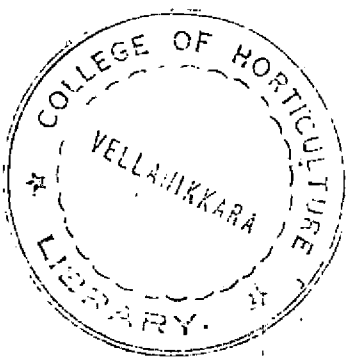
COMPARISON OF DIFFERENT TECHNIQUES FOR THE ESTIMATION OF GENOTYPE-ENVIRONMENT INTERACTION

By

LALY JOHN C.



THESIS

Submitted in partial fulfilment of the

requirements for the degree of

Master of Science (Agricultural Statistics)

Faculty of Agriculture

Kerala Agricultural University

Department of Statistics

COLLEGE OF VETERINARY & ANIMAL SCIENCES

Mannuthy, Trichur.

1984

To

My loving parents

DECLARATION

I hereby declare that this thesis entitled "COMPARISON OF DIFFERENT TECHNIQUES FOR THE ESTIMATION OF GENOTYPE-ENVIRONMENT INTERACTION" is a bonafide record of research work done by me during the course of research and that the thesis has not been previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title of any other University or Society.

Mannuthy
14-6-1984.

Laly John
(LALY JOHN. C)

CERTIFICATE

Certified that this thesis, entitled "COMPARISON OF DIFFERENT TECHNIQUES FOR THE ESTIMATION OF GENOTYPE-ENVIRONMENT INTERACTION" is a record of research work done independently by Miss. LALY JOHN. C, under my guidance and supervision and that it has not previously formed the basis for the award of any degree, fellowship or associateship to her.

(V.K.GOPINATHAN UNNITHAN)
(CHAIRMAN, Advisory Board)
ASSOCIATE PROFESSOR OF AGRL. STATISTICS,
COLLEGE OF HORTICULTURE,
VELLANIKKARA.

Mannuthy,
14-6-1984.

ACKNOWLEDGEMENTS

With immense pleasure, I express my deepest sense of gratitude to Sri.V.K.Gopinathan Unnithan, Associate Professor of Agricultural Statistics and Chairman of the Advisory Committee for his inspiring guidance, generous help and co-operation in the preparation of the thesis.

I am extremely grateful to the late Dr.P.U.Surendran, former Professor of Statistics, who was a member of the Advisory Committee.

My heartfelt thanks are due to Dr.K.C.George, Professor and Head of the Department of Statistics, for proposing the problem for the thesis and also for his valuable suggestions and timely help. I am equally grateful to Dr. (Mrs) Sosamma Iype, Associate Professor of Animal Breeding and Genetics and Sri.K.L.Sunny, Assistant Professor of Agricultural Statistics for the help and encouragement rendered by them as members of the Advisory Committee.

I am thankful to Kerala University for providing the library facilities in the collection of references.

I am grateful to Dr.K.V.Peter, Professor and Head, Department of Olericulture, Miss P. Indira and Sri.V.S.Devadas, Junior Assistant Professors, for providing the necessary data.

I would like to express my sincere thanks to the Dean, College of Veterinary and Animal Sciences, Mannuthy for providing necessary facilities for the study.

I sincerely acknowledge the monetary assistance awarded by Kerala Agricultural University, in the form of fellowship.

I extend my sincere thanks to the staff, Department of Statistics and to all my friends for their valuable help and co-operation.

Thanks are also due to Sri.T.K.Prabhakaran, for typing the manuscript neatly.

(LALY JOHN.C)

CONTENTS

GLOSSARY OF SYMBOLS AND ABBREVIATIONS

CF	:	Correction Factor
df	:	degrees of freedom
EMS	:	Error mean square
ER	:	Eberhart and Russell
FP	:	Freeman and Perkins
GE	:	Genotype-Environment
PJ	:	Perkins and Jinks
SS	:	Sum of squares
S_e^2	:	Error mean square pooled over environments
Y_{ijk}	:	Performance of i^{th} genotype (variety) in the k^{th} replicate of the j^{th} environment.
Y_{ij}	:	Mean performance of the i^{th} genotype in the j^{th} environment.
e_{ij}	:	error associated with the i^{th} genotype in the j^{th} environment.
		$i = 1,2. . . ., t.$
		$j = 1,2. . . ., s.$
		$k = 1,2. . . ., r.$
t	:	number of genotypes
s	:	number of environments
r	:	number of replications
$Y_{i..}$	:	sum of Y_{ijk} over the suffix omitted
$Y_{i.}$	:	sum of Y_{ij} over the suffix omitted
		Similar notations are followed for $Y_{.j.}$, $Y_{...}$, $Y_{.j}$ and $Y_{..}$
b_i	:	regression coefficient under ER model
β_i	:	regression coefficient under PJ model
b_i'	:	regression coefficient under FP model
I_j	:	Environmental index under ER and PJ models
Z_j	:	Environmental index under FP model.

S_d^2 : Second parameter of stability under ER and PJ models.

$S_d'^2$: Second parameter of stability under FP model

$\sum_{j=1}^{s} \frac{\delta_{i.j}^2}{s-2}$: Deviation mean square for the i^{th} genotype under ER and PJ models

$\sum_{j=1}^{s} \frac{\delta'^2_{i.j}}{s-2}$: Deviation mean square for the i^{th} genotype under FP model.

W_i : Ecovalence ratio of the i^{th} genotype

σ_i^2 : Stability variance for the i^{th} genotype.

INTRODUCTION

INTRODUCTION

One of the most important advances in biometrical techniques during the last few years has been in the investigation, elucidation and understanding of genotype-environment interactions. They are of major importance to the plant breeder in developing improved varieties and had been of concern to him for many years. Inspite of early recognition of its importance, it was regarded as intractable till recently. Some fruitful work had been carried out only by the last two decades.

"A phenotype is the result of an interplay of a genotype and its environment". A change in environment may have a greater effect on some genotypes than on others. In otherwords, there may be a change in the ranking of genotypes when measured over varying environments. For instance, a genotype 'A' may be superior to another genotype 'B' under one environment, but inferior to it under another. This interplay of genetic and non-genetic effects on the phenotypic expression is called genotype-environment interaction.

In presence of interaction, the phenotypic value 'P' of an individual can be expressed as $P = G+E+I_{GE}$,

where G is the genotypic value, E the environmental value and I_{GE} the interaction between genotype and environment.

The environment of an individual is made up of everything other than the genotype of the individual, that affects its development. Comstock and Moll (1963) classified the environment into two categories namely, micro and macro environments.

Micro-environmental differences are those environmental fluctations, among individuals that are apparently treated alike. Its interaction with the genotypes is usually very small. Micro-environments are uncontrollable and unpredictable and hence its interaction with genotypes could not properly be studied so far.

Macro-environment is the environment which is associated with a general location and period of time and is a collection of micro-environments. It includes controllable variables such as the level of fertilizer application, sowing dates, sowing density etc. A high level of interaction with macro-environments would be desirable to produce the maximum increase in performance. It is the macro-environmental deviation and its interaction with genotypes that can be isolated and tested for significance.

Stability in performance is one of the most desirable

properties of a genotype to be released as a variety for wide cultivation. Breeding for stable varieties has received much attention recently.

A genotype is said to be stable relative to a set of genotypes, if its response to differing environments is similar to the overall response.

Very many methods are now in use to assess the relative stability of genotypes. Many of them have the same approach and have apparently different stability parameters. A critical study and comparison of all these methods is ofcourse very much needed at this juncture. Hence the present study is taken up with the following objectives:

i) To study the different techniques for estimation of genotype-environment interaction in detail.

ii) To detect which technique is suitable to which situation.

iii) To perform a comparative study of the different techniques of estimating genotype-environment interaction.

iv) Illustration of the techniques by suitable examples.

REVIEW OF LITERATURE

REVIEW OF LITERATURE

The existence of interaction between genotypes and environmental factors had been recognized long ago and various methods have been proposed for its statistical analysis from time to time.

Sprague and Federer (1951) used variance components approach to separate out the effects of genotypes, environments and their interactions by equating the observed mean squares in the analysis of variance to their expectations on the random model.

Many others followed this proceedure. Miller, Williams and Robinson (1959) introduced the concept to plant breeding in an experiment on cotton. Miller, Robinson and Pope (1962) found that three factor interaction of varieties with sites and years was important. Allard and Bradshaw (1964) emphasised the importance of interactions to plant breeders.

Transformation of data which is a well known statistical procedure (Bartlett, 1947; Tukey, 1949) could sometimes be used to eliminate interactions. Mather (1971) considered the question of scale of measurement in detail by giving an example in which interactions were eliminated by a log transformation. He pointed out that such interactions should be

brought explicitly into the analysis inspite of trying to eliminate it. Morley Jones and Mather (1958) discussed how genotype-environment interactions could influence variances and covariances used in biometrical genetical models.

Breeding for stable varieties has received much attention. A number of statistical methods have been proposed for determining the stability of potential varieties when they are tested over a series of environments.

Lewis (1954) suggested 'stability factor' as a simple measure of phenotypic stability. It is given by S.F. = $\frac{\bar{X}_{HE}}{\bar{X}_{LE}}$ where S.F. stands for Stability Factor, $\bar{X}_{HE}$ and $\bar{X}_{LE}$ are the mean values in the high and low yielding environments respectively. A value of 'unity' for the stability factor indicates maximum phenotypic stability. Genotypes with S.F. farther away from unity can be considered as unstable. The drawback of this measure is that it does not take the variability of the genotypes over the varying environments into account.

Plaisted and Peterson (1959) adopted the procedure of obtaining combined analysis of variance at all locations for each pair of variety and computed variety X location component of variance for each pair. Mean value of this

variance component was then taken as a stability measure. The variety with the smallest mean value was considered as the most stable. The major drawback of this procedure is that computation becomes tedious with increase in the number of varieties.

Wricke (1966) developed a method to estimate the ecovalence (W_i) of genotypes grown under several environments, to measure the stability of performance. Ecovalence (W_i) is the percentage contribution of the i^{th} genotype to the genotype-environment interaction sum of squares. The varieties with small W_i value were considered to be stable. This method allows the partitioning of the genotype-environment interaction sum of squares into components attributable to the different genotypes, but it does not allow the prediction of the performance of genotypes over environments.

Shukla (1972) proposed 'stability variance' (σ^2_i) as a measure of stability of the i^{th} genotype and he developed an 'F' test taking into account the within environmental component of variance (σ^2_e). A genotype is called stable if its stability variance is equal to within environmental component of variance and large values of this variance indicate more stability of the genotype. 'Stability variance' and ecovalence are closely related.

A method of partitioning the interaction sum of squares had been given by Yates and Cochran (1938), though it was largely neglected for years. They regressed the yield of each variety on the mean of all varieties. They observed that the regression sum of squares accounted for a large part of the interaction sum of squares, in a set of barley trials.

Finlay and Wilkinson (1963) adopted the same technique for the analysis of adaptation in a trial with 277 varieties of barley in seven environments. They observed that genotype-environment interactions were linearly related to the environmental effects, when these were measured on the same scale as the genotypic effects. They defined an ideal variety as the one with the maximum yield potential and maximum genotypic stability.

