International Journal of Agriculture Innovations and Research
Volume 7, Issue 5, ISSN (Online) 2319-1473
Manuscript Processing Details (dd/mm/yyyy):
Received: 25/01/2019 | Accepted on: 28/02/2019 | Published: 16/03/2019

Non-parametric Measures of Yield Stability in Job's Tear (*Coix lacryma–jobi L.)*

H.L. Raiger* **& N.K. Jajoriya**
*Corresponding author email id: Hanuman.Raiger@icar.gov.in

Abstract **– Multi-environmental trials (MET) play an important role in identifying superior genotypes for large scale propagation in future by assessing the stable performance of improved genotype across over environments before variety release. The aim of the present study is to select job's tear genotypes that have high seed yield and stable performance across different environments. The test of significance for genotype x environment (GE) interaction and eight non-parametric measures of stability analysis were used to identify high seed yield stable genotype across the seven environments. The non-parametric measures for GxE interaction were highly significant (p<0.05), cause the rank change among the genotype to the test environment. Based on low value of non-parametric measures, H-2279 was identified most stable as well as high yielding genotype. These non-parametric measures were observed to be associated with high mean seed yield. The rank correlation coefficient calculated was used to measure the relationship between the stability parameters. The relationships among the non-parametric methods was assessed by hierarchical cluster analysis based on non-weighted values of genotypes. The eight stability measures divided into four groups.**

Keywords **– Job's Tear [*Coix Lacryma – Jobi* (L)], Hierarchical Cluster Analysis, Non-Parametric Stability Analysis, Seed Yield.**

I. INTRODUCTION

Job's tear or adlay [*Coix lacryma – jobi* (L)] is a tall (3–6 ft in height), erect, diploid (2n =20) annual plant with broad leaves. This is a minor cereal belonging to family Gramineae / Poaceae. The plant is monoecious with terminal loose spike which bears large, shining, pear shaped fruits showing fanciful resemblance to tears. The fruits contain a whitish or light brownish grain similar to rice. Job's tear is considered to be a good substitute for rice. Rather, it is considered to be more wholesome by virtue of its higher fat and protein content. It can be used in preparation of any food item that is usually made from rice with same degree of palatability. Milling and baking trials in Philippines showed that its flour is suitable for baking purposes when mixed with wheat. A light beer 'Dzu' is made from adlay by the Nagas [1]. The fruits are used in medicine either as tincture or as decoction for catarrhal infection of the air passage and inflammation of the urinary passage. The foliage may be used as fodder for cattle, horses and elephants. It can also be turned into silage.

An important step in a crop improvement programme is to assess the performance of improved varieties in multi-environmental (multi-location, multi-year or both) trials for identifying promising varieties (genotypes) for large-scale propagation. If possible, the breeder would like to have genotypes, which show high performance for yield and other agronomic traits over as a wide range of environmental conditions as possible. However, in actual practice, the genotypes perform differently in different environments. Leading to alteration of their rankings in these environments. This causes difficulty in the identification of superior varieties. In order to overcome this difficulty an attempt is usually made by the plant breeder to reduce the GE interaction, i.e. dependence of the genotypic ranking on environmental conditions through special breeding techniques like resistance breeding. Since only a minor part of the GE interaction can be attributed to controllable environmental determinants, much reduction in the interaction cannot be achieved. This means that the breeder can no longer hope to find varieties which could excel everywhere and in all the years. The most practical alternative then would be to attempt to produce progressively better adapted populations to the existing or specific subsets of environments. For the final choice of varieties for general/ specific adaptation, apart from the mean performance the stability characteristics of the trial genotypes have to be given due consideration

