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A Non-Parametric Method of Assessing the Yield Stability Using Principal Coordinate Analysis

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Abstract: *The Westcott (1986) method of stability analysis based on principal co-ordinate analysis is a simply non parametric method.The method depends ultimately on the choice of a suitable measure of similarity between genotypes.In the present study, there are 19 bread wheat genotypes for yield per plot under six environments are taken and as a result, there are two genotypes namely K7903 and Sonalika came out as stable genotypes. Further HUW100 and H1784 are stable for low yielding environments and HD2233, HD2214, HD2285 and CPAN1798 are stable for high yielding environments. Most of the stability information appears in a sequence of plots, where genotypes are immediately highlighted as consistently more remote points.*

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I. Introduction

Most of the measures relating to stability appeared in the literature are based on parametric methodology. Among those methods the Ebarhart and Russell (1966) methods,Finley and Wilkinson (1963) methods etc. are widely used approaches, which have some limitations. However here is need to look into a method which is robust and consistent in the assessing the stability of varieties when either certain locations are omitted or when sub-sets of varieties are analyzed. One such method is discussed by Westcott (1986) based on principal co-ordinate analysis.as this method is non parametric then no certain assumptions is needed. Hence it is easy to handle for the researcher and the breeder.

II. Materials and methods

Nineteen diverse genotype of bread wheat were taken for the present study. These genotypes were sown in three subsequent years with each at with a high and very low top dressing of boron respectively, making 6 six environments in all. Natural sets of environments can also be partitioned into the high and very low boron environments in turn. The method of study which is presented here is based on suitable measure of similarity between genotypes. In a particular environment, if L and S denotes the largest and smallest genotypes yields, then the similarity between genotypes' yields x_i and x_j is defined by$S(x_i,x_j)= (L-(x_i+x_j)/2)/(L-S)$ if i and j are unequal ,while $(x_i,x_j) = 1$.The higher yielding the genotypes, as measured by their means, the more dissimilar, they according to this measure. The similarity is standarised by dividing by the yield range for the environment. When a set of environments is being considered, the similarity between *x* and *y* is just the mean of the similarities at advantage of the similarity matrix defined here is that in its principal coordinates analysis (Gower, 1966), no negative eigenvalues are obtained.Coordinates of points in a Euclidean space thus result, referred to principal axes, such that the distance between two points represents the dissimilarity between the corresponding genotypes. Each analysis produces a two-dimensional picture, in which the first two principal coordinates are plotted for each genotype. If distances are adequately approximated in this representation for a particular set of environments, genotypes which are above average yielding over these environments will be more dissimilar to the lesser yielding genotypes than the latter will be to each other and so will be represented by points which are more remote. Such plots show their value when the stability assessment is best on the sequential accumulation of environments. Thus, for the low-yielding environments, the first cycle (called LI) involves the analysis of the lowest-yielding environment, the second cycle (L2) involves analysing the two lowest-yielding environments, the third cycle (L3) adds the next lowest yielding environment.The lowest-yielding environment of those remaining being added at each cycle. Similarly, cycles HI, H2 and H3 respectively involve the highest-yielding environment, two highest yielding and three highest yielding environments based on the sequential accumulation of environments. Similarity matrix was also calculated considering all environments (cycle ALL). The environments are first ranked in descending order of mean yield and the low- and high-yielding environments are then examined in cycles' environments. Analysing these cycles produces a succession of pictures, in each of which the first two principal coordinates are plotted for each

genotype. The methodology of principal co-ordinate analysis is used to reduce the high-dimensionality of the raw data and to obtain geometrical configuration of points in a low-dimensional space, without distorting the original relationship between items (Gower,1966). This is done by taking into account the two largest Eigen values along with its principal co-ordinates (PCs). The good genotypes are simply the ones furthest from the centre and their identification is generally immediate. The stable genotypes are then just the ones which are consistently good over cycles.

III. Result and Discussion

The analysis was performed using Microsoft Excel 2010 and R-3.4.3 (32/64). The similarity matrix is calculated using the above mentioned formula by Microsoft Excel. And the eigen value and eigen vector are calculated from the matrix using R and figures are drawn using SPSS version 20. The eigen value (the highest two) and their corresponding eigen vectors (from both high and low yielding environments) for all cycles are shown in the following tables (Table 1-3) and figures (fig.1.1-3).