The regression technique of Finlay and Wilkinson (1963) was improved upon by Eberhart and Russell (1966) by adding another stability parameter, namely, the deviation from regression (S_d^2).

Tai (1971) presented a method of genotypic stability analysis, where genotype-environment interaction of a variety is partitioned into two components-linear response to environmentaleffects (α) and the deviations from the linear

response (λ). A perfectly stable variety was characterised by $\hat{\alpha} = -1$ and $\hat{\lambda} = 1$. $\hat{\alpha}=0$ and $\hat{\lambda} = 1$ of Tai correspond to unit regression coefficient and S_d^2 equal to zero respectively of Eberhart and Russells' model (1966). These values of α and λ also had coincidence with Shukla's definition of stability, where Shukla (1972) defined a genotype as stable if the performance of the genotype is the sum of additive genetic effect, additive environmental effect and a random error without any interaction between genotype and environment.

The variance components approach and the regression approach discussed above did not relate to parameters in a biometrical genetical model. A third approach is based on the fitting of models which specify the contributions of genetic, environmental and genotype-environment interaction effects to the generation means and variances which allow for the contribution of additive, dominance and epistatic gene effects to the genetic and interaction components.

Eucio Alanis (1966) developed a mathematical model to measure the genotype-environment interaction when only two homozygous parents were grown under a large number of environments.

Bucio Alanis and Hill (1966) extended the above model to include F_1 between two homozygous parents.

Perkins and Jinks (1968, a) extended the technique of Bucio Alanis (1966) and Bucio Alanis and Hill (1966) to cover many inbred lines and crosses among them.

Perkins and Jinks (1968,b) further extended the methodology to a large number of miscellaneous F_1's which may not have any systematic relationship with one another by redefining the model for individual F_1 as $F_{(il)}$ obtained by crossing parents P_i and P_l.

Bucio Alanis, Perkins and Jinks (1969) extended the model of Bucio Alanis and Hill (1966) to include F_2 and the backcrosses B_1 and B_2.

In all the above cases, the genotype-environment interaction component was linearly related to the environmental values. It was found that the phenotypic mean of any generation derivable from two inbred parents grown under any environment could be predicted from the parental and F_1 generations.

This approach is superior in its predictive vâhe across generations and this is nôt possible from alternative approaches of Finlay and Wilkinson (1963), Eberhart and Russell (1966)

and Perkins and Jinks (1968, a & b).

Breese (1969) applied this technique to yield data in herbage plants. It could give a remarkably accurate prediction of the relative response over very wide range of environments.

Using plant height in Nicotiana rustica, Jinks and Perkins (1970) showed that the means of F_2, B_1 and B_2 families could be satisfactorily predicted from estimates of the parameters obtained from the parental and F_1 families. They further extended the methodology to F_1 hybrids in a diallel set.

The major weaknesses of the regression techniques developed by Yates and Cochran (1938), Finlay and Wilkinson (1963), Eberhart and Russell (1966) and Perkins and Jinks (1968) were pointed out by Freeman and Perkins (1971). They criticized the improper choice of sums of squares and degrees of freedom and also of measure of environment in the works quoted above.

Fripp and Caten (1971) made a comparative study of the three regression approaches of Eberhart and Russell (1966), Perkins and Jinks (1968) and Freeman and Perkins (1971).

Rawlo and Das (1978) adopted the regression approach

of Eberhart and Russell (1966) and suggested the reciprocal of the modulus of the regression coefficient as stability index. A variety was termed stable, if the stability index was unity.

Shukla (1972) reparametrised the model of Perkins and Jinks (1968) by taking deviation of individual regression coefficients from the mean of all regression coefficients. Then the problem of testing the equality of regression coefficients became equivalent to testing the presence of the non-additivity term introduced by this reparametrisation, provided the environmental effects were fixed. Further, he considered an extension of the model by taking a covariate, (Z_j), which is a measure of some characteristic of the j^{th} environment, into account. He observed that stability was rendered for some genotypes by taking a covariate into account, and concluded that the instability was due to the linear effect of the covariate.

Sapate and Atale (1983) proposed $S_{b_i} = \frac{1}{1 + |b_i|} \times 100$ as the stability index of the i^{th} genotype where b_i is the regression coefficient of the i^{th} genotype in Eberhart and Russell (1966) model. A value of 100% indicates the most stable variety, and zero, the most unstable one. They proposed the percentage of the coefficient of determination as a second measure of stability.

Thote, Sapate and Jahagirdar (1983) pointed out that the adaptability of Freeman and Perkins (1971) model based on the linear relationship between genotype-environment interaction and environment was rarely possible and restricted its scope.

Sapate and Thote (1983) showed that regressing phenotypic effect instead of genotype-environment interaction as done by Freeman and Perkins was bound to affect the estimate of regression coefficient (β_i) by an amount equal to the combined regression coefficient ($\bar{\beta}$). They suggested that the ranking of genotypes by the regression coefficient could be made after subtracting the combined regression coefficient from the individual regression coefficients.

Fripp and Caten (1971) found that significant part of the genotype-environment interaction was accounted for by differences in linear sensitivity of genotypes. They also observed that a single control genotype could well be used to assess the environment.

Perkins and Jinks (1971) observed that reactions of genotypes to environments were specific to the character under study and the genotype-environment interaction would differ for different kinds of environmental variables.

Fripp (1972) considered different environmental

measures for the regression approach and observed that the bias in using non-independent measure was very small and that the linearity of regression reduces with increase in distance of the environmental measures from the genotypes under study. He found that a single assessment genotype could very satisfactorily be used as the environmental measure.

Perkins and Jinks (1973) investigated the statistical and biometrical genetical advantages and disadvantages of using dependent and independent assessments of the environmental values with inbred lines. They concluded that ranking of the genotypes by the regression coefficients could satisfactorily be made using the dependent environmental measures.

Hardwick and Wood (1972) showed that the bias in the estimate of regression coefficient of genotypes on environmental mean reduces with increase in the number of genotypes and the ratio of variation between environment to the error mean square. They also considered multiple linear regression on a number of environmental variables.

Shukla (1983) proved theoritically that the regression coefficient under Perkins and Jinks model is estimated as a relative measure-relative to the other genotypes in the trial. He suggested that the bias in the estimates of

regression coefficients would be reduced with large numbers of genotypes and environments. He also considered multiple regression on a number of environmental variables.

Principal component analysis of the sum of squares and sum of products matrix of the genotypes over environments was carried out by Perkins (1972) and found that the score of each genotype in the first principal component was directly related to the regression coefficient of the genotype on the non-independent environmental measure.

Freeman and Dowker (1973) observed that principal component analysis could identify the genotypes as well as environments which gave significant contribution to the interaction.

Freeman (1973) discussed the various methods of stydying genotype-environment interaction and suggested multivariate analysis.

Fripp and Caten (1973) examined the relationship between genetical systems determining mean expression and sensitivity to change in environment for the character dikaryotic growth rate in Schyzophyllum commune. They pointed out the drawback in studying the genetic relationship between two characters without reference to the environment.

MATERIALS AND METHODS

MATERIALS AND METHODS

Secondary data had been used for the present study. The following different sets of data had been utilised for the comparison of different methods of estimating stability parameters.

1. Observations on 'mean ears per plant' (calculated from five plants in a plot) from an experiment of ten varieties of barley tried at five different locations in randomised block design with three replications in each location form the first set of data. They are taken from Singh and Choudhary (1977). The mean data averaged over replications are given in table 3.1.

Table 3.1. 'Mean ears per plant' of ten varieties of barley over five locations.

Varieties	Locations				
	L-I	L-II	L-III	L-IV	L-V
1.	43.13	30.73	23.40	26.77	31.70
2.	38.67	33.43	24.17	24.60	29.50
3.	29.60	43.83	33.67	28.83	27.00
4.	40.33	26.13	26.60	29.90	29.50
5.	41.47	40.43	27.97	32.43	27.40
6.	33.43	38.73	28.27	32.27	36.78
7.	40.70	34.90	26.97	27.00	29.63
8.	32.27	27.60	22.50	23.27	24.50

Varieties	Locations				
	L-I	L-II	L-III	L-IV	L-V
9.	36.27	27.57	24.47	24.97	31.60
10.	30.23	32.43	28.83	17.87	32.40

2. The second set of data is based on an experiment on 25 amaranth genotypes, conducted in randomised block design with two replications and repeated in 11 seasons, in the department of Olericulture, College of Horticulture. The data were taken from Devadas, V.S. (1982). Only the means over replications in each season and the corresponding analysis of variance was available. The character selected was 'length of 5th leaf on 30th day of sowing'. The mean data averaged over replications are given in table 3.2.

3. The third set of data was from Indira, P. (1982). The data were generated from an experiment of 15 chilli genotypes in a split-plot experiment with four levels of ethephon sprays in the main-plots. There were three replications. The four ethephon levels were taken as four environments. The character chosen was 'the number of days to first fruit set', which alone showed interaction between genotypes and environments. The error mean squares in the four main plots were not homogeneous and that was the reason for selecting

Table 3.2. Mean length of 5th leaf (cm) on 30th day of sowing of 25 amaranth genotypes in 11 seasons.

Genotypes	Environments										
	E_1	E_2	E_3	E_4	E_5	E_6	E_7	E_8	E_9	E_{10}	E_{11}
1.	12.22	9.23	8.26	7.12	8.35	11.79	9.25	5.99	9.96	9.63	11.51
2.	12.17	12.53	8.64	4.09	11.77	10.77	9.67	6.77	11.67	12.29	16.23
3.	13.30	11.34	9.35	10.15	9.88	11.51	11.38	8.22	10.44	11.93	15.39
4.	11.32	13.05	10.17	11.62	10.61	10.74	9.77	8.95	11.18	12.65	16.33
5.	12.24	13.98	14.77	8.20	10.52	9.15	11.00	11.12	12.70	13.40	14.98
6.	14.11	11.12	10.77	7.28	10.68	12.93	7.57	8.40	12.08	9.45	14.06
7.	7.00	4.55	6.67	3.87	6.24	5.04	3.69	4.68	5.60	5.32	9.17
8.	5.14	13.07	11.22	12.23	13.14	9.81	9.90	9.34	13.36	11.68	20.13
9.	4.25	11.27	10.01	5.61	10.08	13.01	10.08	10.39	12.35	12.24	15.63
10.	11.77	10.95	13.74	11.48	11.78	11.27	9.78	8.90	9.04	10.72	13.84
11.	9.36	10.59	9.22	6.56	10.30	9.25	8.62	6.33	9.43	10.98	9.00
12.	10.58	10.37	8.03	7.14	5.58	7.05	5.58	3.23	11.08	10.84	9.99
13.	12.34	10.64	9.62	6.54	9.52	9.53	6.83	8.59	11.31	11.80	15.99
14.	17.58	13.55	10.35	6.63	17.81	12.32	6.74	10.15	15.34	13.67	17.32
15.	12.23	12.02	14.55	10.62	10.75	13.06	10.50	10.24	11.92	11.42	16.65
16.	15.29	11.53	10.47	8.92	11.59	11.54	7.40	11.25	11.95	10.65	12.32
17.	13.16	14.09	10.67	6.49	9.45	12.60	9.30	13.03	13.60	13.30	13.06
18.	10.25	11.67	13.43	7.51	10.55	13.84	11.67	7.88	14.30	13.45	16.33
19.	11.75	14.31	12.14	6.55	8.97	11.24	6.55	11.20	10.04	11.20	16.09
20.	6.86	6.03	6.05	3.93	6.40	6.86	3.89	4.93	7.12	6.90	9.00
21.	10.50	7.76	7.50	7.09	7.26	7.32	7.55	6.72	7.18	5.70	8.92
22.	10.41	7.28	4.14	4.58	7.23	6.78	7.00	5.11	8.64	7.65	11.40
23.	10.89	9.15	9.02	4.64	9.10	7.29	8.10	5.09	8.44	9.03	11.66
24.	10.86	11.07	7.84	6.61	8.25	7.83	8.25	5.78	9.05	7.64	9.77
25.	5.63	4.33	5.68	4.82	4.62	5.75	6.35	4.72	6.68	5.30	7.75

this peculiar type of data. The mean data averaged over replications are given in table 3.3.

