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GENOTYPE x SITE INTERACTION AMONG MUTAGEN-DERIVED BARLEY POPULATIONS*

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Abstract

Investigations were conducted on genotype x site interaction of mutagen-derived barley lines in comparison to control over four different sites in South Australia.

Seeds of five cultivars (Clipper, C.I. 3576, Proctor, Ketch and Prior) having different yields and adaptation characteristics were treated with 0.04 M ethyl methanesulphonate (EMS) for 8 hours and populations of M_2-derived treated and control lines were assessed in replicated yield trials in the M_4 generation.

Analyses of variance of yield combined over all sites were carried out separately on the treated and control populations of each cultivar. The control populations of each cultivar did not exhibit genotypes x site (G X E) interaction in any of these analyses, indicating a homogeneity of response across all sites among the control lines. In contrast, most of the treated populations showed significant G X E interaction, indicating that EMS treatment had induced heterogeneity of response across sites among treated lines. Furthermore, the significant interaction sum of squares were partitioned into its components using a regression analysis. In most cases the interaction term was due mainly to deviation from regression.

Introduction

Many workers have used different mutagens on a range of crop plants to induce genetic variability in quantitative characters. (Gregory, 1955; Oka *et al.*, 1958; Rawlings *et al.*, 1958; Brock & Latter, 1961, Krull & Frey, 1961; Brock, 1965; Gaul, 1965; Miah & Yamaguchi, 1965). They also have observed negative or positive shifts in the mutated population means.

These studies showed that mutagens are effective in generating variability in quantitative characters. However, just as in plant breeding programmes based on hybridization, the realized selection commonly was less than that predicted from estimates of the geno-

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typic variance of the population from which the selections were made. This discrepancy was ascribed to non-additive genetic effects and to genotype x environment interactions (Brock & Latter, 1961; Aastveit & Gaul, 1967). The genotype x environment interaction component could not be measured in these early mutation studies because tests were conducted in only one environment. However, some recent work of Gaul *et al.* (1969) has involved the testing of successive generations of M_2-derived barley families at two locations. Their study revealed that the genotypic variance for yield was inconsistent between generations and between locations within generations. However, their experiments were not specifically designed to estimate genotype x environment interactions.

In addition, the yield performance of several macro-mutations of cereals have been compared with the parent cultivars over a range of environments (Gustafsson, 1951; Froier, 1954; Bogyo *et al.*, 1969; Pacucci and Frey, 1972) and these studies have provided evidence of G X E interactions among mutagen-derived material. Recently Fatunla & Frey (1974) have studied the G X E interactions of randomly selected irradiated and non-irradiated strains of oats from different bulk populations.

Information on the G X E interactions of randomly selected populations derived from chemical mutagenic treatments is scanty. The present investigations were therefore designed to study the induced genotypic variance and the magnitude of G X E interactions in EMS-treated material of barley cultivars with diverse yields and adaptation pattern.

Materials and Methods

Five barely cultivars (Clipper, C.I. 3576, Proctor, Ketch, Prior) were chosen on the basis of adaptation performance (Table 1), determined in comprehensive barley trials

Table 1. Adaptation parameters of cultivars selected for mutation studies.

Source	Cultivar	Parameters estimated on natural scale		
		Mean yield (gm/plot)	Regression coefficient (b)	S.E. (b)
(a) Sparrow (1972)	Proctor	245	1.46	0.14
40 cultivars tested over	C.I. 3576	341	0.92	0.25
15 environments	Prior	265	0.84	0.15
(b) Sparrow (unpublished)	Clipper (W. I. 2200)	352	1.23	0.13
13 cultivars tested over				
13 environments	Ketch (W.I. 2137)	325	0.61	0.18

conducted over a range of sites and seasons in South Australia by Dr. D.H.B. Sparrow of the Waite Agricultural Research Institute.

The mutagenic treatment consisted of immersing 200 seeds of each cultivar in 200 ml of freshly prepared unbuffered aqueous solution of EMS (0.04 M) in Petri dishes for 8 hr at 23°C. Details of M_1 generation have been reported earlier (Ghafoor Arain, 1974).