Table 1: Results of low yielding environments

SL.NO	Genotype	PC1	PC2	SL.NO	Genotype	PC1	PC2	SL.NO	Genotype	PC1	PC2
1	HP1376	-0.231	-0.024	1	HP1376	-0.220	-0.025	1	HP1376	-0.209	-0.012
2	HD2329	-0.219	-0.051	2	HD2329	-0.223	-0.018	2	HD2329	-0.225	-0.004
3	HD2233	-0.256	0.021	3	**HD2233**	**-0.278**	**0.032**	3	HD2233	-0.254	0.013
4	HUW190	-0.213	-0.073	4	HUW190	-0.232	-0.014	4	HUW190	-0.212	-0.010
5	**K7903**	**-0.181**	**-0.292**	5	**K7903**	**-0.159**	**-0.433**	5	**K7903**	**-0.151**	**-0.668**
6	K7906	-0.261	0.028	6	K7906	-0.258	0.020	6	K7906	-0.256	0.000
7	**SONALIKA**	**-0.123**	**0.940**	7	**SONALIKA**	**-0.123**	**0.887**	7	**SONALIKA**	**-0.147**	**0.743**
8	HUW100	-0.264	0.032	8	**HUW100**	**-0.278**	**0.031**	8	**HUW100**	**-0.302**	**0.005**
9	HW135	-0.219	-0.051	9	HW135	-0.241	-0.002	9	HW135	-0.252	0.000
10	BR2094	-0.234	-0.017	10	BR2094	-0.221	-0.028	10	BR2094	-0.235	-0.003
11	CPAN1823	-0.219	-0.054	11	CPAN1823	-0.197	-0.081	11	CPAN1823	-0.215	-0.008
12	HD2270	-0.219	-0.054	12	HD2270	-0.195	-0.096	12	HD2270	-0.208	-0.011
13	HD2214	-0.207	-0.093	13	HD2214	-0.220	-0.025	13	HD2214	-0.202	-0.013
14	HD2285	-0.230	-0.022	14	HD2285	-0.215	-0.040	14	HD2285	-0.205	-0.013
15	H1784	-0.270	0.038	15	**H1784**	**-0.290**	**0.039**	15	**H1784**	**-0.278**	**0.003**
16	HP1467	-0.258	0.029	16	HP1467	-0.244	0.002	16	HP1467	-0.235	0.013
17	HD2314	-0.235	-0.007	17	HD2314	-0.231	-0.014	17	HD2314	-0.226	-0.005
18	CPAN1798	-0.231	-0.023	18	CPAN1798	-0.218	-0.034	18	CPAN1798	-0.243	-0.002
19	UP115	-0.245	0.004	19	UP115	-0.252	0.016	19	UP115	-0.250	-0.001
	L1 Highest two eigen value=13.858,and 0.858				**L2 Highest two eigen values are 12.119 and 0.918**				**L3 Highest two eigen values are 10.778 and 0.8705**		

