Identification of environments suitable for conducting selection[1]

B. S. Dhillon[2]

Punjab Agricultural University, Ludhiana 141 004

Abstract

Identification of environments favouring selection of superior genotypes should help plant breeders reduce the costs of multi-environment evaluations. The objectives of this study were to develop indices which measure suitability of environments for conducting selection and to apply the indices to a multi-location experiment in maize (*Zea mays* L.). The indices were derived using the rationale that selection in a suitable environment should lead to a high response in the target environments. The value of a selection environment was found to be a product of linear regression coefficient of the observed performance of genotypes in the target environment on the performance in the selection environment and standard deviation of the performance in the selection environment. It was termed as an index of general response to selection (GR index) when based on the performance averaged over a number of target environments. The correlation (r_{Ts}) between the average performance across target environments and that in a selection environment was shown to quantify the GR index and the ratio of response to indirect vs. direct selection. The 18 locations evaluated differed for GR index, r_{Ts} and discriminability (DA; linear regression of the performance of genotypes in a selection environment on the average performance across all target environments); r_{Ts} was closely correlated with GR index; and some locations possessed high GR index as well as DA with respect to maize grain yield. The study gave the indices that are useful in characterizing the suitability of environments for conducting selection and in choosing environments better than others for conducting selection for grain yield in maize.

Key words : Selection environment, response to selection, discriminability, maize, grain yield

Introduction

The prevalence of genotype-environment (GE) interaction in plant breeding experiments is of major concern to plant breeders. The interaction can complicate identification of superior genotypes and reduce gain from selection. Plant breeders, therefore, have to conduct selection over a number of environments. Multi-environment selection experiments require large resources and must be made as efficient as possible.

Various environments may be expected to contribute differently to GE interaction and to the masking effects on genotypes. Some may be more favourable than others for selection of genotypes that perform better across target environments or in a specific zone. The identification of environments that foster selection of superior genotypes should enable plant breeders to more reliably test a larger number of genotypes with given resources and increase the rate of genetic progress. Such environments should particularly be useful for preliminary evaluations.

Several indices, namely environmental mean, heritability, expected response to selection (R), correlation coefficient ($r_{\bar{a}s}$) between the performance of genotypes in an environment (y_{ij}, i = 1, 2, ..., m genotypes, j = 1, 2, ..., n environments) and the mean performance of genotypes across all n environments ($\bar{y}_{i.}$) (in $r_{\bar{a}s}$, $\bar{a}$ stands for all environments and s for a given selection environment), linear regression coefficient ($b_{s\bar{a}}$) of y_{ij} on $\bar{y}_{i.}$ and related statistics have been proposed to choose the optimum test environments [1-6]. Hamblin et al. [4] suggested the use of $r_{\bar{a}s}$; Brown et al. [5], $r_{\bar{a}s}^2$; and Utz [1], screening ability ($r_{\bar{a}s}^2 H$, H defined relative to $\bar{y}_{i.}$).

The objectives of the present study were to develop the measures of suitability of environments for conducting selection so as to maximize the response

to selection in target environments, and to apply the measures to a multi-location experiment in maize.

Materials and methods

Theory

Indices of response to selection : Let the observed performance of the genotype i in the selection environment s ($y_{i|s}$) be designated as s_i, the performance in the target environment t($y_{i|t}$) as t_i, and the average performance across $n - 1$ target environments (excluding environment s) as $\bar{t}_i$. Let $\sigma^2_{(p)}$ be the phenotypic variance and $\sigma^2_{(g)}$ be the genotypic variance of s_i, t_i and $\bar{t}_i$ as specified by the subscripts, s, t and $\bar{t}$, respectively. Unless stated otherwise, let σ denote a standard deviation.