In the M_2 generation, drastically mutant plants were removed and the remainder were then thinned at random to have 5 plants per pot. At maturity, one normal-appearing plant per pot was selected *at random* and harvested as a M_3 seed. In July, 1969, the M_3 seeds from each of the 65 randomly selected M_2 plants were sown in the field in single rows 3.05 m long. These rows were grown at 36 cm spacing with the aim of obtaining sufficient M_4 seed.

Five sites differing in annual rainfall pattern and soil type in the cereal-growing areas of South Australia were selected (Ghafoor Arain, 1973). The sites chosen were situated near the towns of Monarto South (referred to herein as Bundaleer, the name of the farm), Roseworthy (at the Agricultural College), Minlaton, Adelaide (at the Waite Institute) and Clinton.

Because of the large size of the field plots used by the Plant Breeding Section at the Waite Institute, and the limited availability of seed and experimental space, it was not possible to utilize all 65 treated M_2-derived and control lines of each cultivar for testing. In order to keep a balance between the need to test a large number of treated lines and to retain a reasonable number of control lines for comparison, a compromise was made. It was decided to include 35 treated and 25 control lines from each of Clipper, C.I. 3576, Proctor and Ketch cultivars, with at least 200 gm of M_4 seed, in the field experiments. Unfortunately, many of the M_3 single rowe of Prior did not produce the required quantity of seed for use in field trials, hence only 25 treated and 15 control ines of this cultivar were included in the field experiments.

The seeds of the treated and control lines were grown in a two-replicate randomized layout in M_4 generation at each of the five selected sites during 1970. The treated and control lines of each cultivar were randomized within a sub-block with two border plots of the parent cultivar separating each sub-block.

The experimental plots were sown with a magazine-loaded cone seeder using 20 gm of seed per plot (67 kg/ha). The individual plots consisted of four rows 4 m in length and 15 cm apart, with 30 cm space between adjacent plots and 1 m wide path ways between bays of plots.

No results were obtained from the Clinton site in 1970 since most of the plots were destroyed by field mice soon after germination. Hence, data for yield were recorded for each plot at the remaining four sites: Bundaleer, Roseworthy, Minlaton and Waite.

At the maturity, plants upto 30 cm length at each end were removed and the re-

mainder of the plot (3.40 m) was harvested with a "Waite Gravelly Harvester". The weight of clean grain was recorded in gm/plot.

An analysis of variance (ANOVA) was undertaken for (a) yield data at individual sites (b) the data combined over all sites. In the first analysis the error variances for sites were tested for homogeneity by Bartlett's (1937) X^2 test before combining the data for all sites.

The mathematical model used for ANOVA combined over all sites was:

$$Y_{ijk} = \mu + G_i + E_j + (GE)_{ij} + R_{jk} + e_{ijk} \quad (1)$$

where

Y_{ijk} = yield of line (i) at site (j) and in replicate (k).

μ = population mean, i.e. mean yield of all lines over all sites and replicates.

G_i = mean genotypic effect of line (i).

E_j = mean effect of site (j).

$(GE)_{ij}$ = interaction effect of line (i) at site (j).

R_{jk} = effect of replicate (k) within site (j).

e_{ijk} = error of line (i) at site (j) and in replicate (k)

Estimates of the variance components $\sigma^2 p$ (genotypic variance due to lines), $\sigma^2 ps$ (line x site interaction variance) and $\sigma^2 e$ (error variance) were obtained according to the formulae used by Johnson *et al.* (1955). Contribution of individual lines to G X E interaction was identified by calculating "W" values as proposed by Wricke (1962, 1966).

For the regression analysis of yield data, a statistical approach described by Eberhart and Russell (1966) was used. The mathematical model used in the ANOVA (1) was extended to:

$$Y_{ijk} = \mu + G_i + E_j + b_i I_j + \sigma_{ij} + R_{jk} + e_{ijk} \quad (2)$$

Where

b_i = linear regression coefficients of line (i) over all sites,

I_j = environmental index

$= E_j - E$

Where E_j = measure of environment at site (j) and E = mean of all E_j.