Table 3.3. 'Mean number of days to first fruit set'of 15 chilli genotypes in four environments.

Geno-types	Environments E_0	E_1	E_2	E_3
1.	41.07	51.80	57.00	56.53
2.	61.53	61.07	63.93	62.27
3.	38.53	51.00	54.33	55.93
4.	48.93	52.73	56.80	56.07
5.	44.73	50.13	57.33	55.67
6.	43.47	52.40	55.00	56.87
7.	44.13	50.27	52.93	56.00
8.	47.13	50.20	54.33	56.53
9.	43.20	53.00	56.87	56.73
10.	42.07	54.07	56.40	55.93
11.	44.33	52.20	56.20	56.47
12.	45.00	51.93	56.60	57.07
13.	43.40	52.07	54.20	56.27
14.	43.73	52.13	55.53	55.33
15.	47.00	52.40	55.53	57.00

Analysis of variance was performed in each of the environment in all the three sets of data. Homogenity of error variances in different environments was tested using Bartlett's test, in each case.

Unweighted analysis of variance of the data in first two sets, pooled over the different environments in each case was carried out to test the significance of GE interaction. Weighted analysis was performed in the third set of data for the same purpose since the error variances were found to be heterogeneous in the different environments. Tables 3.4.1 and 3.4.2 respectively give the details of the unweighted and weighted analysis of variance of the data pooled over the different environments.

Table 3.4.1. Unweighted analysis of variance of pooled data.

Source	df	SS	MS
Total	$st-1$	$\sum_{i=1}^{t}\sum_{j=1}^{s} Y_{ij}^2$ — C.F.	
Genotypes (G)	$t-1$	$\sum_{i=1}^{t} \frac{Y_{i.}^2}{s}$ — C.F.	
Environments (E)	$s-1$	$\sum_{j=1}^{s} \frac{Y_{.j}^2}{t}$ — C.F.	
GE interaction	$(t-1)(s-1)$	Total SS — Genotypes SS — Environments SS	MS_1
Pooled error	$s(t-1)(r-1)$		$\frac{S_e^2}{r}$

Where,

$$C.F. = \frac{\left(\sum_{i=1}^{t}\sum_{j=1}^{s} Y_{ij}\right)^2}{st}$$

Significance of GE interaction was tested using the F - ratio, $F = MS_1/S_e^2$.

Table 3.4.2. Weighted analysis of variance of the pooled data

Source		SS
Total		$\sum_{j=1}^{s} W_j S_j - C$
Environments	$\frac{1}{t}$	$\sum_{j=1}^{s} W_j P_j^2 - C$
Genotypes		$\frac{\sum_{i=1}^{t} (\sum_{j=1}^{s} W_j Y_{ij})^2}{\sum_{j=1}^{s} W_j} - C$
GE interaction (I)		Total SS - Environments SS - Genotypes SS

The terms in the analysis of variance were obtained as follows:

$W_j = \frac{r}{s_j^2}$, where s_j^2 is the error mean square in the j^{th} environment and r is the number of replications in each environment.

S_j = Crude SS for the j^{th} environment.

P_j = Total for the j^{th} environment

$$C = \frac{G^2}{t \sum_{j=1}^{s} W_j}$$

Where $G = \sum_{j=1}^{s} W_j P_j$

$$= \sum_{i=1}^{t} \left(\sum_{j=1}^{s} W_j Y_{ij} \right)$$

Significance of GE interaction was tested using the χ^2 test,

$$\chi^2 = \frac{(n-4)(n-2)}{n(n+t-3)} \; I \quad \text{with}$$

$$d.f. = \frac{(s-1)(t-1)(n-4)}{(n+t-3)}$$

Where n = The number of d.f. on which the error mean square is based in each environment.

I = Interaction sum of squares.

Once the GE interaction was found significant, stability of each genotype was assessed from the mean performance over the different environments by the different methods as follows:

1. Eberhart and Russell model

$$Y_{ij} = \mu_i + b_i I_j + \delta_{ij},$$

Where

μ_i = Mean of i^{th} variety over all environments

b_i = regression coefficient that measures the response of i^{th} variety to varying environments

I_j = Environmental index, obtained as deviation of the mean of all varieties at the j^{th} environment from the grand mean

and δ_{ij} = Deviation from regression of the i^{th} variety in the j^{th} environment.

I_js which are the independent variables on which Y_{ij}s are regressed, were obtained as

$$I_j = \sum_{i=1}^{t} \frac{Y_{ij}}{t} - \sum_{i=1}^{t} \sum_{j=1}^{s} \frac{Y_{ij}}{st}$$

so that $$\sum_{j=1}^{s} I_j = 0$$

The two parameters of stability under this model are

$$bi = \frac{\sum_{j=1}^{s} Y_{ij} I_j}{\sum_{j=1}^{s} I_j^2}$$

$$S_{di}^2 = \frac{\sum_{j=1}^{s} \delta_{ij}^2}{s-2} - \frac{S_e^2}{r}$$

Where $\sum_{j=1}^{s} \delta_{ij}^2 \qquad \sigma_{Vi}^2 - b_i \sum_{j=1}^{s} Y_{ij} I_j$

$$\sigma^2_{v_i} = \sum_{j=1}^{s} Y_{ij}^2 - \frac{Y_{i.}^2}{s} ,$$

$$b_i \sum_{j=1}^{s} Y_{ij} I_j = \frac{(\sum_{j=1}^{s} Y_{ij} I_j)^2}{\sum_{j=1}^{s} I_j^2} .$$

Since the error variances were heterogeneous in the third set of data, only $\sum_{j=1}^{s} \frac{\delta_{ij}^2}{s-2}$ was calculated instead of $S_{d_i}^2$.

The detailed analysis of variance under ER model is given in table 3.5.

Table 3.5. Analysis of variance under ER model (General).

Source	df	SS	MS
Total	st-1	$\sum_{i=1}^{t} \sum_{j=1}^{s} Y_{ij}^2 - C.F.$	
Varieties	t-1	$\frac{1}{s} \sum_{i=1}^{t} Y_{i.}^2 - C.F.$	MS_1
Environments+ Varieties X Environments	$(s-1)+(s-1)(t-1)=t(s-1)$	$\sum_{i=1}^{t} \sum_{j=1}^{s} Y_{ij}^2 - \sum_{i=1}^{t} \frac{Y_{i.}^2}{s}$	
Environment (linear)	1	$\frac{1}{t} \frac{(\sum_{j=1}^{s} Y_{ij} I_j)^2}{\sum_{j=1}^{s} I_j^2}$	
Variety X Environment (linear)	(t-1)	$\frac{\sum_{i=1}^{t} (\sum_{j=1}^{s} Y_{ij} I_j)^2}{\sum_{j=1}^{s} I_j^2}$ - SSdue to environments (linear)	MS_2

Source	df	SS	MS
Pooled deviation	$t(s-2)$	$\sum_{i=1}^{t}\sum_{j=1}^{s}\delta_{ij}^2$	MS_3
Variety 1	$(s-2)$	$\sum_{j=1}^{s}\delta_{1j}^2$	
.	.	.	
.	.	.	
.	.	.	
.	.	.	
Variety t	$(s-2)$	$\sum_{j=1}^{s}\delta_{tj}^2$	
Pooled error	$s(t-1)(r-1)$		$\frac{s_e^2}{r}$

Where I_j and $\sum_{j=1}^{s}\delta_{ij}^2$ are as defined above.

Here, the SS due to environment and varieties X environments interaction is partitioned into SSs due to environments (linear), varieties X environments (linear) and deviation from the regression model with d.f. one, (t-1) and t (s-2) respectively.

The following F tests were made use of:

(1) $F = \frac{MS_2}{MS_3}$, to test the equality of regression coefficients.

(2) $F = \frac{\sum_{j=1}^{s}\delta_{ij}^2/(s-2)}{s_e^2}$, to test the individual deviation from regression.

A variety with unit regression coefficient (bi = 1) and $S_{d_i}^2$ not significantly different from zero ($S_{d_i}^2 = 0$) could be considered as stable.

To test whether the regression coefficients of individual varieties differed significantly from unity, the following 't' test was applied .

$$t = \frac{bi - 1}{SE\ (b)}$$

Where SE (b) $= \left[\frac{\text{MS due to pooled deviation}}{\sum_{j=1}^{s} I_j^2}\right]^{\frac{1}{2}}$

2. Perkins and Jinks model (PJ model)

$$Y_{ij} = \mu + d_i + \varepsilon_j + g_{ij} + e_{ij} ,$$

Where

μ = grand mean of all genotypes over all environments.

d_i = additive genetic effect of the i^{th} genotype.

ε_j = additive environmental effect of j^{th} environment.

g_{ij} = GE interaction effect of the i^{th} genotype at the j^{th} environment.

The effects are defined as follows:

$$\mu = \frac{Y_{..}}{st}$$

$$d_i = \frac{Y_{i.}}{s} - \mu$$

$$\varepsilon_j = \frac{Y_{.j}}{t} - \mu$$

$$g_{ij} = Y_{ij} - d_i - \varepsilon_j + \mu$$

g_{ij} was further defined as

$g_{ij} = \beta_i \varepsilon_j + \delta_{ij}$ so that the model becomes

$$Y_{ij} = \mu + d_i + (1+\beta_i)\varepsilon_j + \delta_{ij} + e_{ij}$$

The regression coefficient under this model is nothing but that in ER model reduced by unity. S_{di}^2 remains exactly same as that of the ER model.

The analysis of variance under this model, adopting earlier notations is given in table 3.6.

Table 3.6. Analysis of variance under PJ model.