The expected response to selection (R_s) when the same environment s is employed to select and to evaluate the selected genotypes, following Falconer [7], is :

$$R_s = SH = k\sigma^2_{s(g)}/\sigma_{s(p)} \tag{1}$$

Where S is the selection differential, k is the standardized selection differential ($k = S/\sigma_{s(p)}$) and H is heritability in narrow sense ($H = \sigma^2_{s(g)}/\sigma^2_{s(p)}$). The response to selection ($R_{t(s)}$) when selection is conducted in environment s and the selected genotypes are evaluated in environment t, can be computed, following the approach of correlated response to selection [7] as:

$$R_{t(s)} = b_{ts(g)} R_s \tag{2}$$

Here $b_{ts(g)} = \sigma_{t.s(g)}/\sigma^2_{s(g)}$ is the additive genetic regression coefficient of t_i on s_i; $\sigma_{t.s(g)}$ being the additive genetic covariance between t_i and s_i. By substituting the values of $b_{ts(g)}$ and R_s, $R_{t(s)}$ can be rewritten as:

$$R_{t(s)} = (\sigma_{t.s(g)}/\sigma^2_{s(g)})\,(k\sigma^2_{s(g)}/\sigma_{s(p)})$$

$$= k\sigma_{t.s(g)}/\sigma_{s(p)} = kb_{ts}\,\sigma_{s(p)} \tag{3}$$

Here $b_{ts} = \sigma_{t.s(g)}/\sigma^2_{s(p)}$ is the regression of t_i on s_i. Note that the variances of t_i and s_i are the phenotypic variances ($\sigma^2_{t(p)}$ and $\sigma^2_{s(p)}$, respectively) whereas the covariance is the genotypic covariance ($\sigma_{t.s(g)}$) since t and s are independent environments. It is added that

the covariance is due to additive and additive × additive genetic variability in case pure lines are evaluated in different environments and due to all types of genetic variability (additive, dominance and epistasis) when hybrids are evaluated. The effects of dominance and epistasis are not considered but these are not expected to have any practical implication with respect to the indices given in the present study.

The relationship (Eq. 3) holds good even when the numbers of selection and/or target environments are greater than one, as long as the two types of environments are independent. The expected response to selection ($R_{\bar{t}(s)}$) when the selection is done in environment s and the selected genotypes are tested in $n - 1$ target environments (excluding environment s), is found by generalizing Eq. 3 as:

$$R_{\bar{t}(s)} = k\sigma_{\bar{t}.s(g)}/\sigma_{s(p)} = kb_{\bar{t}s}\,\sigma_{s(p)} \tag{4}$$

Where $b_{\bar{t}s} = \sigma_{\bar{t}.s(g)}/\sigma^2_{s(p)}$ is the regression coefficient of $\bar{t}_i$ on s_i and $\sigma_{\bar{t}.s(g)}$ is the covariance between $\bar{t}_i$ and s_i.

The value of k can be considered constant for a given experiment; and $R_{\bar{t}(s)}/k$ and $R_{t(s)}/k$ can be termed as indices of general (GR index) and specific (SR index) response to selection, that is :

$$\text{GR index} = \sigma_{\bar{t}.s(g)}/\sigma_{s(p)} = b_{\bar{t}s}\,\sigma_{s(p)} \text{ and} \tag{5}$$

$$\text{SR index} = \sigma_{t.s(g)}/\sigma_{s(p)} = b_{ts}\,\sigma_{s(p)} \tag{6}$$

The number of target environments should be large to get reliable estimates of GR index. If the number is not large or if the objective is to examine zoning of the target area, one can compute SR index. The higher the estimates of GR and SR indices, the greater is the expected genetic gain in the target environment(s) resulting from selection made in the selection environment. For GR and SR indices to be practically useful, their estimates must be based on a series of experiments conducted over years and genotypes; otherwise these will be biased due to GE interaction.

The GR index can be expressed in terms of the genetic correlation [$r_{\bar{t}s(g)} = \sigma_{\bar{t}.s(g)}/(\sigma_{\bar{t}(g)}\,\sigma_{s(g)})$] between $\bar{t}_i$ and s_i as below :

$$\text{GR index} = (\sigma_{\bar{t}.s(g)}/\sigma_{s(p)})\,(\sigma_{\bar{t}(g)}\,\sigma_{s(g)}/\sigma_{\bar{t}(g)}\,\sigma_{s(g)})$$

$$= r_{\bar{t}s(g)}\,H^{0.5}\,\sigma_{\bar{t}(g)} \tag{7}$$

For a given sample of target environments, $\sigma_{\bar{t}(g)}$ is constant (considering all n environments as target environment), and $r_{ts(g)} H^{0.5}$ measures GR index (H defined relative to s_j). Allen et al. [3] used this expression to denote the value of a test environment.