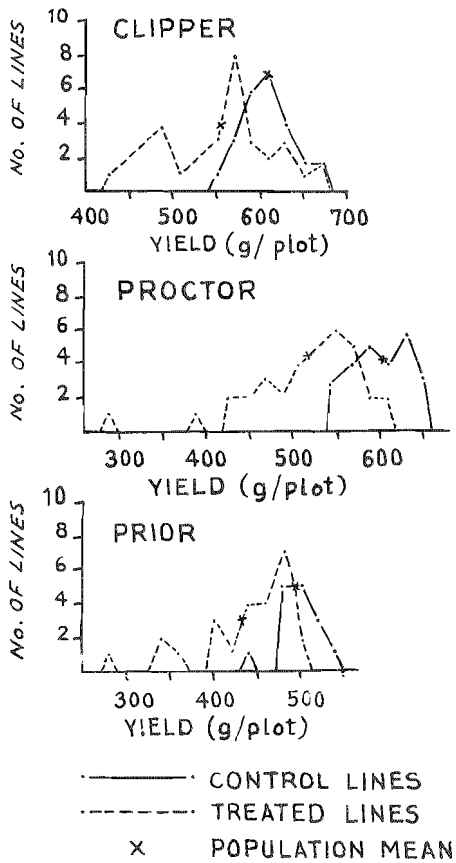
σ_{ij} = deviation from regression of line (i) at site (j).

Results

(a) Mean yield and frequency distributions

The mean yields over all sites for treated and control lines of each cultivar are summarized in frequency distributions shown in Figure 1. A characteristic of the frequency distribution curves was a pronounced shift of the EMS-treated lines away from their respective controls towards lower yield in the M_4 generation.

The mean yields of the treated lines of each cultivar were significantly less than the means of corresponding control populations in all cases. Even though the overall mean yield was reduced, some of the treated lines of Clipper performed similar to that of the highest yielding control lines and with C.I. 3576 three of the treated lines out-yielded the highest yielding control line.



	POP. MEANS	
	TREAT.	CON.
CLIPPER	553·8 ± 12·3	610·6 ± 14·1
C.I. 3576	608·1 ± 13·3	677·9 ± 15·1
PROCTOR	515·3 ± 11·7	603·0 ± 14·5
KETCH	499·3 ± 10·4	536·2 ± 12·5
PRIOR	435·0 ± 8·3	495·4 ± 10·5

Fig. 1. Frequency Distribution of Yield Combined over all Sites of M_2-Derived Treated and Control Lines of Five Barley Cultivars in M_4 Generation (1970).

(b) Analyses of variance combined over all sites

These analyses were performed separately for the control and treated populations of each cultivar involving lines, sites and replicates within sites. The error variances on natural scale for sites were tested for heterogeneity by Bartlett's X^2 test in each analysis before attempting combined analysis of variance. Where error variances were significant on natural scale, the data were transformed to logarithmic scale in an attempt to induce homogeneity of error and Bartlett's X^2 tests are shown in Table 2. However, in many cases the error variances between sites remained heterogeneous on the log scale and then a weighted analysis was performed according to Lawrence (1970).

Although the unweighted analysis on natural scale is statistically invalid in most cases, it has been commonly used by plant breeders because it is more easily understood in biological terms. Moreover, error variances between sites for control groups of different cultivars were homogenous on different scales (Table 2) and there was no common analy-

Table 2. Bartlett's x^2 tests for homogeneity of residual (error) variance over sites for different cultivars, 1970.

Cultivar	Lines	Scale	X^2 values (3 d.f.) Between sites.
Clipper	Control	Natural	21.795 ***
		Log_{10}	3.843 NS
	Treated	Natural	27.961 ***
		Log_{10}	14.607 **
C.I. 3576	Control	Natural	27.308 ***
		Log_{10}	40.525 ***
	Treated	Natural	15.812 **
		Log_{10}	17.336 ***
Proctor	Control	Natural	28.474 ***
		Log_{10}	6.226 NS
	Treated	Natural	31.829 ***
		Log_{10}	10.604 *
Ketch	Control	Natural	41.233 ***
		Log_{10}	27.852 ***
	Treated	Natural	54.150 ***
		Log_{10}	56.750 ***
Prior	Control	Natural	5.536 NS
	Treated	Natural	32.928 ***
		Log_{10}	28.899 ***

NS = Non-significant ** = significant at 1%
* = significant at 5% *** = significant at 0.1%

sis available where both control and treated groups of each cultivar could be compared on the same scale except unweighted analysis on natural scale (approximate analysis).