Source	df	SS	MS
Genotypes	(t-1)	$\sum_{i=1}^{t} \frac{Y_{i.}^2}{s} - \frac{Y_{..}^2}{st}$	
Environments (Joint regression)	(s-1)	$\sum_{j=1}^{s} \frac{Y_{.j}^2}{t} - \frac{Y_{..}^2}{st}$	
Genotype X Environment interaction (GxE)	(t-1)(s-1)	$\sum_{i=1}^{t}\sum_{j=1}^{s} Y_{ij}^2 - \sum_{i=1}^{t} \frac{Y_{i.}^2}{s} - \sum_{j=1}^{s} \frac{Y_{.j}^2}{t} + \frac{Y_{..}^2}{st}$	

Source	df	SS	MS
Heterogenity among regressions	$(t-1)$	$\dfrac{\sum_{i=1}^{t}\left[\sum_{j=1}^{s} Y_{ij}\left(\dfrac{Y_{\cdot j}}{t}-\dfrac{Y_{\cdot\cdot}}{st}\right)\right]^2}{\sum_{j=1}^{s} I_j^2}$	
		- SS due to environments	
Remainder	$(t-1)(s-2)$	(GxE) SS -SS due to heterogenity	
Error	$s(t-1)(r-1)$		S_e^2

Here, the GE interaction SS is partitioned into two components, viz, heterogenity among regressions with (t-1) d f and remainder SS with (t-1) (s-2) df.

The environments (joint regression) SS with (s-1) df in this case is the same as the environments (linear) SS of Eberhart and Russell, with df =1. Similarly, SS due to heterogenity among regressions in this case is equal to the variety X environment (linear) SS of ER model, both with df = (t-1). The pooled deviation SS with t (s-2) df in the former case is equal to the remainder SS with (t-1)(s-2) df in this case.

3. Freeman and Perkins model (FP Model)

The environmental index is the deviation of the mean value of the genotypes at the particular environment from the grand mean, in the case of both the models discussed earlier. Freeman and Perkins (1971) proposed other methods for estimating environmental index.

(1) using a seperate replication for measuring the environment.

(2) using a single assessment genotype.

In the first and third sets of data, the third replication was used for assessing the environment and the other two replications were used for measuring the GE interaction.

In the second set, one of the 25 genotypes, which was a very common one, was taken as the assessment genotype. The observations on this genotype was included in the estimation of GE interaction also.

The symbol Z_j was used for the environmental index thus obtained, to indicate that it is an independent measure.

FP model is actually an extension of PJ model and is given by

$$Y_{ij} = \mu + d_i + \bar{\beta} z_j + \bar{\delta}_j + \beta_{d_i} z_j + \delta_{d_{ij}}$$

μ = mean of all genotypes over all environments.

d_i = effect of i^{th} genotype.

β_i = regression coefficient of i^{th} genotype in the j^{th} environment.

$\bar{\beta}$ = combined regression coefficient (equal to mean of all β_i).

β_{d_i} = difference between the regression coefficient of i^{th} genotype and the combined regression coefficient (ie. $\beta_i - \bar{\beta}$). It is the coefficient for the regression of g_{ij} on to Z_j.

δ_{ij} = deviation of the i^{th} genotype from the regression on Z_j.

$\bar{\delta}_j$ = deviation of the mean of all genotypes in the j^{th} environment from the combined regression line ($\Sigma_j - \bar{\beta} Z_j$).

$\delta_{d_{ij}}$ = deviation of the i^{th} genotype from its linear regression on Z_j in the j^{th} environment minus $\bar{\delta}_j$ (ie. $\delta_{ij} - \bar{\delta}_j$).

The two parameters of stability were computed as

$$b_i = \sum_{j=1}^{s} Y_{ij} Z_j \Big/ \sum_{j=1}^{s} Z_j^2$$

$$S_{d_i}^2 = \frac{\sum_{j=1}^{s} \delta_{ij}^2}{s-2} - \frac{S_e^2}{r}$$

where $\sum_{j=1}^{s} \delta_{ij}^2 = \sigma_{v_i}^2 - b_i \sum_{j=1}^{s} Y_{ij} Z_j$ and

$$\sigma_{v_i}^2 = \sum_{j=1}^{s} Y_{ij}^2 - \frac{Y_{i.}^2}{s}$$

S_e^2 is the pooled error mean square which is obtained from the first two replications.

Analysis of variance takes the form as given in table 3.7 below.

Table 3.7. Analysis of variance under FP model (General).

Source	df	SS	MS
Genotypes (G)	(t-1)	$\sum_{i=1}^{t} \frac{Y_{i..}^2}{rs} - \frac{Y_{...}^2}{rst}$	
Environments (E)	(s-1)	$\sum_{j=1}^{s} \frac{Y_{.j.}^2}{rt} - \frac{Y_{...}^2}{rst}$	
Combined regression	1	$\frac{(\sum_{j=1}^{s} Y_{.j.} Z_j)^2}{rt \sum_{j=1}^{s} Z_j^2}$	
Environmental residual	(s-2)	By subtraction from E	
Genotype X environment interaction (GxE)	(t-1)(s-1)	$\sum_{i=1}^{t} \sum_{j=1}^{s} \frac{Y_{ij.}^2}{r} - \sum_{i=1}^{t} \frac{Y_{i..}^2}{rs} - \sum_{j=1}^{s} \frac{Y_{.j.}^2}{rt} + \frac{Y_{...}^2}{rst}$	
Heterogenity among regressions	(t-1)	$\sum_{i=1}^{t} \frac{(\sum_{j=1}^{s} Y_{ij.} Z_j)^2}{r \sum_{j=1}^{s} Z_j^2} - \frac{(\sum_{j=1}^{s} Y_{.j.} Z_j)^2}{rt \sum_{j=1}^{s} Z_j^2}$	
(GxE) residual	(t-1)(s-2)	By subtraction from (GxE)	
Pooled error	s(t-1)(r-1)		S_e^2

Here, the SS due to environments with df (s-1) is partitioned into SS due to combined regression with one df and environmental residual with df (s-2). The interaction SS is divided into SS due to heterogenity among regressions and (GxE) residual with df (t-1) and (t-1) (s-2) respectively.

The significance of each item was tested by using F ratio against the pooled error mean square.

The above three methods used the theory of regression. The SS due to GE interaction was split up into components attributable to the different genotypes in the following two methods.

1. Wricke (1966) suggested ecovalence ratio as the percentage contribution of a genotype to the SS due to GE interaction.

ie. Ecovalence for i^{th} genotype is

$W_i = \sum_{j=1}^{s} (Y_{ij} - \frac{Y_{i.}}{s} - \frac{Y_{.j}}{t} + \frac{Y_{..}}{st})^2$ expressed as percentage of the total of all W_is.

A variety having least ecovalence was considered most stable and a variety with large ecovalence value, least stable.

2. 'Stability variance', σ_i^2 of i^{th} genotype as per Shukla (1972) is

$$\sigma_i^2 = \frac{1}{(s-1)(t-1)(t-2)} \left[t(t-1) \sum_{j=1}^{s} \left(Y_{ij} - \frac{Y_{i.}}{s} - \frac{Y_{.j}}{t} + \frac{Y_{..}}{st}\right)^2 - \sum_{i=1}^{t} \sum_{j=1}^{s} \left(Y_{ij} - \frac{Y_{i.}}{s} - \frac{Y_{.j}}{t} + \frac{Y_{..}}{st}\right)^2 \right]$$

The mean of σ_i^2 s give the interaction mean square. A variety having σ_i^2 value less than the within environmental variance σ_0^2 (σ_0^2 is estimated as the pooled error mean square) or having negative σ_i^2 value was defined as stable. Furthermore, an F test given by $F = \frac{\sigma_i^2}{\sigma_e^2}$ with df (s-1, s(t-1)(r-1)) was used to test the significance of σ_i^2.

σ_i^2 could be expressed as a linear function of W_i as shown below:

$$\sigma_i^2 = \frac{1}{(s-1)(t-1)(t-2)} \left[t(t-1) W_i - \sum_{i=1}^{t} W_i \right]$$

$$= \frac{1}{(s-1)(t-1)(t-2)} \left[t(t-1) \frac{W_i \times I}{100} - I \right]$$

$$= \frac{It}{100(s-1)(t-2)} W_i - \frac{I}{(s-1)(t-1)(t-2)}$$

$$= A W_i - B$$

Where $W_i = \sum_{j=1}^{s} \left(Y_{ij} - \frac{Y_{i.}}{s} - \frac{Y_{.j}}{t} + \frac{Y_{..}}{st}\right)^2$

$$A = \frac{It}{100(s-1)(t-2)}$$

$$B = \frac{I}{(s-1)(t-1)(t-2)}$$

A method suggested in the present study is to form different groups of genotypes so that the GE interaction is not significant within any group, but significant between any two groups. The genotypes within any group could be considered as having same stability or similar response to differing environments.

The split up of the interaction SS between k groups is given in table 3.8.

Table 3.8. Split up of interaction SS (General).

Interaction	df	SS
Within group 1	$(t_1-1)(s-1)$	I_1
Within group 2	$(t_2-1)(s-1)$	I_2
.	.	.
.	.	.
.	.	.
.	.	.
Within group k	$(t_k-1)(s-1)$	I_k
Between group	$(k-1)(s-1)$	By subtraction
Total	$(t-1)(s-1)$	I

Where I_u, the SS due to interaction within the u^{th} group is given by

$$I_u = \sum_{i=1}^{t_u} \sum_{j=1}^{s} Y_{ij}^2 - \sum_{i=1}^{t_u} \frac{Y_{i.}^2}{s} - \frac{1}{t_u} \sum_{j=1}^{s} \left(\sum_{i=1}^{t_u} Y_{ij} \right)^2 + \frac{1}{st_u} \left[\sum_{i=1}^{t_u} \sum_{j=1}^{s} Y_{ij} \right]^2$$

and

$$I = \sum_{i=1}^{t} \sum_{j=1}^{s} Y_{ij}^2 - \sum_{i=1}^{t} \frac{Y_{i.}^2}{s} - \sum_{j=1}^{s} \frac{Y_{.j}^2}{t} + \frac{Y_{..}^2}{st}$$

t_u, $u = 1,2,\ldots,k$ is the number of genotypes in the u^{th} group so that $\sum_{u=1}^{k} t_u = t$.

Efficiency of the various stability parameters was assessed in the light of this grouping.

Correlation coefficient was calculated for each pair of stability parameters to see whether there is any agreement between them or not. Correlation coefficient was also obtained between the environmental indices used.

RESULTS

RESULTS

The results obtained by the various analyses of the three sets of data used in the present study are given below:

4.1. Multilocational trial of ten barley varieties.

The mean data for the character 'number of ears per plant' (average for five plants) of ten barley varieties in five locations averaged over three replications are given in table 3.1.

The error mean squares (EMS) in the analyses of variance carried out in the five different locations were as follows:

Location	1	2	3	4	5
EMS	26.514	44.172	16.457	23.860	37.272

They were found to be homogeneous using Bartlett's test. (χ^2= 5.11 at df = 4). Hence the analysis of variance of the data pooled over the five locations (given in table 3.1) was performed and is provided in table 4.1.1.

The variety X location interaction was found significant at 5% level. Stability parameters were, therefore estimated under different methods.

The analysis of variance under ER model is given in table 4.1.2. Variety X location (linear) component was non-significant. Pooled deviation from regression was significant at 5% level. This was because of the significance of deviation from regression for varieties 3 and 10. The deviation from regression was significant for none of the other varieties.

The analysis of variance under PJ model for the same data is given in table 4.1.3. Heterogeneity ($\hat{e}$) among regressions was not significant and the remainder part of the variety X location interaction was significant.

One of the three replications in each location was used for the measure of environment under FP model. The remaining two replications were used for the analysis of variance and the same is given in table 4.1.4. From the table, it could be inferred that heterogeneity ($\hat{e}$) among regressions was not significant and the remainder part of the variety X location interaction was significant in this case also.