It may, however, be shown that the simple correlation $(r_{ts} = \sigma_{t.s(g)} / \sigma_{\bar{t}(p)} \sigma_{s(p)})$ between $\bar{t}_j$ and s_j quantifies the GR index as well as the ratio of response to indirect and direct selection.

$$\text{GR index} = (\sigma_{t.s(g)} / \sigma_{s(p)})(\sigma_{\bar{t}(p)} / \sigma_{\bar{t}(p)})$$

$$= r_{ts} \sigma_{\bar{t}(p)} \qquad (8)$$

The $\sigma_{\bar{t}(p)}$ being constant for a given sample of target environments (considering all n environments as target environment), the value of a selection environment is also measured by r_{ts}.

The ratio of response to indirect and direct selection $(R_{\bar{t}(s)} / R_{\bar{t}})$ is:

$$R_{\bar{t}(s)} / R_{\bar{t}} = [(\sigma_{t.s(g)} / \sigma_{s(p)}) / (\sigma_{\bar{t}(g)}^2 / \sigma_{\bar{t}(p)})](\sigma_{\bar{t}(p)} / \sigma_{\bar{t}(p)})$$

$$= r_{ts} (\sigma_{\bar{t}(p)}^2 / \sigma_{\bar{t}(g)}^2) \qquad (9)$$

The $\sigma_{\bar{t}(p)}^2 / \sigma_{\bar{t}(g)}^2$ ($1/H$; H defined relative to $\bar{t}_j$) being constant for a given sample of target environments (considering all n environments as target environment), r_{ts} measures $R_{\bar{t}(s)} / R_{\bar{t}}$ It can also be shown that the genotypic regression coefficient of $\bar{t}_j$ on s_j obtained from the standardized variables is equal to $R_{\bar{t}(s)} / R_{\bar{t}}$

In practice, m genotypes may be tested in n environments with the objective of evaluating all n environments as selection environments ($j = 1, 2, ..., s, ..., n$). In such a study, each of the n environments, in turn, may be considered as the selection environment s and the remaining $n - 1$ as the target environments. Thus, there will be n estimates of both $\sigma_{\bar{t}(p)}$ (Eq. 8) and $\sigma_{\bar{t}(p)}^2 / \sigma_{\bar{t}(g)}^2$ (Eq. 9). If n is large, the differences in the n estimates of $\sigma_{\bar{t}(p)}$ and $\sigma_{\bar{t}(p)}^2 / \sigma_{\bar{t}(g)}^2$ may be negligible; and r_{ts} may provide a measure of GR index as well as $R_{\bar{t}(s)} / R_{\bar{t}}$ The maximum value of r_{ts} is unity, which indicates that the selection in environment s may be expected to be as effective as that based on the mean performance across all $n - 1$ target environments.

The r_{ts} is as easily calculable and interpretable as the GR index defined earlier (Eq. 5). The estimate of r_{ts} and differences between two or more estimates can be tested for significance, and two or more estimates can be combined together. Furthermore, r_{ts} is independent of units and, hence, can be compared over experiments and characters.

Discrimination ability: A good selection environment should also allow easy discrimination of genotypes [Utz, 1]. The DA (discriminability) of an environment can be computed as a regression ($b_{s\bar{t}}$) of s_j on $\bar{t}_j$. An estimate of $b_{s\bar{t}} = 1$ means that the DA of the selection environment s is as good as that based on $\bar{t}_j$; and $b_{s\bar{t}} > 1$ or < 1 indicates that the DA is better or poorer, respectively. Utz [1], Hamblin et al. [4] and Brown et al. [5] considered $\bar{y}_j$ in place of $\bar{t}_j$ and computed $b_{s\bar{a}}$ or related statistics.