Hence, in addition to statistically valid analyses of variance, approximate analyses based on unweighted natural data were included for comparative purposes. These analyses are presented in Tables 3, 4, 5, 6, 7.

(i) Site effects – The mean squares for sites were highly significant for both control and treated lines of each cultivar confirming that there were wide differences between sites in 1970.

(ii) Line effects – None of the mean squares attributable to lines were significant among the control lines of each cultivar except with Ketch, where these were significant at 5% level in the valid analysis, but not in the approximate analysis. Thus, there was no evidence of genetic heterogeneity among the control lines of any of the cultivars except possibly with Ketch. It should be noted, however, that Ketch control lines did not show significant heterogeneity within any of the individual sites (Ghafoor Arain, 1973).

On the other hand, highly significant line mean squares occurred among the treated lines from all cultivares. With Ketch the line mean squares were significant in the valid analysis but not in the approximate analysis. Thus the EMS-treatments have generated significant variability in all cultivars but apparently to a lesser extent in Ketch.

(iii) Genotype X environment interactions - No significant lines X sites interaction mean squares were obtained among the control lines from each cultivar, indicating that all control lines of each cultivar performed consistently across all sites. In contrast, significant interaction mean squares were observed with the treated lines of each cultivar except with Ketch. In the valid analyses the levels of significance for the lines X sites interaction terms varied from 0.1% with Prior and Proctor to 1% with Clipper and C.I. 3576.

The results obtained with control and treated lines taken together clearly indicate that the EMS treatments have resulted in inducing genetic variability among M_2-derived lines which performed relatively differently when tested over a range of environments, thus showing significant genotype x environment interaction terms in the analyses of variance.

The next question concerns whether the significant G X E interaction terms can be accounted for by linear responses to change in environments or to deviations from a linear model. Consequently the lines X sites interactions sum of squares were partitioned into these two components (Tables 3, 4, 5, 7). In most cases the interaction term was due mainly to deviations from regressions. Thus the deviation component was significant with treated lines of Clipper, Proctor and Prior. Significant linear components occurred only in the valid analyses and then only in treated lines of Clipper and C.I. 3576 ($P \geqslant .05$). The differential response to environments of treated lines of Clipper and C.I. 3576 could thus be explained partly by regression of individual yields on site means as suggested by Finlay and Wilkinson (1963).

Table 3. Analyses of variance combined over all sites for yield, components of variances, and heritability values of M_2-derived treated and control lines of CLIPPER in M_4 generation, 1970.

	Approximate analysis				Statistically valid analysis			
Analysis of Variance	Unweighted natural scale				Log_{10} scale unweighted		Natural scale weighted	
Source	Control lines		Treated Lines		Control lines		Treated lines	
	df	MS	df	MS	df	MS	df	MS
(Env.)	3	2,250,170***	3	2,913,510***	3	1,38860***	3	2,733,560***
Replicates within sites	4	16,244*	4	42,933***	4	.009975**	4	14,701**
Lines	24	8048.7 NS	34	33,208***	24	.003917 NS	34	22,023***
Lines X Sites interaction	72	5469.2 NS	102	8811.9*	72	.002778 NS	102	7147.3**
Linear			34	9115.4 NS			34	9786.2*
Deviation			68	8660.1*			68	5827.9*
Residual	96	5756.6	136	6154.6	96	.002773	136	4116.4
Variance components								
$\sigma^2 p$		322.44		3049.51				
$\sigma^2 ps$		0.0		1326.65				
$\sigma^2 e$		5756.60		6154.60				
Heritability								
H		0.3094		0.7346				

Table 4. Analyses of variance combined over all sites for yield, components of variances, and heritability values of M_2-derived treated and control lines of C.I. 3576 in M_4 generation, 1970.