Use of parametric stability statistics and their significance tests require assumption about distribution of variate and the homogeneity of variance. The different approaches are available for the analysis and interpretation of GE interaction, excellent reviews of which have been provided by researchers [2, 3]. The choice among these approaches depends on the particular situations and the type of data generated. The analysis of variance method [4] is the fundamental analysis to confirm the presence of GE interaction and to estimate the fraction of total variance attributable to this component. A galaxy of workers [5, 6, 7, 9, 10, 11] have contributed to the development of this approach. A major drawback of the parametric method is that it gives only the individual aspects of adaptability and stability and does not provide an overall picture of the response. For example, a genotype assessed stable in biological sense may prove to be unstable in agronomic sense or vice versa. Use of parametric stability statistics and their significance tests require assumption about distribution of variate and the homogeneity of variance. In most of the situations the parent distribution and the knowledge of the population parameters may not be readily available. The problems is most acute when the sample size is small and the central limit theorem does not hold there by making non-parametric analysis the only plausible alternative to parametric methods. Non-parametric measures are distribution-free and are not as sensitive to measurement errors as are parametric measures. The non-parametric analysis of GE interaction is also robust against the addition or deletion of observations. Yet another consideration in the use of non-parametric measures is the following. Not every GE interaction causes rank changes among the genotypes (rank interaction). From the stand point of a breeder, the interaction might be tolerable so long as it does not affect rank orders. If the interaction is so large as to cause rank changes among genotypes, then one can speak of rank interaction, which is also termed qualitative or crossover interaction. In this type of interaction the true treatment differences vary not only in magnitude but also in direction. In contrast in quantitative or non-crossover interaction the treatment differences vary only in magnitude. Whatever may be the inference on the merits of various stability measures from theoretical grounds, the final judgment on the suitability of these measures for stability assessment has to be based on their performance on multi-location yield data [12, 13]. A procedure, which performs well from both the angles, theoretical as well as practical, can safely be recommended for wider application. Several non-parametric measures [14, 15, 16] were also proposed. Four non-parametric measures of phenotypic stability ($S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$ and $S_i^{(6)}$) based Phenotypic Rank Order were proposed [14], and a variety is considered stable over a set of environments if its ranks are similar over these environments. [16]. Proposed as non-parametric stability measure [16] based on ranks of adjusted means of the genotypes in each environment, and These measures were improved by considering the rank median instead of rank mean in mean deviation formula, because mean deviation is minimum taken from the median. Here the denominators are based on uncorrected ranks while the numerators on corrected ones. Accordingly, the purpose of this paper is to study the performance of eight non-parametric stability measures using Job's tear data.

However, there are many questions about job's tear productions, commercialization and genetic improvement in India. Hardly any work has been taken up on genetic improvement of this species so far in India due to their underutilized status. At a global level information on genetic improvement, adaptability and genotype environment interaction of jobs' tear is restricted to few publications. The stability yield has not been investigated in job's tear due to their underutilized status in India. The aims of present study were: (i) to identify job's tear genotype that has high seed yield as well as stable performance across different environment; (ii) to investigate the nature of relationship among non-parametric stability measures.

II. MATERIALS AND METHODS

Plant Material:

The study was carried out with 11 job's tear superior geno type in trials conducted for three years (2006-08) at three locations in India. The locations consisted of Ranichauri, Palampur and Shillong. The trial was not conducted at Ranichauri centre in 2008 and Palampur in 2007. The agro-climate data of these test experiment (year x locations) is given in Table 1. Eleven genotypes tested were developed by NBPGR regional station, Shillong centre of AICRN on Underutilized Crops in India. The names, source of these genotypes are given in Table 2.

Experimental Details:

The experimental layout was a randomized complete block design with three replications at each location. The sowing was done by experimental drill in 3 m x 1.35 m plots, consisting of the 3 rows with 20 cm distance between the rows and plant to plant 15 cm. distance. The seed yield was estimated by the plot basis and converted into kg per ha. for each genotype at each tested environment

Table 1. Agro-climatic Data of testing environments

Environments		**Mean seed yield (kg ha^{-1})**	**EMS**	**Latitude longitude**	**Altitude (m)**	**Soil condition (Texture)**
Location	**Year**					
Palampur	2006	577.0	17300	32°7' N 76°3' E	1290 m	Silty clay loam
	2008	568.0	58200			
Ranichauri	2006	400.0	1000	30°6' N 78°4' E	2000 m	Silty clay loam
	2007	162.0	400			
Shillong	2006	1275.0	30900	25°42' N 88°24' E	1520 m	Silty clay loam
	2007	744.0	18600			
	2008	539.0	21500			

Table 2. Genotype name and origin of 11 job's tear genotypes with mean seed yield.