The environmental indices I_j and Z_j are given in table 4.1.5. Eberhart and Russell (1966) and Perkins and Jinks (1968) used the same environmental indices. A correlation coefficient of 0.97 was obtained between I_j and Z_j which showed that they were in close agreement.

Stability parameters for the ten varieties under the three models are provided in table 4.1.6. S_d^2 values are same for ER and PJ models.

None of the regression coefficients was found significant.

The values of W_i and σ_i^2 and F values for testing the significance of σ_i^2 are given in table 4.1.7. Only varieties 3 and 10 had significantly high σ_i^2 values. The W_is were also high for these varieties. σ_i^2 could be obtained from W_i by the relation, $\sigma_i^2 = 1.9725\ W_i - 2.1917$.

Correlation coefficients between the various pairs of stability parameters are given in table 4.1.8. A correlation coefficient of unity was obtained between W_i and σ_i^2. Hence, σ_i^2 had the same coefficient of correlation with other parameters as W_i had with them. The regression coefficients b s and b' s showed negative correlation with W_i. S_d^2 and W_i were highly correlated.

Ranking of varieties by the stability parameters could be taken as a clue for grouping them so that interaction within any group is insignificant, but between any two groups is significant. The split up of the interaction SS obtained by the grouping is given in table 4.1.9.

It was observed that grouping based on W_i or σ_i^2 values was most efficient. When variety 3 alone was seperated, the GE interaction for the rest of the varieties were found to be insignificant. This implied that all other varieties had similar response to the differing environments.

4.2. Multiseasonal trial of 25 amaranth genotypes.

The data on 25 amaranth genotypes over 11 seasons, averaged over two replications for the character 'length of fifth leaf on 30th day of sowing' are provided in table 3.2.

The seasonwise analysis of the data gave the following EMS.

Season	1	2	3	4	5	6	7	8	9	10	11
EMS	2.70	1.32	4.15	4.43	3.43	3.94	2.45	2.35	3.88	1.86	4.95

Bartlett's test showed them to be homogeneous (χ^2 = 18.04 at df =10). The analysis of variance of the pooled data over the 11 seasons is given in table 4.2.1.

The GE interaction was significant at 5% level. Therefore, stability parameters were estimated by different methods. The analysis of variance under ER model is given in table 4.22. The pooled deviation was significant at 5% level when compared against pooled error and the GE interaction (linear) component was significant at 5% level when compared against pooled deviation. Deviation from regression was significant

for varieties 8, 9, 12, 14, 17 and 19 and this was the reason for the significance of pooled deviation.

The analysis of variance under PJ model is given in table 4.2.3.

Remainder term was significant at 5% level when compared against pooled error. Heterogenity among regressions was significant in comparison with pooled error, but it was not significant when compared against remainder mean square at 5% level.

As there were only two replications in each season, one replication as a whole could not be taken for assessing the environment in FP model. Hence, the mean values of one of the 25 genotypes, which was considered as a popular variety, was taken as the environmental measure.

Analysis of variance under FP model is given in table 4.2.4. The regressions were heterogeneous. Significance of environmental residual indicated either that the environmental indices could not assess the environment adequately or that the regression model was inadequate. Deviation from regression component (interaction residual) was also significant at 5% level.

The environmental indices I_j and Z_j are given in table 4.2.5. A correlation coefficient of 0.93 was obtained

between the two indices and this high correlation restricted the need for FP model.

The regression coefficients and S_d^2 values under the three models are given in table 4.2.6. The regression coefficients for varieties 2 and 14 were significant as per t-test.

The values of W_i and σ_i^2 and F values for testing the significance of σ_i^2 aregiven in table 4.2.7. The varieties 2, 8, 9, 12, 14, 17 and 19 were found to have significantly high σ_i^2 value. Deviation mean squares were significant for all varieties among these except variety 2. But 't' values identified only varieties 2 and 14 as having significant regression coefficients.

σ_i^2 could be obtained from W_i by the relation

$\sigma_i^2 = 0.7750\ W_i - 0.1292$.

The correlation coefficients between the various pairs of stability parameters are given in table 4.2.8. Coefficient of correlation between W_i and σ_i^2 was unity. Regression coefficients and W_i values did not show high correlation, whereas W_i s had high correlation with S_d^2 values. b and b^1 as well as $S_d'^2$ and S_d^2 were highly correlated.

The ranking of genotypes based on the various stability parameters could be used as a clue for grouping them so

that interaction within any group is insignificant and that between any two groups is significant. W_i and σ_i^2 values gave good grouping. Out of the 25 genotypes, 20 genotypes excluding genotypes 8, 9, 12, 14 and 17 formed a group. The split up of the interaction SS into the groups is given in table 4.2.9. The grouping showed the efficiency of W_i and σ_i^2 in giving relevant information about the performance of genotypes over varying environments.

4.3. Trial of 15 chilli genotypes under four varying levels of ethephone

The mean data averaged over three replications of 15 chilli genotypes in four environments for the character 'number of days to first fruit set' are given in table 3.3.

The following EMS are obtained by the analyses of variance at the four environments.

Environment	1	2	3	4
EMS	17.2969	6.4388	2.6217	0.7611

Bartlett's test showed that they are heterogeneous (χ^2 = 62.1297, df = 3). The GE interaction was found to be significant when weighted analysis of variance was carried out (χ^2 =37.76, df = 25).

The analysis of variance under ER model is given in table 4.3.1. The pooled deviation as well as individual

deviation SS could not be tested for their significance since the pooled error mean square was not available. The GE interaction (linear) sum of squares was tested for significance against pooled deviation mean square and was found significant. This meant that the linear regression coefficients accounted for a major part of the GE interaction.

Analysis of variance under PJ model is given in table 4.3.2. In the absence of pooled error mean square, the significance tests of the various items was not possible. Heterogeneity among regressions was significant when compared with residual mean square. This is an indication for the linear regression coefficients to account for a large part of GE interaction.

The environmental indices under PP model were estimated using one of the three replications. The other two replications were used for the analysis of variance and is given in table 4.3.3. Since the pooled error mean square could not be found, the tests of significance of various items were not possible here also. Heterogeneity among regressions was found significant when tested against interaction residual which implied that linear regression coefficients could account for a major part of the GE interaction.

The environmental indices I_j and Z_j are given in

table 4.3.4. A correlation coefficient of 0.9986 between them showed that they were in close agreement.

Regression coefficients b_i, β_i and b_i' and deviation mean squares $\frac{\sum_{j=1}^{s} \delta_{i,j}^2}{s-2}$ and $\frac{\sum_{j=1}^{s} \delta_{i,j}'^2}{s-2}$ are given in table 4.3.5. Regression coefficient was significant for genotype 2.

The values of W_i and σ_i^2 are given in table 4.3.6. Variety '2' had the largest values for W_i and σ_i^2. The F test for σ_i^2 was not possible since pooled error mean square was not available. σ_i^2 could be obtained from W_i by the relation,

$$\sigma_i^2 = 0.6155\ W_i - 0.2931.$$

The correlation coefficient between the various pairs of stability parameters are given in table 4.3.7. W_i and σ_i^2 had a correlation coefficient equal to unity and hence both of them had the same correlation with the other stability parameters. W_i had negative correlation with the regression coefficients.

Ranking of varieties by the stability parameters was taken as a clue for grouping them so that interaction within any group is insignificant but between any two groups is significant. Weighted analysis of variance was used for grouping. All the varieties except variety '2' could be

grouped together so that interaction was insignificant within the group. Genotype '2' had the largest W_i and σ_i^2 values. Also, regression coefficient was significant for genotype 2 only.

The split up of interaction χ^2 within and between groups obtained by the weighted analysis of variance is given in table 4.3.8.

Table 4.1.1 Pooled analysis of variance for barley varieties.

Source	df	SS	MS	F
Total	49	1664.6838		
Varieties	9	282.5232	31.3915	
Locations	4	750.9464	187.7366	
Varieties X Locations	36	631.2142	17.5337	1.7709*
Pooled error	90		9.901	

*Significant at 5% level.

Table 4.1.2. Analysis of variance under ER model for barley varieties.

Source	df	SS	MS	F
Total	49	1664.6838		
Varieties	9	282.5232	31.3915	
Environments + (Varieties X Environments)	40	1382.1605		
Environments (linear)	1	750.9464		
Varieties X Environments (linear)	9	105.0146	11.6661	0.6651
Pooled deviation	30	526.1995	17.5400	1.7715*
Variety 1	3	39.5585	13.1862	1.3318
Variety 2	3	0.7787	0.2596	0.0262
Variety 3	3	170.6705	56.8902	5.7459*
Variety 4	3	77.3722	25.7907	2.6649
Variety 5	3	52.5997	17.5332	1.7709
Variety 6	3	46.8805	15.6268	1.5783
Variety 7	3	3.5407	1.1802	0.1192
Variety 8	3	3.2778	1.1259	0.1157
Variety 9	3	31.3284	10.4428	1.0547
Variety 10	3	100.1927	33.3976	3.3732*
Pooled error	90		9.901	

* Significant at 5% level.

Table 4.1.3. Analysis of variance under PJ model for barley varieties.

Source	df	SS	MS	F
Varieties	9	282.5232	31.3910	
Environments (joint regression)	4	750.9464	187.7370	
Varieties X Environments	36	631.2142		
Heterogenity among regressions	9	105.0146	11.6680	0.5987
Remainder	27	526.1995	19.4890	1.9684*
Error	90		9.901	

* Significant at 5% level.

Table 4.1.4. Analysis of variance under FP model for barley varieties.

Source	df	SS	MS	F
Varieties	9	505.4769		
Environments	4	1467.1864		
Combined regression	1	1296.6813		
Environmental residual	3	170.5051	56.8350	3.8096
Variety X Environment Interaction	36	1747.7956		
Heterogenity among regressions	9	133.5849	14.8428	0.2483
Interaction residual	27	1614.1747	59.7842	4.0073*
Error	45	1342.6954	14.9188	

*Significant at 5% level.

Table 4.1.5. Environmental indices I_j and Z_j for barley varieties.

Location	I_j	Z_j
1	5.877	5.760
2	2.845	2.650
3	-4.048	-4.210
4	-3.942	-5.140
5	-0.732	0.940

Table 4.1.6. b_i, β_i, b_i', S_d^2 and $S_d'^2$ for barley varieties.

Variety	b_i	β_i	b_i'	$S_{d_i}^2$	$S_{d_i}'^2$
1	1.5640	0.5640	1.0303	3.3995	-3.0277
2	1.4111	0.4111	1.2307	-9.5414	-8.4566
3	0.3855	-0.6145	0.6724	47.1002	108.1798
4	0.8552	-0.1448	0.7605	16.0007	8.4243
5	1.3000	0.3000	0.8315	7.7432	35.0481
6	0.5072	-0.4928	0.2768	5.5368	2.2386
7	1.3475	0.3475	1.2509	-8.6098	9.9056
8	0.8979	-0.1021	1.0072	-8.6794	-7.3788
9	0.9452	-0.0548	1.0059	0.6528	18.5133
10	0.7865	-0.2135	0.6641	23.6076	2.0571

Table 4.1.7. W_i, σ_i^2 and F values for testing the significance of σ_i^2s, for barley varieties.