	Approximate analysis				Statistically valid analysis			
Analysis of Variance	Unweighted natural scale				Log_{10} scale unweighted		Natural scale weighted	
Source	Control lines		Treated Lines		Control lines		Treated lines	
	df	MS	df	MS	df	MS	df	MS
Sites (Env.)	3	2,350,850***	3	3,026,750***	3	2,704,840***	3	3,197,410***
Replicates within sites	4	23,533 NS	4	16,181 NS	4	17,507*	4	17,288*
Lines	24	9189.5 NS	34	72,795***	24	6398.2 NS	34	54,772***
Lines X Sites interaction	72	8708.5 NS	102	10,903*	72	6265.5 NS	102	9206.5**
Linear			34	13,467 NS			34	13,832*
Deviation			68	9620.6 NS			68	6893.5 NS
Residual	96	11,809	136	7751.2	96	6558.1	136	5828.2
Variance components								
$\sigma^2 p$		60.15		7736.50				
$\sigma^2 ps$		0.0		1575.90				
$\sigma^2 e$		11,809.0		7751.20				
Heritability								
H		0.0391		0.8502				

Table 5. Analyses of variance combined over all sites for yield, components of variance and heritability values of M_2-derived treated and control lines of PROCTOR in M_4 generation, 1970.

	Approximate analysis				Statistically valid analysis			
Analysis of Variance	Unweighted natural scale				Log_{10} scale unweighted		Natural scale weighted	
Source	Control lines		Treated Lines		Control lines		Treated lines	
	df	MS	df	MS	df	MS	df	MS
Sites (Env.)	3	2,342,650***	3	2,575,470***	3	21.3755***	3	1,819,480***
Replicates within sites	4	17,419*	4	50,746***	4	.005718 NS	4	21,625***
Lines	24	7906.6 NS	34	35,442***	24	.004769 NS	34	20,318***
Lines X Sites interaction	72	5966.7 NS	102	9430.6***	72	.003197 NS	102	5933.1***
Linear			34	8877.0 NS			34	7045.2 NS
Deviation			68	97 07.4***			68	5378.5***
Residual	96	6706.5	136	4105.6	96	.003158	136	2288.7
Variance components								
$\sigma^2 p$		242.49		3251.43				
$\sigma^2 ps$		0.0		2662.50				
$\sigma^2 e$		6706.50		4105.60				
Heritability								
H		0.2244		0.7339				

Table 6. Analyses of variance combined over all sites for yield, components of variance, and heritability values of M_2-derived treated and control lines of KETCH in M_4 generation, 1970.

Analysis of Variance	Approximate analysis				Statistically valid analysis			
	Unweighted natural scale				Weighted natural scale			
Source	Control lines		Treated Lines		Control lines		Treated lines	
	df	MS	df	MS	df	MS	df	MS
Sites (Env.)	3	1,679,590***	3	2,245,850***	3	1,506,010***	3	2,281,910***
Replicates within sites	4	10,503 NS	4	16,186*	4	4019.1 NS	4	9692.6**
Lines	24	5221.6 NS	34	7407.5 NS	24	4413.4*	34	5165.5**
Lines X Sites interaction	72	4346.6 NS	102	5652.7 NS	72	1376.7 NS	102	2916.7 NS
Residual	96	6983.5	136	5442.3	86	2272.8	136	2248.3
Variance components								
$\sigma^2 p$		109.38		21[illegible].35				
$\sigma^2 ps$		0.0		105.20				
$\sigma^2 e$		6983.50		5442.30				
Heritability								
H		0.1113		0.2369				

Table 7. Analyses of variance combined over all sites for yield, components of variance, and heritability values of M_2-derived treated and control lines of PRIOR in M_4 generation, 1970.

Analysis of variance	Statistically valid analysis		Approximate analysis		Statistically valid analysis	
	Unweighted natural scale†		Unweighted natural scale		Weighted natural scale	
Source	Control lines		Treated lines		Treated lines	
	df	MS	df	MS	df	MS
Sites (Env.	3	342,454***	3	293,454***	3	348,648***
Replicates within sites	4	35,196***	4	26,699***	4	12,803***
Lines	14	4,029.4 NS	24	23,499***	24	23,835***
Lines X Sites interaction	42	3,482.8 NS	72	9,827.6**	72	5,675,3***
Linear			24	10,640.0 NS	24	7,501.7 NS
Deviation			48	9,421.6**	48	4,762.1**
Residual	56	3,812.2	96	4,882.7	96	2,397.1
Variance components						
$\sigma^2 p$		68.33		1,708.93		
$\sigma^2 ps$		–		2,472.45		
$\sigma^2 e$		3,812.20		4,882.70		
Heritiability						
H		0.1254		0.5818		

† In the case of control lines, unweighted analysis on natural scale is statistically valid as its error variances for sites are homogeneous on natural scale.

