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Repeatability of stability estimators for downy mildew incidence in pearl millet

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Summary. Repeatability of mean downy mildew (*Sclerospora graminicola* (Sacc.) Schroet.) incidence, regression coefficients and deviation mean squares were investigated for 25 pearl millet (*Pennisetum typhoides* (Burm.) Stapf. & Hubb.) genotypes in 20 environments by correlating arrays of these stability parameters over subsets of the 20 environments arranged according to the year-wise, random, stratified and extreme methods of environmental division. Correlation coefficients between arrays of mean downy mildew incidence from different pairs of subsets ranged from 0.57 to 0.98 and those of deviation mean squares from 0.58 to 0.96 indicating good repeatability of these parameters. Arrays of regression coefficients from different subsets, on the other hand, showed correlation coefficients that ranged from –0.58 to 0.96. Apparently, the regression index of stability was not repeatable for the genotypes and environments studied. Therefore, in order to identify a widely adapted genotype, testing is required to be carried out over a wider range of environments.

Key words: Downy mildew – Pearl millet – Stability parameters – Repeatability – Multilocation testing

Introduction

Following the breakdown of downy mildew resistance in pearl millet hybrids during the early seventies, several multilocation evaluation programmes were initiated to identify genotypes with stable resistance.

The data from such programmes have already been subjected to the genotype-environment interaction models of Finlay and Wilkinson (1963); Eberhart and Russell (1966) and Perkins and Jinks (1968) by Pethani et al. (1980); Sarr and Sy (1981) and Chahal and Virk (1984) on the assumption of generalised host-pathogen interactions. Three stability parameters, namely the mean disease score, regression coefficient and deviations from regression, are used for identifying genotypes with general or specific adaptability. For the selection of the stable genotypes to be widely effective, these stability indexes must be repeatable over samples of environments.

Therefore, in the present paper we examine the repeatability of these estimators across environmental sets in formulating a testing strategy for downy mildew incidence.

Materials and methods

Materials

The data used in the present investigations were extracted from the International Pearl Millet Downy Mildew Nursery (IPMDMN) trials of the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT). The material consisted of 19 pearl millet inbred lines, 5 F_1 hybrids and a susceptible 7042 and check, NHB-3. These entries were promoted from the pre-international pearl millet downy mildew nursery. These materials were tested for the stability of resistance to downy mildew at 10 locations in India and West Africa (Table 1) during 1979/1980. At each site the experiments were laid out in a randomised block design with two replicate blocks.

Testing procedures

At each site the experiments were conducted in downy mildew infested plots where primary oosporic inoculum was available in abundance. The secondary sporangial inoculum was provided by the infector rows, planted with highly susceptible pearl millet materials. To make sure that equal amounts of indirect infections are available to each experimental row, every third row was planted with the infector materials. These rows were sown two to three weeks prior to the sowing of the experimental material so that the test genotypes were exposed to severe attacks of the disease right from the time of emergence. Incidence of disease was scored as percent of infected plants for each genotype.

Table 1. Environments included in the subsets formulated with the year-wise, random, stratified and extreme methods of division and mean downy mildew scores and environmental ranges for 25 pearl millet genotypes grown in each environment

Year-wise		Random		Stratified		Extreme	
Subset I (1979)	Subset II (1980)	Subset I	Subset II	Subset I	Subset II	Subset I	Subset II
1 = Aurangabad	11 = Aurangabad	5	3	11	18	11	15
2 = Jam Nagar	12 = Jam Nagar	8	20	14	19	18	9
3 = Hissar	13 = Hissar	14	4	6	10	19	7
4 = Mysore	14 = Myosore	2	15	5	17	14	20
5 = Ludhiana	15 = Ludhiana	17	6	13	16	6	12
6 = ICRISAT	16 = ICRISAT	18	10	15	9	10	3
7 = Pune	17 = Pune	12	13	20	7	5	1
8 = Hyderabad	18 = Kano	1	11	3	12	17	4
9 = Coimbatore	19 = Samaru	7	16	1	4	16	8
10 = Kamboinse	20 = Kamboinse	19	9	2	8	13	2
Mean (Overall) 8.858	23.838	15.284	15.412	16.002	14.694	24.692	8.004
Range (i) Overall 0–96.5	0–100	0–100	0–100	0–100	0–100	0–100	0–93
(ii) Environmental means 4.48–11.3	7.1–75.64	4.48–52.44	5.92–75.64	4.48–75.64	5.92–52.44	8.9–75.64	4.48–8.72

Environmental numbers in all classifications correspond to locations shown under year-wise categorization

Formulation of environmental sets

To test the repeatability of the stability estimators, it was necessary to have two estimates of each parameter for each pearl millet genotype. These pairs of estimates were obtained by dividing the 20 environments into two subsets of 10 environments each. The following four methods were used to construct environmental subsets:

(a) Year-wise classification – the environments were divided into two subsets of 10 locations according to the year of assessment.