Variety	W_i	σ_i^2	F
1	10.0518	17.6355	1.7812
2	2.1342	2.0180	0.2038
3	31.5320	60.0052	6.0605*
4	12.5048	22.4740	2.2699
5	9.4043	7.7432	1.6522
6	10.3167	5.5368	1.8340
7	1.9979	1.7493	0.1767
8	0.6432	-0.9229	-0.0932
9	4.9992	7.6693	0.7746
10	16.4159	30.1886	3.0490*

* Significant at 5% level.

Table 4.1.8. Correlation coefficients between the various pairs of stability parameters for barly varieties.

Stability parameters between which correlations were obtained.	Coefficient of correlation
b_i and W_i	-0.6193
b_i and b_i'	0.7747 *
W_i and $S_{d_i}^2$	0.9871 *
b_i' and W_i	-0.5738
W_i and $S_{d_i}'^2$	0.8088 *
$S_{d_i}^2$ and $S_{d_i}'^2$	0.7909 *
W_i and σ_i^2	1.0000 *

* Signicant at 5% level

Table 4.1.9. Split up of interaction SS for barley varieties.

Interaction	df	SS	MS	F
**Within group	32	409.9324	12.8104	1.2938
Between groups (Variety 3 Vs. Rest)	4	221.2818	55.3205	5.5874*
Total	36	631.2142	17.5337	1.7709*

** All varieties except variety 3 were within one group
* Significant at 5% level.

Table 4.2.1. Pooled analysis of variance for amaranth genotypes.

Source	df	SS	MS	F
Total	274	2619.4594		
Genotypes	24	1212.7981	50.5400	
Seasons	10	693.6711	69.3671	
Genotypes X Seasons	240	712.9902	2.9708	1.8432*
Pooled error	264		1.6118	

*Significant at 5% level.

Table 4.2.2. Analysis of variance under EH model for amaranth genotypes.

Source	df	SS	MS	F
Total	274	2619.4594		
Genotypes	24	1212.7981	50.5400	
Environments + (genotypes X environments)	250	1406.6613		
Environments (linear)	1	693.6711		
Genotypes X environments (linear)	24	104.8591	4.3691	1.6435*
Pooled deviation	225	608.1312	2.6584	1.6493*
Genotype 1	9	16.9104	1.8789	1.1657
" 2	9	13.5548	1.5061	0.9344
" 3	9	15.0371	1.6708	1.0366
" 4	9	15.7716	1.7524	1.0872
" 5	9	24.5534	2.7282	1.6926
" 6	9	15.6032	1.7337	1.0756
" 7	9	8.0612	0.8957	0.5557
" 8	9	100.0733	11.1192	6.8986*
" 9	9	74.0610	8.2290	5.1055*
" 10	9	20.1442	2.2382	1.3337
" 11	9	13.7641	1.5294	0.9488
" 12	9	35.2486	3.9165	2.4299*
" 13	9	5.7106	0.6345	0.3937
" 14	9	60.6651	6.7406	4.1820*
" 15	9	14.8189	1.6465	1.0216
" 16	9	24.2708	2.6968	1.6731
" 17	9	33.3532	3.7059	2.2992*
" 18	9	27.0847	3.0094	1.8671
" 19	9	28.5730	3.1748	1.9697*
" 20	9	2.5012	0.2779	0.1724
" 21	9	11.9141	1.3238	0.8213
" 22	9	16.6968	1.8552	1.1510
" 23	9	9.8851	1.0983	0.6814
" 24	9	12.9967	1.4441	0.8959
" 25	9	6.8783	0.7642	0.4742
Pooled error	264		1.6118	

*Significant at 5% level.

Table 4.2.3. Analysis of variance under PJ model for amaranth genotypes.

Source	df	SS	MS	F
Genotypes	24	1212.7981	50.5332	
Environments (joint regression)	10	693.6711	69.3671	
Genotypes X Environments	240	712.9902		
Heterogenty among regressions	24	104.8591	4.3691	1.5519
Remainder	216	608.1311	2.8154	1.7467*
Pooled error	264		1.6118	

*Significant at 5% level.

4.2.4. Analysis of variance under FP model for amaranth genotypes.

Source	df	SS	MS	F
Genotypes	24	1212.7981	50.5400	
Environments	10	693.6711	69.3671	
Combined regression	1	603.7168	603.7168	
Environmental residual	9	89.9543	9.9949	6.2011*
Genotypes X Environment interaction	240	712.9902		
Heterogenity among regressions	24	116.3228	4.8468	1.7546*
Interaction residual	216	596.6674	2.7623	1.7138*
Error	264		1.6118	

*Significant at 5% level.

Table 4.2.5. Environmental indices I_j and Z_j for amaranth genotypes.

Environment	I_j	Z_j
1	1.00	1.57
2	0.78	1.93
3	-0.15	-1.96
4	-2.63	-6.51
5	-0.22	1.17
6	0.08	0.17
7	-1.58	-0.93
8	-1.96	-3.83
9	0.73	1.07
10	0.50	1.69
11	3.45	5.63

Table 4.2.6. b_i, β_i, b'_i, $s_{d_i}^2$, and $s_{d_i}'^2$ for amaranth genotypes.

Genotype	b_i	β_i	b'_i	$s_{d_i}^2$	$s_{d_i}'^2$
1	0.8683	-0.1312	0.4419	0.2671	0.3046
2	1.8198	0.8198	1.0000	-0.1057	-1.6118
3	0.9189	-0.0811	0.4550	0.0590	0.2347
4	0.9333	-0.0667	0.4144	0.1406	0.8097
5	0.9504	-0.0496	0.4330	1.1164	1.7008
6	1.2428	0.2428	0.5583	0.1219	1.2245
7	0.7885	-0.2115	0.3324	-0.7161	-0.0973
8	1.1031	0.1031	0.4866	9.5074	10.4788
9	1.0272	0.0272	0.5618	6.6172	6.1716
10	0.4770	-0.5230	0.1540	0.6264	1.0483
11	0.5378	-0.4622	0.3335	-0.0824	-0.4932
12	1.1167	0.1167	0.4854	2.3047	3.3821
13	1.5333	0.5333	0.7050	-0.9773	0.4384
14	1.9355	0.9355	1.0008	5.1228	4.9388
15	0.9182	-0.0818	0.3461	0.0347	1.2248
16	0.7398	-0.2602	0.3177	1.0850	1.5872
17	0.9343	-0.0657	0.4750	2.0941	2.1405
18	1.3028	0.3028	0.6382	1.3976	1.8542
19	1.4091	0.4091	0.6027	1.5630	3.4186
20	0.8452	-0.1548	0.3910	-1.3339	-0.9253
21	0.3451	-0.6549	0.1439	-0.2880	-0.1643
22	1.1134	0.1134	0.5936	0.2434	-0.0633
23	1.1287	0.1287	0.5871	-0.5134	-0.6256
24	0.7064	-0.2936	0.3693	-0.1677	-0.2278
25	0.3584	-0.6416	0.1601	-0.8475	-0.7526

Table 4.2.7. W_i, σ_i^2 and F values for testing the significance of σ_i^2s, for amaranth genotypes.

Genotype	W_i	σ_i^2	F
1	2.4319	1.7555	1.0892
2	4.4930	3.3529	2.0802*
3	2.1319	1.5230	0.9449
4	2.2320	1.6006	0.9931
5	3.4624	2.5541	1.5846
6	2.4086	1.7374	1.0079
7	1.3090	0.8853	0.5493
8	14.0891	10.7897	6.6942*
9	10.3920	7.9245	4.9166*
10	3.6986	2.8922	1.7944
11	2.7671	2.0153	1.2503
12	4.9880	3.7365	2.1382*
13	1.8920	1.3371	0.8290
14	11.8822	9.0795	5.6631*
15	2.1083	1.5048	0.9336
16	3.6662	2.7121	1.6827
17	4.6905	3.5029	2.1751*
18	4.1458	3.0838	1.9133
19	4.6559	3.4791	2.1585*
20	0.4435	0.2146	0.1337
21	3.3441	2.4625	1.5278
22	2.3840	1.7184	1.0661
23	1.4520	0.9961	0.6180
24	2.1650	1.5487	0.9690
25	2.5670	1.8602	1.1541

* Significant at 5% level.

Table 4.2.8. Correlation coefficients between various pairs of stability parameters for amaranth genotypes.

Stability parameters between which correlations were obtained.	Coefficient of correlation
b_i and W_i	0.3709
b_i and b_i'	0.9701 *
W_i and $S_{d_i}^2$	0.9638 *
b_i' and W_i	0.3727
W_i and $S_{d_i}'^2$	0.9017 *
$S_{d_i}^2$ and $S_{d_i}'^2$	0.9636 *
W_i and σ_i^2	1.0000 *

* Significant at 5% level.

Table 4.2.9. Split up of interaction SS for amaranth genotypes.

Interaction	df	SS	MS	F
**Within group	190	372.4981	1.9605	1.2163
Between group	50	340.4921	6.8098	4.2250*
Total	240	712.9902	2.9708	1.8432*

** All genotypes except genotypes 8, 9, 12, 14 and 17 were within one group.
* Significant at 5% level.

Table 4.3.1. Analysis of variance under ER model for ohilli genotypes.

Source	df	SS	MS	F
Total	59	1857.8145		
Genotypes	14	432.2998	30.8786	
Environments + (Genotypes X Environments)	45	1425.5148		
Environments (linear)	1	1265.4953		
Genotypes X Environments (linear)	14	123.3858	8.8153	7.2175*
Pooled deviation	30	36.6338	1.2211	
Genotype 1	2	0.9442	0.4721	
" 2	2	3.1334	1.5667	
" 3	2	2.5788	1.2894	
" 4	2	1.4159	0.7080	
" 5	2	6.1125	3.0563	
" 6	2	1.3999	0.7000	
" 7	2	3.5986	1.7993	
" 8	2	5.6330	2.8165	
" 9	2	1.0255	0.5128	
" 10	2	6.8111	3.4056	
" 11	2	0.0474	0.0237	
" 12	2	0.4065	0.2033	
" 13	2	1.9353	0.9677	
" 14	2	0.7780	0.3890	
" 15	2	0.8127	0.4069	

*Significant at 5% level.

Table 4.3.2. Analysis of variance under PJ model for chilli genotypes.

Source	df	SS	MS	F
Genotypes	14	432.2998	30.8786	
Environments (joint regression)	3	1265.4953	421.8318	
Genotypes X Environments	42	160.0196	3.8100	
Heterogenity among regressions	14	123.3858	8.8153	6.7359*
Remainder	28	36.6338	1.3084	

*Significant at 5% level.

Table 4.3.3. Analysis of variance under FP model for chilli genotypes.

Source	df	SS	MS	F
Genotypes	14	1000.1150		
Environments	3	2883.0066		
Combined regression	1	2866.9343		
Environmental residual	2	16.0723		
Genotype X Environment Interaction	42	331.9784		
Heterogenity among regressions	14	230.1176	16.4370	4.8338*
Interaction residual	28	101.8608	3.6379	

*Significant at 5% level.

Table 4.3.4. Environmental indices I_j and Z_j for chilli genotypes.