(c) Variance components and heritability

The three variance components: σ^2p (genotypic variance due to lines), σ^2ps (lines X sites interaction variance) and σ^2e (error variance) and H (heritability values) were calculated for both control and treated lines of each cultivar from the mean squares of unweighted analyses on naural scale. These estimates are shown in Tables 3-7.

The σ^2p provides a relative magnitude of the genetic variability occurring among lines under varying environmental conditions. The magnitude of σ^2p induced by EMS-treatment among the treated material of each cultivar was several-fold greater than corresponding controls except with Ketch, where it showed only a two-fold increase. The largest σ^2p was obtained with the treated lines of C.I. 3576 followed in order by Prior, Proctor, Clipper and Ketch treated lines.

In order to study the differential performance of treated lines over a range of environments, estimates of σ^2ps were calculated. A high magnitude of σ^2ps is an indication of differential responses of lines to change in environment. Relatively large values of σ^2ps were obtained with treated lines of Clipper, C.I. 3576, Proctor and Prior cultivars. However, the interaction variances were small in magnitude compared with the σ^2p estimates among the treated lines of all cultivars except Prior, where σ^2ps was slightly greater than σ^2p.

In addition, heritability (H) values estimated over a range of environments for treated lines were compared with corresponding controls in each cultivar. The heritability estimates of the treated lines of each cultivar showed almost the same tendency as the σ^2p. Thus greater gains from selection for yield can be anticipated among the EMS-treated material of all cultivars than their respective controls.

(d) Contribution of individual lines to genotype X environment interaction (ecovalence parameter).

After finding significant G X E interaction among the treated lines of Clipper, C.I 3576, Proctor and Prior (Tables 3,4,5,7), the lines contributing most towards these interaction terms, were identified by calculating "ecovalence" (W) values as proposed by Wricke (1962, 1966).

The 'W' values were calculated for both treated and control groups on unweighted natural scale. In addition, these values were calculated for treated lines using weighted data. The 'W' values from weighted (natural scale) analyses were much the same as those derived from unweighted (natural scale) analyses, as shown by Spearman's rank correlations (Snedecor and Cochran, 1967) of .978***, .990***, .805***, .991*** in the case of treated lines of Clipper, C.I. 3576, Proctor and Prior respectively.

The frequency distributions of the 'W' values calculated from the unweighted analyses on natural scale were plotted so that the performance of the treated lines could

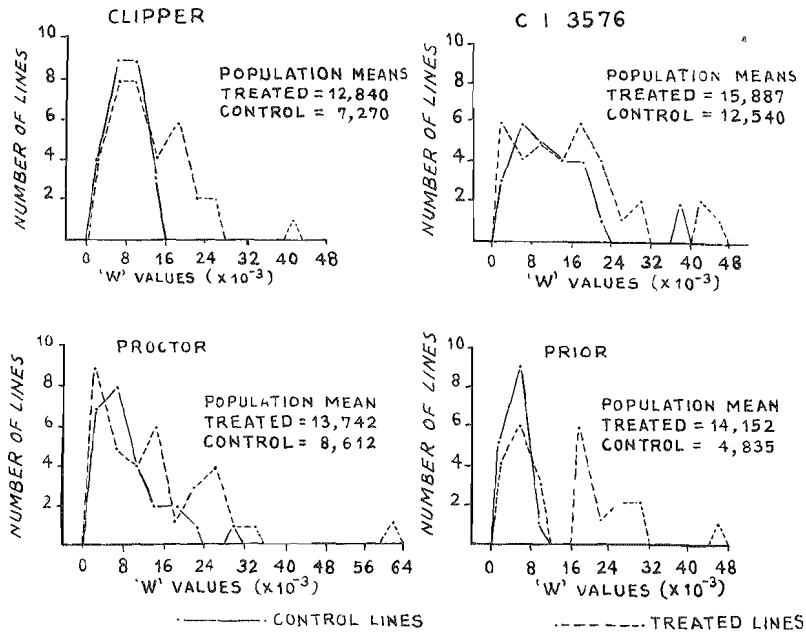


Fig. 2. Frequency Distribution of "W" Values for Treated and Control Lines of Four Barley Cultivars, Derived from Analyses of Yield DATA on Natural Scale (1970).

be compared with that of controls on a common scale (Figure 2). These 'W' values for the treated lines of each cultivar showed a much wider range of variation as compared with the respective control lines.

