]	sl(r-1)	M_r	$\sigma_e^2 + g\sigma_r^2$
L	(l-1)	M_l	$\sigma_e^2 + r\sigma_{gls}^2 + rg\sigma_{sl}^2 + rl\sigma_{gs}^r + rgl\sigma_s^2$
S	(s-1)	M_s	$\sigma_e^2 + r\sigma_{gls}^2 + rg\sigma_{sl}^2 + rs\sigma_{gl}^2 + rgg\sigma_l^2$
G	(g-1)	M_g	$\sigma_e^2 + r\sigma_{gls}^2 + rl\sigma_{gs}^2 + rs\sigma_{gl}^2 + rls\sigma_g^2$
L x S	(l-1)(s-1)	M_{ls}	$\sigma_e^2 + r\sigma_{gls}^2 + rg\sigma^2 sl$
L x G	(l-1)(g-1)	M_{lg}	$\sigma_e^2 + r\sigma_{gls}^2 + rl\sigma_{gs}^2$
S x G	(s-1)(g-1)	M_{gs}	$\sigma_e^2 + r\sigma_{gls}^2 + rs\sigma_{gl}^2$
L x S x G	(l-1)s-1)g-1)	M_{gls}	$\sigma_e^2 + r\sigma_{gls}^2$
Error[*3]	sl(r-1)(g-1)	M_e	σ_e^2

[*1] see text

[*2] Reps within L and S SS = sum of Rep SS in all L and all S

[*3] Error SS or (G x Rep/L/S) SS = sum of error SS in all L and all S

Appendix 5. Method of determination of estimates of variance components (Source: Comstrock, *et al.*, 1963)

Variance component		Method of determination
S	σ_s^2	$(M_s - M_{sl} - M_{gs} + M_{gls})/rlg$
L	σ_l^2	$(M_l - M_{sl} - M_{gl} + M_{gls})/rsg$
S x L	σ_{sl}^2	$(M_{sl} - M_{gls})/rg$
G	σ_g^2	$(M_g - M_{gl} - M_{gs} + M_{gls})/rls$
G x L	σ_{gl}^2	$(M_{gl} - M_{gls})/rs$
G x S	σ_{gs}^2	$(M_{gs} - M_{gls})/rl$
G x S x L	σ_{gsl}^2	$(M_{gls} - M_e)/r$
Plot error	σ_e^2	M_e

Appendix 6: Regression analysis (Finlay and Wilkinson, 1963, model)

Source of variation	df	SS
G	$(g-1)$	$\frac{1}{n}\sum_i y_{i.}^2 - CF$
E	$(n-1)$	$\sum_j I_j^2 - (\sum I_j)^2/n$
G x E	$(G-1)(n-1)$	$\sum_i \sum_j y^2_{ij} - \sum_j y^2_{i.}/n$
Regressions	$(g-1)$	$\sum_i \left[(\sum_j y_{ij} I_j)^2/E\ SS\right]$
Deviation from regressions	$(g-1)(n-2)$	$\sum_j \sigma^{2*}_{ij}$
Average error	$\frac{n}{r}(g-1)(r-1)$	Pooled over environments averaged over replicates.

$$^*\sum_j \sigma^2_{ij} = \left[\sum_j y^2_{ij} - (y^2_{i.}/n)\right] - b_i \sum_j y_{ij} I_j$$

Appendix 7. Regression analysis (Eberhart and Russell, 1966, Model)

Source of variation	df		SS	MS
Total	ng-1		$\sum_i \sum_j y^2_{ij} - CF$	
GE	g-1		$\frac{1}{n} \sum_i y^2_{i.} - CF$	M_1
E	n-1	g(n-1)	$\sum_i \sum_j y^2_{ij} - \sum y^2_{i.}/n$	
G x E	(g-1)(n-1)			
E(linear)	1		$\frac{1}{8}(\sum_j y_{.j} I_j)^2/\sum_j I^2_j$	
G x E (linear)	g-1		$\sum_i [(\sum_j y_{ij} I_j)^2/\sum_i I^2_j] -$ E (Linear) SS	M_2
pooled deviations	g(n-2)		$\sum_i \sum_j \delta^2_{ij}$	M_3
G_1	n-2		$[\sum_j y^2_{ij} - \frac{(y_{1.})^2}{n}] - (\sum_j y_{ij} I_j)^2/\sum_j I^2_j = \sum_j \delta^2_{Ij}$	
G_2	n-2		$\sum_j \delta^2_{2j}$	
⋮	⋮		⋮	
G_n	n-2		$\sum_j \delta^2_{nj}$	
Mean error	$\frac{n}{r}(r-1)(g-1)$		SS([illegible]) (pooled over all E)	

Appendix 8. Phenotypic Regression (b_i) Analysis of each Genotype (Source: Perkins and Jinks, 1968 a)