Environment	I_j	Z_j
1	-7.4380	-6.5700
2	-0.1620	0.2302
3	3.5440	2.9367
4	4.0560	3.4034

Table 4.3.5. b_i, β_i, b_i', $\frac{\sum_{j=1}^{s} \delta_{ij}^2}{s-2}$ and $\frac{\sum_{j=1}^{s} \delta_{ij}'^2}{s-2}$ for chilli genotypes.

Genotype	b_i	β_i	b_i'	$\frac{\sum_{j=1}^{s} \delta_{ij}^2}{s-2}$	$\frac{\sum_{j=1}^{s} \delta_{ij}'^2}{s-2}$
1	1.3919	0.3919	1.6336	0.4721	0.4014
2	0.1373	-0.8637	0.2158	1.5667	2.6168
3	1.4764	0.4764	1.7952	1.2894	0.1855
4	0.6666	-0.3334	1.1318	0.7080	0.0993
5	1.0449	0.0449	1.1653	3.0563	8.4566
6	1.1115	0.1115	1.3281	0.7000	0.5329
7	0.9286	-0.0714	1.0704	1.7993	7.7863
8	0.7485	-0.2514	1.3376	2.8165	2.2679
9	1.2060	0.2060	1.5026	0.5128	0.5749
10	1.2453	0.2453	1.4068	3.0456	1.4094
11	1.0672	0.0672	1.0215	0.0237	0.0127
12	1.0543	0.0543	1.0746	0.2033	1.7631
13	1.0558	0.0558	1.3287	0.9677	0.0037
14	1.0373	0.0373	1.0295	0.3890	2.5517
15	0.8288	-0.1712	1.3707	0.4069	0.8231

Table 4.3.6. W_i and σ_i^2 for chilli genotypes.

Genotype	W_i	σ_i^2
1	8.6980	5.0604
2	41.1640	25.0419
3	13.5980	8.0759
4	6.7300	3.8490
5	3.9150	2.1162
6	1.5390	0.6541
7	2.5170	1.2560
8	6.8400	3.9166
9	2.8880	1.4845
10	7.4440	4.2883
11	0.2690	-0.1278
12	0.4070	-0.0425
13	1.3790	0.5558
14	0.5630	0.0533
15	2.0500	0.9687

Table 4.3.7. Correlation coefficient between various pairs of stability parameters for chilli genotypes.

Stability parameters between which correlations were obtained.	Coefficient of correlation
b_i and W_i	- 0.5860 *
b_i and b'_i	0.8462 *
W_i and b'_i	-0.5497 *
W_i and σ_i^2	1.0000 *
W_i and $\frac{\sum_{j=1}^{s} \delta_{ij}^2}{s-2}$	0.2230
W_i and $\frac{\sum_{j=1}^{s} \delta'^2_{ij}}{s-2}$	-0.0080
$\frac{\sum_{j=1}^{s} \delta_{ij}^2}{s-2}$ and $\frac{\sum_{j=1}^{s} \delta'^2_{ij}}{s-2}$	0.5413 *

* Significant at 5% level.

Table 4.3.8 Split up of interaction χ^2 for chilli genotypes.

Interaction	df	χ^2 value
** Within group	24	24.0859
Between group (Genotype 2 Vs. Rest)	1	13.6743*
Total	25	37.7602

** All genotypes except genotype 2 formed a single group

* Significant at 5% level.

DISCUSSION

DISCUSSION

The regression approaches by Eberhart and Russell (1966), Perkins and Jinks (1968) and Freeman and Perkins (1971) do not differ very much. Although they used different models, the stability parameters under all the three models measure almost the same. Regarding stability, the first two methods lead to the same conclusion, only difference being in the value ofthe regression coefficient. That is, regression coefficient in PJ model is obtained by subtracting unity from that in ER model. Freeman and Perkins (1971) used a different measure of the environment and comments that a value of unity or near to unity for the combined regression coefficient ($\bar{\beta}$) is needed for meaningful conclusions. But when $\bar{\beta}$ is equal to 'one', parameters estimated under this model will be same as those under PJ model. This amounts to saying that all the three methods do not differ substantially.

There had been much confusion on the splitting up of the total SS and df into components. All the three methods differ in this aspect. The partitioning of the SS and the corresponding df by Freeman and Perkins (1971) is correct. But nothing had been mentioned as to what exactly was the problem in the other two methods.

Eberhart and Russell (1966) partitioned the (~~variety~~ environment + variety X environment) SS into SS due to environment (linear), variety X environment (linear) and pooled deviation from regression. The corresponding df were one, (t-1) and t (s-2) respectively. It may be noted that the SS between environments has the same value as that of the SS due to environments (linear), the df being (s-1) and 'one' respectively. This was because the environmental SS is split into environments (linear) and environment (non linear), the corresponding df being 'one' and (s-2) respectively. But under this model, the SS due to environments (non linear) becomes zero, because the environmental means themselves were chosen as the environmental index. The SS due to environment (non linear) or SS due to deviation from combined regression is included in the SS due to pooled deviation under this model.

In the analysis of variance, Perkins and Jinks (1968) had given (s-1) as the degrees of freedom for the SS due to combined regression, which is wrong. The SS due to combined regression should have only 'one'df and (s-1) is the df for the SS due to environments. But, as pointed out earlier, the remainder part of the SS due to environments is zero, because of regressing the environmental means on themselves and the corresponding df is (s-2). Though Eberhart and Russell (1966) combined the sum of squares due to deviation

from combined regression along with the SS due to pooled deviation, Perkins and Jinks did not.

A defect of the Eberhart and Russell as well as Perkins and Jinks approaches, pointed out by Freeman and Perkins is that of dependence of the environmental measure used, on the mean of genotypes. As pointed out by Hardwick and Wood (1972) and Shukla (1983), though some of the basic assumptions of the regression model-like measurement of independent variables free from error-are violated in these, these methods as well as that of Freeman and Perkins can very well be used for practical purposes, atleast in cases where the number of genotypes is fairly large. It may be pointed out that S_d^2, given as a second measure of stability, in all these three models is nothing but a measure of reliability of the first measure, namely, the regression coefficient.

The advantage of regression method often pointed out, is of predictability of response. But this is possible only if the environmental measure is available for the environments, where the genotype or genotypes are intended to be introduced. But if the measure is chosen as the environmental mean as is done by Eberhart and Russell (1966) or Perkins and Jinks (1968) or the mean of all genotypes in a replicate not used for the estimation of parameters as done by Freeman

and Perkins (1971), there is no predictability, as, such a measure will not be available for a new environment. This can be made possible if some physical measure of the environments such as weather parameters and soil characteristics are used to get the environmental index. Moreover, in order that predictability under linear regression method is to be satisfactory, the deviation from regression should be very small. In other words, the dependence of the genotype on the environment should be linear. Hence, efforts may be made to estimate the stability parameters, with some physical measure of environments as the environmental index.

The stability variance (σ_i^2) of Shukla (1972) can be obtained by a linear transformation of W_i, Wricke's ecovalence ratio, as shown in chapter 3.

Logically, these are very good measures of stability so far as we define, genotypes having similar sensitivity to differing environments, as stable. Ofcourse, there is no predictability for these parameters.

A method of forming groups of genotypes such that interaction of genotypes with environments is insignificant within any group, but significant between any two groups, is suggested in the present study. The genotypes so included in a group will have same sensitivity to differing environments and thus can be said to be relatively stable. The

ranking of the genotypes by the different stability parameters had been discussed in this context in the illustrative examples.

W_is and σ_i^2s can be used as measures of stability in almost all situations. The regression coefficient can conveniently be used as a measure of relative sensitivity of a genotype to the environment, only if it accounts for all or most of the GE interaction. The grouping technique can be used effectively to verify the comparative effifiency of the various stability parameters as well as to identify genotypes of same stability.

5.1. Multilocational trial of ten barley varieties.

In the analyses of variances under ER, PJ and PP models, heterogeneity among regressions was not significant and deviation from regression was significant as seen from tables 4.1.2., 4.1.3 and 4.1.4. This showed the inadequacy of the linear regression coefficients to account for the GE interaction. Hence the regression approach failed to give any relevant information on the relative stability of genotypes. By the method of grouping of genotypes, it was found that the GE interaction among all the genotypes except genotype '3' was insignificant and that of genotype '3' Vs. rest was significant. That is, all the genotypes except

genotype '3' showed some sensitivity to environmental changes. σ_i^2 was significant for genotypes '3' and '10'. W_i was also large for these two genotypes. It may be noted that genotype 10, which was included in the group of other genotypes had smaller values of W_i and σ_i^2 compared to genotype '3'. None of the regression coefficients was found significant. This means that W_i and σ_i^2 could be served as better measures of stability than the regression coefficients estimated under the three models.

The correlation coefficient between W_i and S_d^2 of EH model was ashigh as 0.987. This could be explained as follows. Since the regression could not explain the interaction SS to any significance, the major portion of the interaction SS was contained in the deviation from regression SS hence in S_d^2 values. W_i is nothing but the contribution of the i^{th} genotype to the interaction sum of squares and hence the high correlation.

The correlation coefficient between the environmental means and the environmental indices of FP model was 0.97. Environmental means could very well be used instead of the different measure used in FP model as they had a correlation coefficient near to unity. It might be noted that the correlation coefficient between b and $\hat{b}$ was only 0.77. This

was because of the difference in the genotypic means based on three and two replications in the two models.

5.2. Multiseasonal trial of 25 amaranth genotypes.

The heterogeneity among regressions was significant under ER and FP models. But it was not significant under PJ model because of the wrong partitioning of the df. The deviation mean squares of genotypes 8, 9, 12, 14, 17 and 19 were significant, when compared against pooled error mean square, as seen from table 4.2.2. This was the reason for the significance of pooled deviation.

Among the 25 genotypes, 20 genotypes except genotypes 8, 9, 12, 14 and 17 could be grouped together by using the grouping technique evolved. Within the group, interaction was nonsignificant showing that those genotypes had similar response to differing environments. The ranking of genotypes based on W_i and σ_i^2 was the efficient guide in group formation. It might be noted that there were seven genotypes with significant σ_i^2 values of which two, having low σ_i^2 values, could be grouped with the rest so that the GE interaction within group was not significant.

In this example, the deviation from regression was significant in all the three regression methods. This meant

that a major portion of interaction was contained in the S_d^2 or $S_d'^2$ values and hence the correlation of S_d^2 and $S_d'^2$ with W_i was very high (.96 and 0.90).

The environmental means and the environmental indices of FP model had a correlation coefficient equal to 0.93. The correlation coefficient between b and b' was also high (0.97). This was because the means of the genotypes used in all the methods were same, that is, based on two replications. Here also, all the three regression methods did not differ in measuring stability parameters.

5.3. Trial of 15 chilli genotypes over four environments.

In the absence of the pooled error mean square, the tests of significance of various items in the analyses of variance were not possible and the second parameter of stability could not be obtained under ER, PJ and FP models.

Regression coefficient was significant for variety '2' only. W_is and σ_i^2 s were highest for this variety. The technique of grouping could group all varieties except variety '2' together so that interaction was not significant within the group.