Discussion

In common with other workers, it was found that EMS treatment of barely cultivars caused a reduction in mean yield and a large increase in genotypic variance for yield. Although all cultivars were given exactly the same EMS treatment, they exhibited different responses with respect to several treats. The maximum reduction in mean in M_4 generation occurred among the treated lines of Proctor, followed in order by those of Prior, C.I. 3576, Clipper and Ketch (Figure 1). These results are closely paralleled to by the response with respect to M_2 chlorophyll mutation frequency and M_1 seed sterility except that in these cases Clipper was less responsive than Ketch (Ghafoor Arain, 1974). On the other hand, the magnitude of induced genotypic variance in M_4 did not follow the same trend except that the least amount occurred in Ketch (Tables 3-7). Gaul (1965) has observed that M_1 survival, chlorophyll mutation frequency, reduction of yield mean and increased genotypic variance are closely correlated phenomena and he has used these joint responses to gauge the effectiveness of the mutagen treatment. Therefore, it can be concluded that in the present study the EMS treatment was most effective with Proctor

and Prior and least effective with Ketch and Clipper. The reasons for these differences are not known but it is possible that the cultivars differ in their seed coat permeability or in the physiological state of the embryo.

The combined analysis of variance is valid only when the experimental error variance between sites is homogeneous but the error variances were found to be heterogeneous in the present study (Table 2). Such heterogeneity of error occurs commonly in the field experiments, even in small trials with few entries (Immer *et al.*, 1934; Salman, 1951). This heterogeneity of error has been ascribed to soil heterogeneity and differences between seasons.

However, in literature many workers have combined yield data over all sites and performed analyses of variance on natural scale without testing for homogeneity of error variances (Comstock and Robinson, 1952; Hanson *et al.*, 1956; Miller *et al.*, 1959; Eberhart & Russell, 1966; Reich & Atkins, 1970; Tai, 1971; Gupton *et al.*, 1974; Patanothai & Atkins, 1974).

Finaly & Wilkinson (1963) used logarithmically transformed data for inducing a reasonable degree of homogeneity of experimental error, but such a transformation was not successful in the present study nor in some other analyses (Lawrence, 1970; Fripp & Caten, 1971). Hence, the weighting procedure suggested by Yatas & Cochran (1938) and used by Lawrence (1970) to analyze yield data of barley varieties, was employed in the present study.

Thse combined anlyses of variance over sites were performed on both unweighted (natural scale) and weighted data. Herein, emphasis was given to the results of the weighted analyses because of its statistical validity. However, since many other workers have employed an unweighted analysis (natural scale) in their studies of G X E interactions and the results of such an analysis give a measure of actual biological response in the field, the unweighted analysis has also been presented for comparative purposes.

The control lines of each cultivar did not exhibit G X E interactions when the performance was examined over sites. Thus for each cultivar, all control lines behaved consistently across sites and this made it simpler to interpret the effects observed with the treated lines. The treated lines of each cultivar generally showed significant G X E interaction. They only exception to this pattern occurred with Ketch where the induced genotypic variance was low. It can be concluded that as a result of mutagen-induced genetic variability, the treated lines of each cultivar show a heterogeneity of response across sites.

The significant G X E interactions observed among the treated lines were partitioned into linear and non-linear components to find the relative contribution of these two components to the overall interaction term. The G X E interactions observed in these analyses were due mainly to deviations from regression. This is expected because of the small number of sites included in 1970 year. However, when the number of environments was increased by combining the M_4 and M_5 (1970 + 1971) results, both linear and

deviation components became significant (unpublished data). Eberhart & Russell (1966) and Tai (1971) working with maize and potato, respectively, showed that the major part of G X E interaction variation in their material was due to deviations from regression.

The occurrence of treated lines showing large ecovalence values provides support for Brock's (1965) suggestion that random mutations are expected to upset the integrated functioning of genes in a plant leading to reduced phenotypic stability and an increased G X E interaction.

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