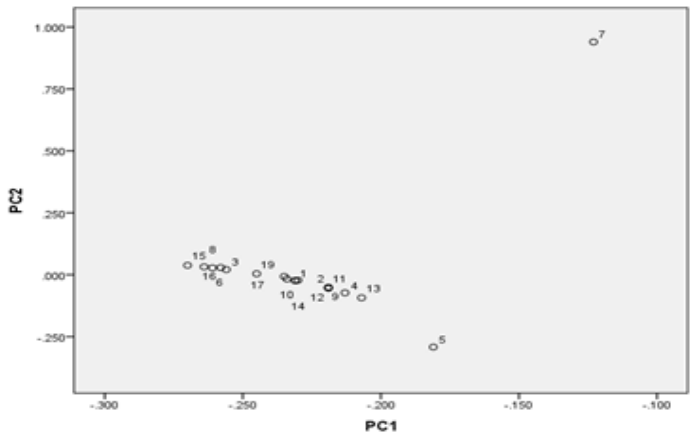

Fig. 1.1: Comparative positions ofgenotypes w.r.t. first two PCs for L1

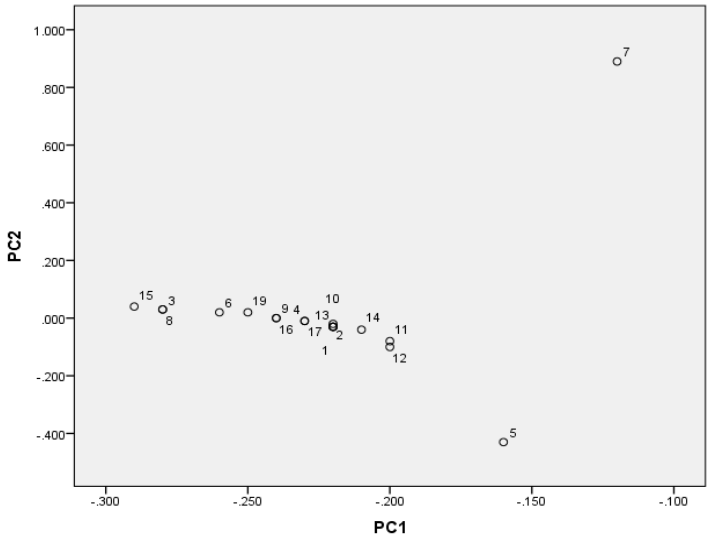

Fig. 1.2: Comparative positions of genotypes w.r.t. first two PCs for L2

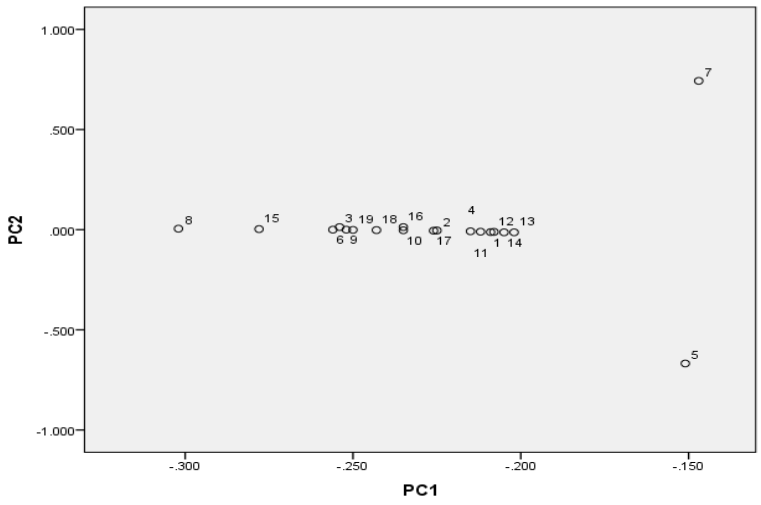

Fig. 1.3: Comparative positions of genotypes w.r.t. first two PCs for L3

Table 2: Results of high yielding environments

SL.NO	Genotype	PC1	PC2	SL.NO	Genotype	PC1	PC2	SL.NO	Genotype	PC1	PC2
1	HP1376	-0.232	-0.008	1	HP1376	-0.232	0.012	1	HP1376	-0.240	-0.013
2	HD2329	-0.254	-0.006	2	HD2329	-0.250	-0.004	2	HD2329	-0.231	-0.012
3	**HD2233**	**-0.125**	**-0.875**	3	**HD2233**	**-0.138**	**-0.738**	3	**HD2233**	**-0.161**	**0.909**
4	HUW190	-0.229	0.005	4	HUW190	-0.234	-0.005	4	HUW190	-0.213	-0.047
5	K7903	-0.220	0.011	5	K7903	-0.211	-0.005	5	K7903	-0.212	-0.047
6	K7906	-0.201	0.027	6	K7906	-0.188	0.025	6	K7906	-0.217	-0.049
7	SONALIKA	-0.238	0.001	7	SONALIKA	-0.255	0.009	7	SONALIKA	-0.211	-0.046
8	HUW100	-0.247	-0.003	8	HUW100	-0.217	0.014	8	HUW100	-0.249	0.014
9	HW135	-0.251	-0.004	9	HW135	-0.294	-0.004	9	HW135	-0.257	0.018
10	BR2094	-0.202	0.026	10	BR2094	-0.218	-0.004	10	BR2094	-0.227	-0.017
11	CPAN1823	-0.219	0.012	11	CPAN1823	-0.226	-0.004	11	CPAN1823	-0.231	-0.012
12	**HD2270**	**-0.155**	**0.179**	12	HD2270	-0.193	-0.004	12	HD2270	-0.207	-0.038
13	**HD2214**	**-0.144**	**0.386**	13	**HD2214**	**-0.164**	**0.052**	13	**HD2214**	**-0.178**	**-0.268**
14	**HD2285**	**-0.150**	**0.224**	14	**HD2285**	**-0.139**	**0.672**	14	**HD2285**	**-0.181**	**-0.299**
15	H1784	-0.299	-0.018	15	H1784	-0.259	-0.004	15	H1784	-0.270	0.009
16	HP1467	-0.259	-0.011	16	HP1467	-0.254	-0.005	16	HP1467	-0.240	-0.006
17	HD2314	-0.259	-0.011	17	HD2314	-0.254	-0.005	17	HD2314	-0.240	-0.006
18	CPAN1798	-0.290	-0.016	18	CPAN1798	-0.290	-0.004	18	**CPAN1798**	**-0.289**	**0.016**
19	UP115	-0.284	-0.014	19	UP115	-0.263	-0.004	19	UP115	-0.265	0.014
	H1 Highest two eigen values are11.5and0.96respectivly				**H2 Highest two eigen values are10.3and0.94 respectively**				**H3 Highest two eigen valuesare 10.52 and .789 respectively**		