(b) Random method – they were assigned randomly into two subsets of 10 environments each.

(c) Stratified method – the 20 environments were divided into 10 pairs (strata) so that the first and second highest scoring environments were in pair one, the third and fourth highest scoring in pair two, and so on. The two members of each pair were then assigned at random to the two subsets of environments.

(d) Extreme method – the 20 environments were linearly ordered and the 10 highest scoring were assigned to subset one and the rest to subset two.

The environments assigned to the two subsets by each method are shown in Table 1. Joint regression analyses for each subset were computed following Perkins and Jinks (1968). The sum of squares due to heterogeneity of regressions was partitioned into components due to concurrence and non-concurrence following Mandel (1961). The degree of repeatability between two arrays of stability estimators obtained from each subset for each of the 25 genotypes was then evaluated through simple correlation coefficients.

Results

Means and ranges for the two subsets of environments formulated by the four methods of classification are presented in Table 1. For the year-wise and extreme divisions, mean values showed large differences between the two subsets but for the random and stratified methods they were nearly identical. Ranges of the two subsets were more uniform for the random and stratified than for the year-wise and extreme methods. The manifestation of the disproportionate number of environments that had high disease incidence is clear from the large differences that exist between the subsets of year-wise and extreme methods.

Joint regression analyses for all 20 environments and for the two subsets of 10 environments within each method of classification have been presented in Table 2. For each method, genotypes, environments and genotype × environment interaction were observed to be highly significant. The component of genotype-environment interactions attributable to heterogeneity among linear regressions was also consistently significant and so were the deviations from regressions. The heterogeneity of regressions MS was significant against deviation MS except for subset 1 with random and subset 2 with extreme methods, thus, revealing the importance of linear regressions. Further, the mean squares due to concurrence were significant against error MS and deviation MS for different subsets except for subset 1 with random and subset 2 with stratified divisions of environments (Table 2). Whereas concurrence reveals the tendency of regression lines to meet at a common point, non-concurrence indicates the tendency of the lines to run parallel. The significance of concurrence mean squares indicates the correlation be-

Table 2. Mean squares from the analysis of variance for downy mildew incidence recorded on 25 pearl millet genotypes tested in 20 environments divided into two sets of 10 environments by year-wise, random, stratified and extreme methods

Item	d.f.	All environments	d.f.	Year-wise		Random		Stratified		Extreme	
				Subset I	Subset II	Subset I	Subset II	Subset I	Subset II	Subset I	Subset II
Reps/environments	20	46.42*	10	29.00	63.84**	47.99*	44.84	64.98**	27.86	71.58**	21.26
Environments	19	8,037.60**	9	148.74**	13,702.85**	5,699.52**	11,268.52**	11,412.89**	5,531.62**	13,046.84**	53.52**
Genotypes	24	5,724.62**	24	2,856.51**	2,915.10**	2,811.80**	2,985.74**	3,400.19**	2,416.03**	3,024.67**	2,792.70**
Genotypes × environments	456	105.85**	216	69.48**	148.76**	122.98**	92.37**	73.41**	139.86**	168.03**	45.12**
Heterogeneity	24	294.25**++	24	99.75**++	315.15**++	390.13**	202.37**++	201.06**++	400.72**++	310.30**++	37.44*
Concurrence	1	2,636.20**++	1	906.33**++	3,325.83**++	16.60	2,135.56**++	3,251.70**++	4.87	3,518.88**++	410.85**++
Non-concurrence	23	192.42**++	23	64.68**	184.25**	406.37**	118.32**	62.42**	417.93**++	170.79**	21.20
Deviations	432	95.38**	192	58.39**	127.96**	747.86**	78.62*	57.46**	107.26**	150.24**	46.08**
Rep × geno/environments (error)	480	25.22	240	28.97	21.47	20.73	29.69	24.66	25.78	26.43	24.01

**,* Significant at the 1% and 5% probability levels, respectively, when tested against error MS
++,+ Significant at the 1% and 5% probability levels, respectively, when tested against deviations MS

Table 3. Correlation coefficients between mean values ($\bar{X}_i$), regression coefficients (b_i) and deviation mean squares (S^2d_i) for subsets within each method of environmental division for 25 pearl millet genotypes tested in 20 environments

Method of env. division	Correlation of	Correlation coefficient	
		Subset I	Subset II
Year-wise	$\bar{X}_i$ vs b_i	0.62**	−0.66**
	$\bar{X}_i$ vs S^2d_i	0.84**	0.84**
Random	$\bar{X}_i$ vs b_i	−0.04	−0.81**
	$\bar{X}_i$ vs S^2d_i	0.82**	0.90**
Stratified	$\bar{X}_i$ vs b_i	−0.82**	−0.02
	$\bar{X}_i$ vs S^2d_i	0.87**	0.84**
Extreme	$\bar{X}_i$ vs b_i	−0.69**	0.68**
	$\bar{X}_i$ vs S^2d_i	0.84**	0.91**
Overall environments	$\bar{X}_i$ vs b_i	−0.62**	
	$\bar{X}_i$ vs S^2d_i	0.87**	