The correlation coefficient between b and b' was 0.85. There was negative correlation between W_i s and b s and

also between W_is and b_is, though not very high. The correlation coefficient between W_i and $\sum_{j=1}^{s} \delta_{ij}^2$ was very low. The low values of the correlation coefficients in this case could not be explained in the absence of the significance tests for heterogenity among regressions and deviation from regression.

A correlation coefficient of 0.9986 between environmental means and environmental indices under FP model showed that the environmental means could very well be used as the measure of environment and hence the three regression methods did not differ in the measure of stability.

The following conclusions could be drawn by the analyses of the data:

There was very high correlation coefficient between the environmental indices of FP and ER as well as PJ models. In such situations, there is no much difference among the three regression models, provided the genotypic means are measured with same precision.

When one replication as a whole is kept apart for the environmental measure as in the case of FP model, the genotypic mean is measured in each environment from the remaining replications. The precision in the estimate of

genotypic means becomes lower in such situations. That is genotypic means with less precision compared to ER or PJ models, were regressed on an environmental measure which has very high linear relationship with that of the models of Eberhart and Russell or Perkins and Jinks, under FP model. This amounts to saying that ER or PJ models seems better compared to that of FP model, in case, one replication is used entirely for the environmental measure.

If the linear regressions explain a lions share of the GE interaction, the correlation coefficient between W_i or σ_i^2 and the regression coefficients will be high. If the regressions cannot explain any significant portion of GE interaction, there will be high correlation between S_d^2 or $S_d'^2$ and W_i or σ_i^2.

Although some of the tests could not be performed due to the heterogeneity of error variances in the example of chilli genotypes, all the stability parameters considered were found quite satisfactory in the light of the grouping method. Still, efforts will have to be made for obtaining statistically valid stability parameters when the error variances become heterogeneous.

SUMMARY

SUMMARY

Different techniques of estimating stability of genotypes were studied in detail with special reference to the regression approaches of Eberhart and Russell (1966), Perkins and Jinks (1968) and Freeman and Perkins (1971), ecovalence ratio of Wricke (1966) and stability variance of Shukla (1972). The three regression approaches do not differ very much. The mistakes crept into the analysis of variance of Perkins and Jinks (1968) were identified and the correct analysis of variance was provided. Difficulties encountered in case of heterogeneity of error variances in the different environments were projected through an example.

Formation of groups of genotypes such that GE interaction is insignificant within any group, but significant between any two groups was suggested in this study. The genotypes coming in a group have similar sensitivity. ie. A genotype of a group is stable in relation to the other genotypes in the group thus formed.

Shukla's stability variance was expressed as a linear function of Wricke's ecovalence ratio.

All the stability parameters were assessed for efficiency in the light of the grouping method suggested in the

present work, in three different sets of data. Correlation coefficients among different stability parameters were also used for comparison.

When the number of genotypes is large, any of the three regression approaches could very well be used, in case the regression explains a large part of the GE interaction. If the regression does not explain a major portion of the GE interaction, the ecovalence ratio or the stability variance could be made use of. The grouping method can be adopted in any situation and ecovalence ratio or stability variance can be better guides for grouping.

Regression technique using the physical measures of environments as the environmental index is suggested for future work.

REFERENCES

REFERENCES

Allard, R.W., and Bradshaw, A.D. (1964). Implications of genotype-environmental interactions in applied plant breeding. Crop Sci., 4 : 503-508.

*Bartlett, M.S. (1947). The use of transformations. Biometrics., 3 : 39-52.

Breese, E.L. (1969). The measurement and significance of genotype-environment interactions in grasses. Heredity., 24 : 27-44.

Bucio Alanis, L. (1966). Environmental and genotype-environmental components of variability. I. Inbred lines. Heredity., 21 : 387-397.

Bucio Alanis, L. and Hill, J. (1966). Environmental and genotype-environmental components of variability. II. Heterozygotes. Heredity., 21 : 399-405.

Bucio Alanis, L., Perkins, J.M. and Jinks, J.L. (1969). Environmental and genotype-environmental components of variability. V. Segregating generations. Heredity., 24 : 115-127.

Bulmer, M.G. (1980). The mathematical theory of quantitative genetics. Oxford University Press, New York.

*Comstock, R.E. and Moll, R.H. (1963). Genotype-environment interactions. In : Statistical Genetics and Plant Breeding. NAS-NRC. Publ., 982 : 164-196.

Devadas, V.S. (1982). Screening for non-bolting type(s) of amaranths suited for year round planting. M.Sc. thesis submitted to College of Horticulture, Vellanikkara.

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

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

Freeman, G.H. and Dowker, B.D. (1973). The analysis of variation between and within genotypes and environments. Heredity., 30 : 97-109.

Freeman, G.H. (1973). Statistical methods for the analysis of genotype-environment interactions. Heredity., 31 (3) : 339-354.

Freeman, G.H. and Perkins, J.M. (1971). Environmental and genotype-environmental components of variability. VIII. Relations between genotypes grown in different environments and measures of these environments. Heredity., 27 : 15-23.

Fripp, Yvonne J. (1972). Genotype-environmental interactions in Schizophyllum commune. II. Assessing the environment. Heredity., 28 : 223-238.

Fripp, Yvonne J. and Caten, C.E. (1971). Genotype-environmental interactions in Schizophyllum commune. I. Analysis and Character. Heredity., 27 : 393-407.

Fripp, Yvonne J. and Caten, C.E. (1973). Genotype-environmental interactions in Schizophyllum commune. III. The relationship between mean expression and sensitivity to change in environment. Heredity., 30 : 341-349.

Hardwick, R.C. and Wood, J.T. (1972). Regression methods for studying genotype-environment interactions. Heredity., 28 : 208-222.

Indira, P. (1982). Response of chilli genotypes to ethephon application. M. Sc. thesis submitted to College of Horticulture, Vellanikkara.

Jain, J.P. (1982). Statistical techniques in quantitative genetics. Tata Mc Graw-Hill publishing Company Ltd., New Delhi.

Jinks, J.L. and Perkins, J.M. (1970). Environmental and genotype-environmental components of variability. VII. Simultaneous prediction across environments and generations. Heredity., 25 : 475-480.

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

*Mather, K. (1971). On Biometrical Genetics. Heredity., 26 : 349-364.

Mather, K. and Jinks, J.L. (1971). Biometrical Genetics. 2nd Edn. Chapman and Hall, London.

Mather, K. and Morley Jone, R. (1958). Interaction of genotype and environment in continuous variation. I. Description. Biometrics., 14 : 343-359.

Miller, P.A., Robinson, H.F. and Pope, O.A. (1962). Cotton variety testing additional information on variety X environment interactions. Crop Sci., 2 : 349-352.

Miller, P.A., Williams, J.C.^Aand Robinson, H.F. (1959). Variety X environment interactions in cotton variety tests and their implications on testing methods. Agron. J., 51 : 132-134.

Morley Jones, R. and Mather, K. (1958). Interaction of genotype and environment in continuous variation. II. Analysis. Biometrics., 14 : 469-498.

Panse, V.G. and Sukhatme, P.V. (1954). Statistical methods for Agricultural Workers. I.C.A.R., New Delhi.

Perkins, J.M. (1970). Environmental and genotype-environmental components of variability. VI. Diallel sets of crosses. Heredity., 25 : 129-40.

Perkins, J.M. (1972). The principal component analysis of genotype-environmental interactions and physical measures of the environment. Heredity., 29 : 51-70.

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

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

Perkins, J.M, and Jinks, J.L. (1971). Specificity of the interaction of genotypes with contrasting environments. Heredity., 26 : 463-474.

Perkins, J.M. and Jinks, J.L. (1973). The assessment and specificity of environmental and genotype-environmental components of variability. Heredity., 30 : 111-126.

*Plaisted, R.L. and Peterson, L.C. (1959). A technique for evaluating the ability of selection to yield consistently in different locations and seasons. Amer. Potato. J., 36 : 381-385.

Rawlo, S. and Das, M.N. (1978). An alternative approach for interpretation of data collected from groups of experiments. J. Indian Soc. Agri. Stat., 30 : 99-107.

Sapate, B.G. and Atale, S.B. (1983). Statistical aspects of stability measures. A paper presented at the 37th conference of ISAS.

Sapate, B.G. and Thote, S.G. (1983). A note on "Freeman and Perkins" stability measure. A paper presented at the 37th conference of ISAS.

Shukla, G.K. (1972 a). Some statistical aspects of partitioning genotype-environmental components of variability. Heredity., 29 : 237-245.

Shukla, G.K. (1983). Use of regression approach in the analysis of genotype-environmental interactions. J. Indian Soc. Agri. Stat., 35 (2) : 129-138.

Singh, R.K. and Choudhary, B.D. (1977). Biometrical methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi - Ludhiana.

Sprague, G.F. and Federer, W.T. (1951). A comparison of variance components in corn yield trials. II. Error, year X variety, location X variety and variety components. Agron. J., 43 : 535-541.

Tai, G.C.C. (1971). Genotypic stability analysis and its application to potato regional trials. Crop Sci., 11 : 184-190.

Thote, S.G., Sapate, B.G. and Jahagirdar, S.W. (1983). A study on limitations of stability models. A paper presented at the 37th conference of ISAS.

*Tukey, J.W. (1949). One degree of freedom for non-additivity. Biometrics., 5 : 232-242.

Verma, M.M. and Gill, K.S. (1975). Ed. Parmindar Singh. Genotype-environment interaction - Its measurement and significance in plant breeding.

*Wricke, G.(1966). Über eine Biometrics che Methode zur Erfassung der okologischen Anpassung. Acta Agri. Scand Suppl. 16 : 98-101.

*Yates, F. and Cochran, W.G. (1938). The analysis of groups of experiments. J. agric. Sci. Camb. 28 : 556-580.

* Original not seen.

COMPARISON OF DIFFERENT TECHNIQUES FOR THE ESTIMATION OF GENOTYPE-ENVIRONMENT INTERACTION

By

LALY JOHN C.

ABSTRACT OF A THESIS

Submitted in partial fulfilment of the

requirements for the degree of

Master of Science (Agricultural Statistics)

Faculty of Agriculture

Kerala Agricultural University

Department of Statistics

COLLEGE OF VETERINARY & ANIMAL SCIENCES

Mannuthy, Trichur.

1984

ABSTRACT

The genotypic stability analyses of Eberhart and Russell (1966), Perkins and Jinks (1968), Freeman and Perkins (1971), Wricke (1966) and Shukla (1972) were studied in detail. The mistakes in the analysis of variance of Perkins and Jinks (1968) were corrected. The first three analyses which used the theory of regression do not differ substantially. These could satisfactorily be used with large number of genotypes, provided, the regression explains a large part of the genotype-environment interaction. On the otherhand, when the regression cannot explain a large part of the genotype-environment interaction, Wricke's ecovalence ratio and Shukla's stability variance could satisfactorily be used.

Shukla's stability variance was expressed as a linear function of Wricke's ecovalence ratio. These two stability measures could be used effectively in almost all situations.

Formation of groups of genotypes such that the genotype-environment interaction is insignificant within any group, but significant between any two groups was suggested in this study. The genotypes in any group have similar sensitivity to differing environments and any one of them is defined as stable in rlation to those in the group. The different stability parameters were assessed for efficiency using this method by making use of three different sets of data.