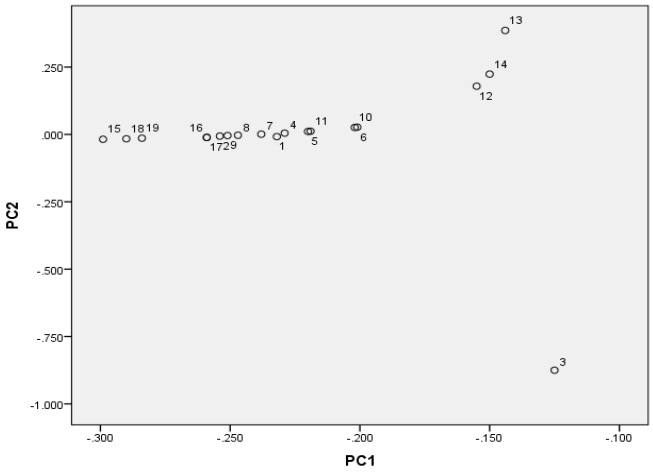

Fig. 2.1: Comparative positions of genotypes w.r.t. first two PCs for H1

Considering Table-1 and Fig.1.1-1.3. it is revealed that genotypes mainly 5th (K7903),7th (Sonalika),8th (HUW-10) and 15th (H1764) are stable in low yielding environments. And similarly for high yielding environments (Table-2 and Fig. 2.1-2.3) genotypes mainly 3rd (HD2233), 13th (HD2214) and 14th (HD2285) are stable. Further it is seen that when all environments are taken under consideration the genotypes 7th, 5th, 13th and 14th *viz.* Sonalika, K7903, HD2214 and HD2285 are stable among all genotypes studied.