Experimental

The theory developed above is applied here to a multi-location experiment in maize. Grain yield data were collected in a national trial organized by the All-India Coordinated Maize Improvement Project during the monsoon season of 1983. In that experiment, 10 composites were evaluated at 18 locations. These locations range from Poonch ($33^\circ 46'$ N, $74^\circ 06'$ E) in the north, Kolhapur ($16^\circ 43'$ N, $74^\circ 14'$ E) in the south, Sabour ($25^\circ 15'$ N, $87^\circ 02'$ E) in the east and Khedbrahma ($24^\circ 03'$ N, $73^\circ 03'$ E) in the west. The experiment was laid out in a randomized complete-block design with four replications at each location. A plot consisted of four rows at locations L10 and L13, nine rows at L4 and six rows at all other locations (see Table 1 for location codes). The row length was 5 m except for 3 m at L4. The distance between rows was 0.60 m at L1, L3, L4, L5, L6, L7, L13, L14, L15 and L16; and 0.75 m at the other locations. The distance between plants within a row was 0.25 m. At grain maturity, data were recorded on ear weight, grain moisture and number of plants. Grain yield at 15 per cent moisture was computed assuming grain to ear ratio of 80 per cent, and was adjusted for the differences in the plant stand using the analysis of covariance technique. The data available in the Annual Report of the Project are entry mean grain yield at each location [8].

In the present study, the regression (b) and correlation (r) coefficients, variances and standard deviations were computed following standard statistical analyses [9]. The $b_{\bar{t}s}$ for the location s was computed as a regression of $\bar{t}_j$ on s_j, and GR index was obtained as a product of $b_{\bar{t}s}$ and $\sigma_{s(p)}$, where $\sigma_{s(p)}^2$ is the mean squares (MS) due to genotypes in the analysis of

Table 1. Estimates of the index of general response to selection (GR index), discriminability (DA) and related statistics of various locations for grain yield in maize

Location Name	Code	GR index[1] (kg/ha)	r_{ts} [1]	DA (b_{st})	b_{ts}	$\sigma_{s(p)}$ (kg/ha)	Mean yield (kg/ha)
Poonch	L1	−24	−0.07	−0.03±0.17	−0.14±0.72	164	4639
Bajaura	L2	104	0.33	0.70±0.70	0.16±0.16	670#	5929
Solan	L3	204	0.67*	1.54±0.60*	0.29±0.11*	697#	5200
Almora	L4	86	0.26	0.30±0.39	0.23±0.30	374	5857
Dhaulakuan	L5	293	0.96**	1.60±0.16**	0.58±0.06**	506#	3358
Gurdaspur	L6	253	0.85**	1.96±0.43**	0.37±0.08**	687#	4282
Ludhiana	L7	216	0.69*	1.11±0.41*	0.43±0.16*	500#	3208
Karnal	L8	272	0.87**	1.12±0.22**	0.67±0.13**	403#	3906
Delhi	L9	221	0.70*	0.80±0.29*	0.61±0.22*	362#	2198
Bhilwara	L10	−41	−0.12	−0.26±0.74	−0.06±0.16	712#	2740
Banswara	L11	282	0.90**	1.08±0.18**	0.75±0.13**	375#	2472
Pantnagar	L12	222	0.75*	2.05±0.64*	0.28±0.09*	806#	5914
Farrukhabad	L13	40	0.12	0.12±0.36	0.12±0.35	335#	3346
Bahraich	L14	182	0.59	1.29±0.62	0.27±0.13	669#	3893
Varanasi	L15	141	0.43	0.41±0.30	0.45±0.34	309#	1313
Sabour	L16	225	0.73*	1.30±0.43*	0.41±0.14*	548#	2538
Khedbrahma	L17	284	0.89**	0.68±0.13**	1.15±0.21**	247#	1841
Kolhapur	L18	131	0.42	0.91±0.70	0.19±0.15	684#	4076
LSD (0.05)			39.2^2	1.277	0.448	46.0^2	

*,**Significant at 0.05 and 0.01 levels, respectively.