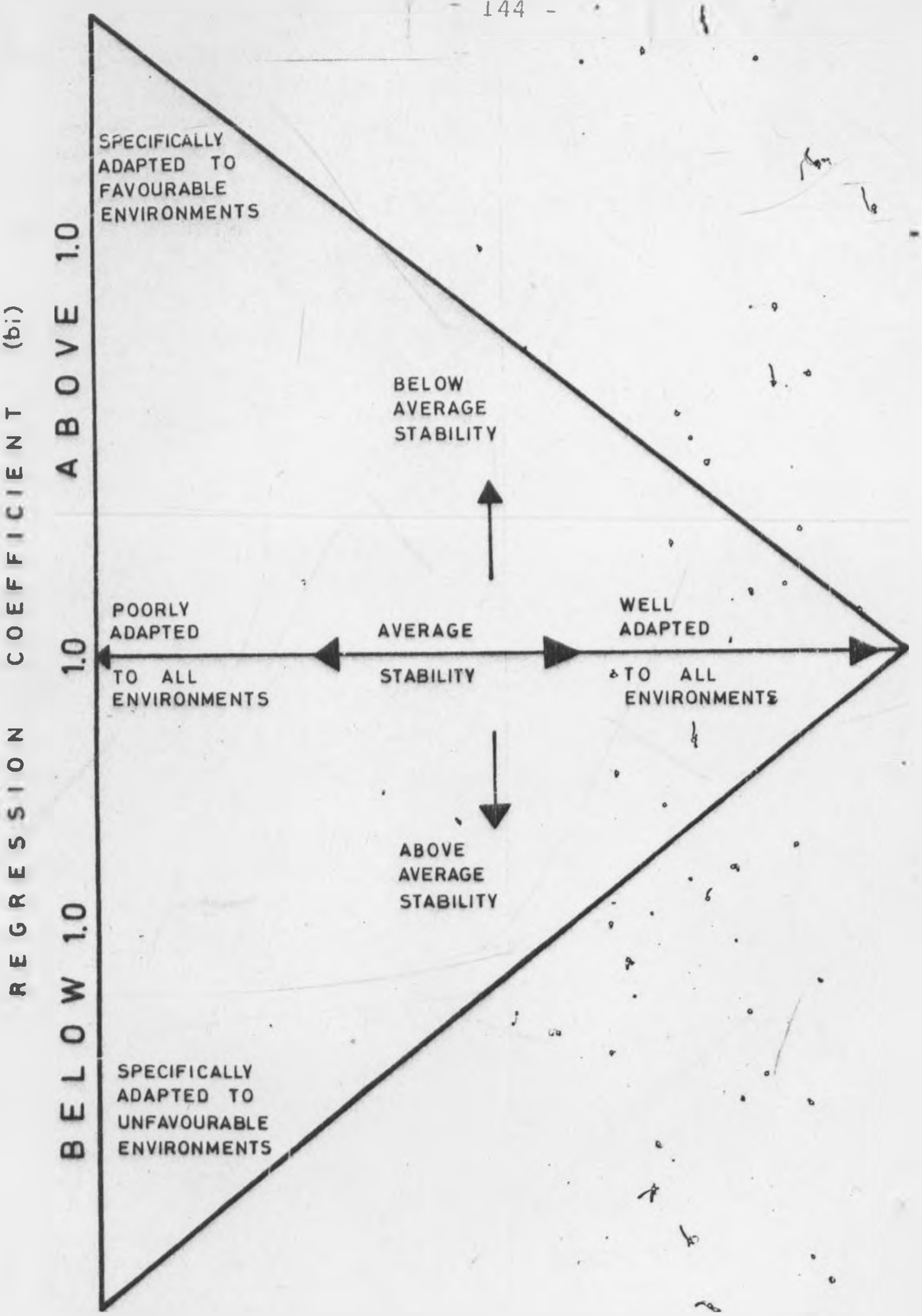
Source of variation	df	SS
Total	n-1	$\sum_j (y_{ij} - y_{i.}/n)^2$
Regression (b_i)	1	$b_i^2 \sum_j I_j^2$
Remainder	n-2	$\sum_j \delta_{ij}^2$

Appendix 9. Genotypic (linear) Regression (B_i) Analysis of each Genotype (Source: Perkins and Jinks, 1968 a)

Source of variation	df	SS
Total	n-1	$\sum_j (y_{ij} - y_{i.}/n)^2$
Regression (B_i)	1	$B_i^2 \sum_j I_j^2$
Remainder	n-2	$\sum_j \delta_{ij}^2$

Appendix 10. Joint Regression Analysis (Source: Perkins and Jinks, 1968 a)

Source of variation	df	SS
G (differences between genotypes)	g-1	$n \sum_{i})^2$
E (joint regression)	n-1	$g \sum_{j} (\underline{r}_{j})^2$
G x E	(g-1)(n-1)	
Heterogeneity between regressions	g-1	$\sum_{j} (B_{i})^2 \sum_{j} (I_{j}^2)$
Remainder	(g-1)(n-2)	$\sum_{ij} \delta_{ij}$
Average error	$\frac{n}{3}(r-1)(g-1)$	σ_e^2



APPENDIX 11. A generalised Interpretation of Adaptability (Source: Finlay and Wilkinson, 1963).