** Significant at the 1% probability level

tween mean downy mildew scores and regression coefficients (Table 3). These correlation coefficients (Table 3) are significant in all cases except for subset 1 of the random and subset 2 of the stratified methods. Large differences between correlation coefficients for corresponding subsets of each environmental division indicate that the repeatability of regression coefficients and mean as the index of responsiveness is not possible. On the other hand, correlations between the mean downy mildew score and residual mean squares are highly significant and independent of the method of environmental classification. Apparently, selection for low disease score will be accompanied with less sensitivity in the mean performance.

Correlation coefficients between the mean values, regression coefficients and deviations mean squares of the two subsets of environments for each of the four methods and the correlations of these stability estimators over all the 20 environments are presented in Table 4. The correlations of mean values and deviation mean squares are highly significant and their magnitude does not depend upon the method of environmental division. Thus, selection for stable genotypes and low disease score from a few environments would identify millet genotypes that were superior over a wide range of environmental conditions.

Correlations between arrays of linear regression coefficients from two subsets of environments and their overall values were interesting in the sense that the bi-values of the two subsets were either not correlated or negatively associated as for subset 1 of the extreme method. In spite of the fact that the correlations of bi-values from the two subsets were non-significant, the correlations of bi-values from the individual subsets were generally significant with the corresponding

Table 4. Correlation coefficients between arrays of mean mildew score, regression coefficients, and deviations mean squares for the various subsets themselves and with the estimates over all 20 environments for 25 pearl millet genotypes

Method of environmental division	Correlation between	Correlation coefficient for		
		Mean	b_i values	deviations MS
Year-wise	subset I vs subset II	0.57**	−0.17	0.58**
	overall vs subset I	0.87**	−0.10	0.65**
	overall vs subset II	0.95**	0.95**	0.99**
Random	Subset I vs subset II	0.98**	0.12	0.90**
	overall vs subset I	0.99**	0.74**	0.94**
	overall vs subset II	0.99**	0.75**	0.99**
Stratified	Subset I vs subset II	0.98**	0.14	0.96**
	overall vs subset I	0.99**	0.76**	0.83**
	overall vs subset II	0.99**	0.75**	0.99**
Extreme	Subset I vs subset II	0.97**	−0.58**	0.94**
	overall vs subset I	0.99**	0.96**	0.99**
	overall vs subset II	0.99**	−0.40*	0.97**

**,* Significant at the 1% and 5% probability levels, respectively

overall estimates. This reflects the change of response of lines with the sample of environments which is amply demonstrated by the extreme method of environmental division where the correlation for the two subsets was negative and significant, and the overall estimates were positively correlated with subset 1 and negatively with subset 2. The estimate for the subset 1 being based on high disease environments are reflected in the overall estimates as against those of subset 2. The regression stability parameter, therefore, appears to be less repeatable across environments for downy mildew incidence and it should be possible to use this parameter to a limited degree for selecting cultivars with stable resistance to downy mildew disease.

Discussion

We have assumed a generalized non-specific type of host-pathogen interaction where the pathogen, with its genetic variation (Shetty and Ahmad 1982), is present in all environments but conditions of moisture, etc., are more conducive to infection in the high score environment. Under these circumstances, the multilocation disease data can be conventiently subjected to regression analysis for obtaining stability indexes for each genotype, as proposed by Finlay and Wilkinson (1963); Eberhart and Russell (1966), and Perkins and Jinks (1968). If the generalized model prevails, all genotypes should have regression coefficients greater than zero and none with $b \leqq 0$, or negative slopes. This was true in the overall analysis, in the present case, where all genotypes showed positive slopes, some being more positive than others. The regression mean squares for the two susceptible entries 7042 and NHB-3 with 73% and 67% mean disease score were, however, non-significant against their corresponding remainder mean squares.

The three stability parameters – mean, regression coefficient and deviations from regression – to be of practical value, must be respectable over other sets of environments. It has been shown that while mean and deviations are highly repeatable, the regression coefficients are not. The most drastic change in the magnitudes of regressions was observed for the extreme method where the regression coefficients in the subset 2 were non-significant ($b_i \triangleq 0$) for most of the genotypes and they had exceptionally large standard errors. This means either the generalized model has failed in subset 2 or that some genotypes show responses which are subjected to thresholds (Jinks and Pooni 1979). Under these circumstances, linear regression analysis must be supplemented with a secondary classification of the environments into two graded sets for which separate regressions can be computed (Verma et al. 1978). In this way, it will be possible to identify a genotype with $b_i = 1.0$ in the low and $b_i \leqq 1.0$ in the high disease environments.

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