#Genotypic MS (mean squares) vs. error MS were significant (0.05 level).

[1]GR Index = $b_{ts}\,\sigma_{s(p)}$; r_{ts} is a measure of GR index under the assumption of no differences among n estimates of $\sigma_{\bar{t}(p)}$.

[2]χ^2 at 17 df (based on z transformed r_{ts} and Bartlett's test of $\sigma^2_{s(p)}$).

variance at location s. Further, r_{ts} was computed as r between $\bar{t}_i$ and s_i. It quantifies GR index under the assumption of no differences among the n estimates of $\sigma_{\bar{t}(p)}$ ($\sigma^2_{\bar{t}(p)}$ = MS due to genotypes in the analysis of variance over $n - 1$ target locations). The DA was computed as a regression of s_i on $\bar{t}_i$ (b_{st}). The i refers to 10 genotypes; s, to the selection environment (one location); and t, to the target environments ($n - 1 = 17$ locations). Each location in turn was considered as a selection environment and the remaining 17, as target environments; to compute the estimates of b_{ts}, $\sigma_{s(p)}$, r_{ts} and b_{st} for all 18 locations. Spearman rank correlations were computed between some selected combinations of variables [9].

The results of the F test of genotypic MS vs. error MS at each location was obtained from the Annual Report of the Project. Bartlett's test of homogeneity of variances [9] was applied to examine the differences among n estimates of $\sigma^2_{s(p)}$ and n estimates of $\sigma^2_{\bar{t}(p)}$.

The estimates of r and rank correlation were compared with the table values [9]. The heterogeneity of various estimates of r was tested by using z transformation [9]. The significance of various b's was examined by an F test for heterogeneity of regression (regression MS vs. deviation MS with 1 and $m - 2$ df, respectively). The SE of b was computed as (deviation MS/SS of the independent variable)$^{0.5}$, where SS is the sum of squares. Extended analysis of variance was carried out to examine the heterogeneity of different b's (b_{ts}, b_{st}) for various locations [9]. The LSD was computed as {2 [pooled deviation MS/(pooled SS of the independent variable/n)]}$^{0.5}t$ at n ($m - 2$) df.

Results and discussion

Extended analysis of variance revealed significant heterogeneity among b_{ts} and b_{st} estimates (Table 2). The estimates of r_{ts} were also significantly heterogenous (Table 1). Thus, the locations differed with respect to b_{ts} (a component of GR index), and r_{ts} (a measure of GR index as well as of the ratio of response to indirect vs. direct selection) and DA.

Table 2. Extended analysis of variance of different linear regressions

Source	df	Mean squares	
		b_{ts}[1]	b_{st}[1]
Heterogeneity of regressions	17	121947*	384392*
Deviations	144	67213	189814

*Significant at 0.05 level.
[1]b_{ts} is a component of the index of general response to selection (GR index) and b_{st} is an estimate of discriminability (DA).

The r_{ts}, b_{ts} and DA estimates of 10 locations, namely L3, L5, L6, L7, L8, L9, L11, L12, L16 and L17 were significant. The MS due to genotypes were significant at all locations except L1 and L4 (see under $\sigma_{s(p)}$, Table 1). The GR index of the above listed 10 locations varied from 204 to 293 and was greater than that of others ($\leq$ 182), particularly L1, L4, L10 and L13 ($\leq$ 85.6). Location L5 had numerically the highest estimate of GR index, r_{ts} and DA; and DA was significantly greater than unity. These results and the significantly positive rank correlations of GR index and r_{ts} with DA estimates (Table 3) indicated the possibility of identifying locations with high GR index as well as DA.

Differences among locations with respect to their r_{as} or related parameters and $b_{s\bar{a}}$ (DA as defined by Utz [1]) have been reported by Pollmer et al. [10], Fakorede [11] and Misevic and Dumanovic [12] for grain yield in maize. Further, Misevic and Dumanovic [12] reported that high yielding locations were better test locations than the low yielding ones whereas Pollmer et al. [10] did not observe any such relationship. In the present study rank correlations of mean grain yield with GR index, r_{ts} and DA were not significant (Table 3).