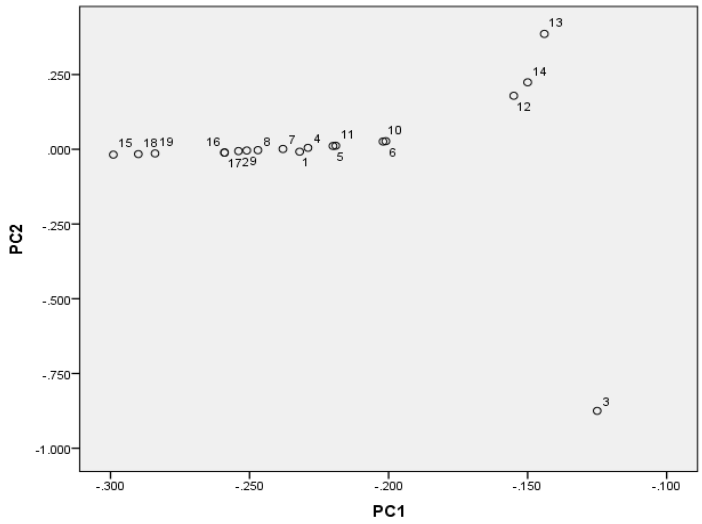

Fig. 2.2: Comparative positions of genotypes w.r.t. first two PCs for H2

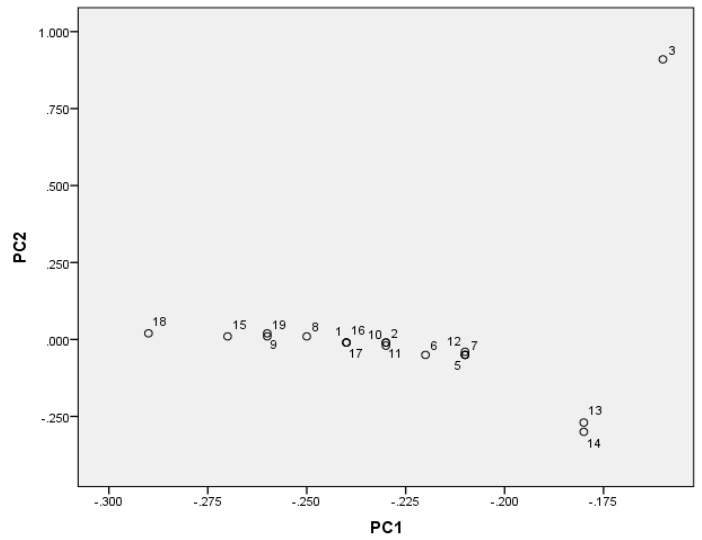

Fig. 2.3: Comparative positions of genotypes w.r.t. first two PCs for H3

The method of stability assessment proposed here can highlight features of performance which might otherwise be overlooked. It is free from the shortcomings of regression methods, cluster analysis and principal components which were detailed by Westcott (1986).

In conclusion, the method accurately reveals those genotypes which are stable for different sets of environments. This is completely assumption free method, which may easily be acceptable by the breeders and researchers as well. Hence for any sets of environments one may reveal such important genotypes, may be used for future breeding program adopted for boron deficient terai zone.

Table 3: Results of all environments

SL.NO	Genotype	PC1	PC2
1	HP1376	-0.225	0.016
2	HD2329	-0.229	0.014
3	HD2233	-0.210	0.032
4	HUW190	-0.213	0.027
5	**K7903**	**-0.182**	**0.561**
6	K7906	-0.238	0.008
7	**SONALIKA**	**-0.179**	**-0.814**
8	HUW100	-0.277	0.000
9	HW135	-0.255	0.005
10	BR2094	-0.231	-0.015
11	CPAN1823	-0.223	-0.016
12	HD2270	-0.207	-0.018
13	**HD2214**	**-0.191**	**0.109**
14	**HD2285**	**-0.194**	**0.084**
15	H1784	-0.275	-0.001
16	HP1467	-0.238	-0.019
17	HD2314	-0.233	0.011
18	CPAN1798	-0.266	0.002
19	UP115	-0.258	-0.013

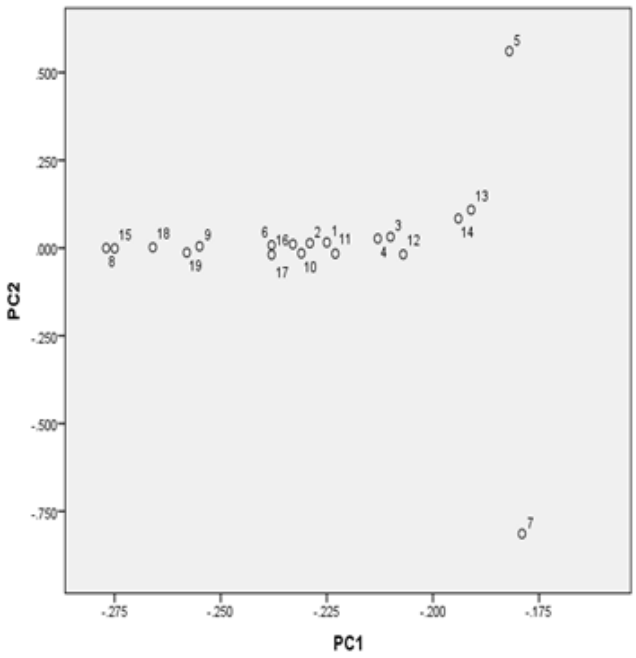

Fig.3: Comparative positions of genotypes w.r.t. first two PCs for ALL

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