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CLUSTERING GENOTYPES BASED ON GENOTYPE x ENVIRONMENT INTERACTION

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Abstract: A procedure to form clusters of genotypes such that a genotype is stable relative to the cluster to which it belongs to and not so relative to any other is suggested.

INTRODUCTION

Stability in performance is one of the most desirable properties of a genotype to be released as a variety for wide cultivation. A genotype is 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. The most commonly used are the regression methods of Eberhart and Russell (1966), Perkins and Jinks (1967 a & b) and Freeman and Perkins (1971). The main drawback of regression approach is, by introduction of a genotype having a response to environments differing from average response of the genotypes under study, the genotypes labelled as stable earlier may become unstable. This, to a certain extent can be overcome by forming clusters of genotypes such that those within a cluster have similar response to environments. The main purpose of this paper is to evolve a procedure to achieve this.

MATERIALS AND METHODS

Stability analysis is carried out only when the genotype x environment interaction is significant. If the interaction is not significant, all the genotypes are considered stable with respect to the available set of genotypes. Hence, if any subset of the genotypes is identified such that their genotype x environment interaction is not significant, any member of this subset can be termed stable with respect to this set. In other words, all those belonging to such a subset will have similar response to differing environments. Therefore, formation of different clusters of genotypes such that each cluster is a maximum set with nonsignificant genotype x environment interaction is proposed for identification of genotypes having similar response to differing environments. Different clusters may or may not be overlapping. The partitioning of the genotype x environment interaction in the analysis of variance, when the clusters obtained are non-overlapping is explained below. Such a partition in the overlapping situation can be obtained in a similar manner.

Assuming there to be s environments and t genotypes partitioned into k non-overlapping groups, the partition of the interaction sum of squares in the analysis of variance table is given in Table 1.

To consider all possible partitions and arrive at the best partition is very tedious. A procedure which eliminates a great many of the undesirable partitions for consideration and arrive at a logically best partition is attempted. It involves ranking of the genotypes based on their contribution to the genotype x environment interaction and arrive at the best partition after considering different partitions such that only genotypes having contiguous ranks will come into a cluster. For this purpose, ecovalence defined by Wricke (1962, 1966) and stability variance defined by Shukla (1972) were considered for ranking genotypes.

Wricke (1962, 1966) defined ecovalence as the percentage contribution of a genotype to the total genotype x environment interaction sum of squares. Ecovalence of the i^{th} genotype is given by

$$W_i = \sum_{j=1}^{s} (Y_{ij} - Y_{i.}/s - Y_{.j}/t + Y../st)^2$$

expressed as the percentage of the total of all W_is.

The stability variance defined by Shukla (1972) can be proved to be a linear function of the ecovalence and hence the genotypes will have the same ranking when they are ranked by ecovalence and by the stability variance. Hence ecovalence and stability variance are equally effective for ranking genotypes.

A more ambitious way of ranking will be based on the graph of interaction effect against the environmental means for each genotype.

RESULTS AND DISCUSSION

The procedure is illustrated using an experiment on 25 amaranth genotypes. The experiment involved testing of 25 amaranth genotypes in 11 environments with two replications in randomised block design. The character taken for study was length of fifth leaf on 30th day of sowing, being the only character for which genotype x environment interaction was significant.

Analysis of variance was done in each environment and error variances were tested for homogeneity. Since the error variances were homogeneous, the data were subjected to pooled analysis for testing the significance of genotype x environment interaction. The interaction was found significant. Hence the genotypes were arranged in descending order of magnitude of their Wj values (ecovalence) as given in Table 2.

Interaction of 20 genotypes, which had ranks from 6 to 25, with environments, was not significant and grouped into one, showing that they had similar response to differing environments. The remaining five genotypes which had high values of Wj could not be combined to form groups. The split up of sum of squares and degrees of freedom are given in Table 3.

The pooled error mean square for testing the significance of interaction was 1.6118.

Table 1. Partitioning of interaction sum of squares

Source	Degrees of freedom	Interaction sum of squares
Within group 1	$(t_1-1)(s-1)$	I_1
Within group 2	$(t_2-1)(s-1)$	I_2
--	--	--
--	--	--
--	--	--
Within group k	$(t_k-1)(s-1)$	Ik
Between groups	$(k-1)(s-1)$	By subtraction
Total	$(t-1)(s-1)$	I

where I_u, the interaction sum of squares within the u^{t} group is given by

$$I_u = \sum_{i=1}^{t_u}\sum_{j=1}^{s} Y_{ij}^2 - (1/s)\sum_{i=1}^{t_u} Y_i^{\,2} - (1/t_u)\sum_{j=1}^{s}\left(\sum_{i=1}^{t_u} V\right) + (1/st_u)\left(\sum_{i=1}^{t_u}\sum_{j=1}^{s} Y_{ij}\right)^2$$

and I, the total interaction sum of squares is given by

$$I = \sum_{i=1}^{t}\sum_{j=1}^{s} V - (1/s)\sum_{i=1}^{t} Y_{i.}^2 - (1/t)\sum_{j=1}^{s} Y_{.j}^2 + (1/st)\, Y_{..}^2,$$

Y_{ij} is the mean performance of i^{t} genotype in j^{t} environment,

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

$$\sum_{u=1}^{k} t_u = t \quad \text{and} \quad Y_{..} = \sum_{i-1}^{t}\sum_{j=1}^{s} Y_{ij}$$

Table 2. Wi values of 25 amaranth genotypes arranged in descending order of magnitude

Rank	Genotype	Wi	Rank	Genotype	Wi
1	8	14.0891	14	25	2.5670
2	14	11.8892	15	1	2.5670
3	9	10.3920	16	6	2.4086
4	12	4.9880	17	22	2.3840
5	17	4.6905	18	4	2.2320
6	19	4.6559	19	24	2.1650
7	2	4.4930	20	3	2.1319
8	18	4.1458	21	15	2.1083
9	10	3.8986	22	13	1.8920
10	16	3.6662	23	23	1.4520
11	5	3.4624	24	7	1.3090
12	21	3.3441	25	20	0.4435
13	11	2.7671			

Table 3. Split up of interaction sum of squares

Source	Degrees of freedom	Interaction		F
		Sum of squares	Mean sum of squares	
Within groups	190	372.4981	1.9605	1.2163
Between groups	50	340.4921	6.8098	4.2250*
Total	240	712.9902	2.9708	1.8432*

* Denotes significant at 5% level.

The procedure described helps to form different clusters of genotypes such that those within any cluster have similar response to changing environments. This grouping will not change with the addition or deletion of one or more genotypes, whereas the conventional stability indices will change. The selection of a genotype for cultivation in a track reduces to selection of the best in the cluster which is appropriate for the track.

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