Table 3. Estimates of rank correlation coefficients for selected pairs of the statistics

Statistics pair[1]	Rank correlation coefficient
Mean vs. GR index	–0.263
Mean vs. r_{ts}	–0.232
Mean vs. DA	0.288
GR index vs. r_{ts}	0.996**
GR index vs. DA	0.686**
GR index vs. b_{ts}	0.876**
GR index vs. $\sigma_{s(p)}$	0.001
r_{ts} vs. DA	0.703**
DA vs. b_{ts}	0.393

**Significant at 0.01 level.
[1]See Table 1 for explanation of various statistics.

The GR index and r_{ts} estimates showed a very strong, positive rank correlation. Thus, r_{ts} was a good measure of the GR index in the present study. It may be added that the 18 estimates of $\sigma^2_{\bar{t}(p)}$ were shown by the Bartlett's test to be homogeneous (χ^2 = 0.41 at 17 df), an assumption required to use r_{ts} as a GR index (Eq. 8).

Both GR index and r_{ts} were significantly correlated with DA. The GR index (Eq. 5) can be written as $(\sigma_{\bar{t}.s(g)}/\sigma_{s(p)})(\sigma^2_{\bar{t}(p)}/\sigma^2_{\bar{t}(p)})$ = $b_{s\bar{t}}(\sigma^2_{\bar{t}(p)}/\sigma_{s(p)})$ = $DA(\sigma^2_{\bar{t}(p)}/\sigma_{s(p)})$. Thus, the correspondence between GR index and DA is influenced by the variation in the estimates of $\sigma^2_{\bar{t}(p)}$ and $\sigma_{s(p)}$. In the present study, Bartlett's test showed the 18 estimates of $\sigma^2_{s(p)}$ to be heterogeneous (Table 1) whereas those of $\sigma^2_{\bar{t}(p)}$ were not, as stated earlier. Thus, GR index and r_{ts} were significantly correlated with DA in spite of heterogeneous estimates of $\sigma^2_{s(p)}$. Further, of its two components, GR index had a strong rank correlation with b_{ts} but had no correlation with $\sigma_{s(p)}$. This indicated a greater importance of b_{ts} in determining GR index in the present study.

Locations L1 and L10 had negative GR index (Table 1). At L1, MS due to genotypes ($\sigma^2_{s(p)}$) were not significant and the b_{ts} was very low. In contrast, L10 had significant and numerically the largest MS due to genotypes, but had very low b_{ts}. A low $\sigma_{s(p)}$ means poor expression of genotypic differences and, therefore, selection may not be expected to be effective at that location. A low b_{ts} estimate, on the other hand, indicates that the location differs from the target environments as represented by the other locations. It may be desirable to weigh locations depending on their GR index, and in extreme cases of very poor index, not to employ such locations for selection purposes. In situations where there is low b_{ts} but high $\sigma_{s(p)}$, such as L10, the location may be used to select genotypes for growing in that specific target area.

The present study showed that the locations differed for their suitability to conduct selection; GR index and r_{ts} had strong, positive correlation with each other and with DA, and GR index had a closer correlation with b_{ts} than with $\sigma_{s(p)}$. These estimates should, however, be interpreted with caution, since these are influenced by the complex interactions of many abiotic (climatic and edaphic) and biotic factors, and such

studies should be based on series of experiments conducted over years and genotypes, and on large and representative samples of target environments.

The extended analysis of variance (Table 2) and LSD's (Table 1) have two limitations. Firstly, the b's ($b_{\bar{t}s}$, $b_{s\bar{t}}$) for various locations are not independent. This is, however, as relevant to $b_{\bar{t}s}$ and $b_{s\bar{t}}$ as to $b_{s\bar{a}}$ [DA as defined by Utz, 1]; the last mentioned estimate being analogous to that obtained in the widely used stability analysis of Eberhart and Russell [13]. Secondly, the deviation MS should be homogeneous to have valid testing of the heterogeneity of b's, a point discussed in detail by Eberhart and Russell [13]. In spite of these limitations, the analysis is illustrative of the differences among $b_{\bar{t}s}$ and $b_{s\bar{t}}$

Utz [1], Hamblin et al. [4] and Brown et al. [5] have proposed $r^2_{\bar{a}s} H$ (H defined relative to $\bar{y}_{i.}$), $r_{\bar{a}s}$ and $r^2_{\bar{a}s}$, respectively, to evaluate test locations. These studies, however, did not appreciate, as expounded here, the genetic meaning of $r_{\bar{t}s}$ in terms of R. Further, $\bar{y}_{i.}$ was used instead of $\bar{t}_i$. Thus, the independent variable $(\bar{y}_{i.})$ is not independent of the dependent variable (s_i) since it includes s_i. Consequently, the covariance between $\bar{y}_{i.}$ and s_i is biased due to GE interaction and error, which may be a serious limitation when n is small. The present approach does not have these shortcomings.

The concept of correlated response to selection has been followed in the present study as well as in that of Allen et al. [3]. Yet, these studies differ. We considered phenotypic observations, defined the indices in terms of genetic covariance and phenotypic variances that are estimable from the phenotypic values, s_i, t_i and $\bar{t}_i$, and presented simple formulations for practical computations of the indices. Allen et al. [3] used genotypic values, and consequently did not discuss the approach as exposited here. They proceeded on to calculate the value of an environment as $r_{\bar{t}s(g)} H^{0.5}$. Further, the present study indicated that simple $r(r_{\bar{t}s})$ may provide a measure of GR index. The present indices, being simpler, are expected to be more precise than $r_{\bar{t}s(g)} H^{0.5}$ of Allen et al. [3].

References

1. **Utz H. F.** 1972. Die Zerlegung der Genotyp × Umwelt-Interaktionen. EDV in Medizin und Biologie, **3**: 52-59.

2. **Vela-Cardenas M. and Frey K. J.** 1972. Optimum environment for maximizing heritability and genetic gain from selection. Iowa State J. Sci., **46**: 381-394.

3. **Allen F. L., Comstock R. E. and Rasmusson D. C.** 1978. Optimal environments for yield testing. Crop Sci., **18**: 747-751.

4. **Hamblin J., Fisher H. M. and Ridings H. L.** 1980. The choice of locality for plant breeding when selecting for high yield and general adaptation. Euphytica, **29**: 161-168.

5. **Brown K. D., Sorrells M. E. and Coffman W. R.** 1983. A method for classification and evaluation of testing environments. Crop Sci., **23**: 889-893.

6. **Glaz B., Miller J. D. and Kang M. S.** 1985. Evaluation of cultivar-testing locations in sugarcane. Theor. Appl. Genet., **71**: 22-25.

7. **Falconer D. S.** 1981. Introduction to Quantitative Genetics. Longman, London, UK.

8. All-India Coordinated Maize Improvement Project. 1983. Unpubl. Annual Report. Indian Agricultural Research Institute, New Delhi.

9. **Snedecor G. W. and Cochran W. G.** 1980. Statistical Methods. Iowa State University Press, Ames, USA.

10. **Pollmer W. G., Eberhard D., Klein D. and Dhillon B. S.** 1980. Stability of performance of high-yielding maize (*Zea mays* L.) hybrids. *In:* Improvement of Quality Traits of Maize for Grain and Silage Use. (ed. W.G. Pollmer and R. H. Phipps). Martinus Nijhoff Publication, Hague, Netherlands, pp. 257-272.

11. **Fakorede M. A. B.** 1986. Selection of sites for preliminary maize yield trials in the rainforest zone of South-Western Nigeria. Euphytica, **35**: 441-447.

12. **Misevic D. and Dumanovic J.** 1989. Examination of methods for choosing locations for preliminary maize yield testing. Euphytica, **44**: 173-180.

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