Genotype name	**Origin**	**Mean (kg/ha)**
AAH-33	Tago, Arunachal Pradesh	599.0
DKH-07	Linchek, K. Anglong	654.0
H-0626	Lephami, Nagaland	568.0
H-0732	Sangsangiyo, Nagaland	619.0
H-2215	Medziphema, Nagaland	590.0
H-2279	Peren, Nagaland	679.0
H-2287	Peren, Nagaland	723.0
H-2902	Sasatgiri, Meghalaya	494.0
H-3738	Shillong, Meghalaya	540.0
Mayeun Local	Shillong, Meghalaya	649.0
Pollin Local	Shillong, Meghalaya	588.0

Table 3. Mean yields of different genotypes at different environments.

Genotype	Environment						$\sum w_j Y_{ij} = G_i$
	1	2	…	j	…	N	
1	Y_{11}	Y_{12}	…	Y_{1j}	…	Y_{1N}	G_1
2	Y_{21}	Y_{22}	…	Y_{2j}	…	Y_{2N}	G_2
:	:	:	…	:	…	:	:
i	Y_{i1}	Y_{i2}	…	Y_{ij}	…	Y_{iN}	G_i
:	:	:	…	:	…	:	:
t	Y_{t1}	Y_{t2}	…	Y_{tj}	…	Y_{tN}	G_t
Total	P_1	P_2	…	P_j	…	P_N	
Crude SS	S_1	S_2	…	S_j	…	S_2	

Test the Significance of Genotype Environment Interaction.

The analysis of variance is a fundamental analysis to find out whether significant interactions are present or not. This analysis must precede any genetic analysis of breeding data including stability analysis with which we are presently concerned. But a non-weighted analysis is valid only when the error variances in the different experiments are homogeneous. When Bartlett's test shows that the experiments have different error structure, the combined analysis requires a weighted analysis of variance taking $W_j = r/S_j^2$. The different steps involved in this case are:

(i) Using the G x E data on mean yields given in Table 3, form the column totals $P_j = \sum_i Y_{ij}$ and determine $W_j P_j$ values.

(ii) Form the row totals $G_i = \sum_j w_j Y_{ij}$

(iii) Form crude sum of squares of entries in each column, S_j

(iv) Obtain the correction factor $C = \left(\sum_i \sum_j w_j Y_{ij}\right)^2 / t \sum_j w_j$

(v) Computation the different sum of squares as follows:

Total *(T)* : $\sum_j w_j S_j - C$

Genotypes (G): $\frac{\sum_i G_j^2}{\sum_j w_j} - C$

Environments (E): $\frac{I}{t} \sum w_j P_j^2 - C$

Unfortunately, the interaction sum of squares *I* has to be obtained by subtraction *(I=T-G-E)*

Following [17], $\frac{(n-4(n-2))}{n(n+t-3)} I$ may be approximated as χ^2 value with the significant point of Chi-square corresponding to $(n-4)(s-1)(t-1)/(n+t-3)$ degrees of freedom, *n* being the error degrees of freedom in different trials. If the experiments differ in size, as a rough approximation the average number of degrees of freedom per experiment is used in place of *n*. A comparison of the computed χ^2 value with the significant point of Chi-square corresponding to $(n-4)(s-1)(t-1)/(n+t-3)$ degrees of freedom will provide the necessary test for GE interaction.

Non Parametric Stability Analysis:

The statistical procedures adopted for the stability analysis of the genotype were those proposed by [14, 15, 16]. The two measures [14] are based on ranks of phenotypes in each environment. The phenotypic values of k genotypes are ranked within each environment $(j = 1, 2 \ldots \ldots N)$, giving the lowest value of rank (r_{ij}) and the highest value of rank k. Then under the biological concept a variety i is considered stable over a set of environments if its ranks are similar over these environments.

$$S_i^{(1)} = \frac{1}{N-1} \sum_{j=1}^{N} (r_{ij} - \bar{r}_i)^2$$

$$S_i^{(2)} = \frac{2}{N(N-1)} \sum_{j=1}^{N-1} \sum_{j=j+1}^{N} |r_{ij} - r_{ij}|$$

The two measures [15]: The genotypic stability, in fact, should be measured independently of genotypic effects, which means that the actual ranks (r_{ij}) have to be based on the corrected (r_{ij}) have to be based on the corrected Y_{ij} values namely $Y_{ij} - \bar{Y}_{i}.\ r_{ij}$ and $\hat{r}_i$ have been determined from these corrected values only. [15] Proposed two other stability measures [15] which combined yield and stability. Here the denominators are based on uncorrected ranks while the numerators on corrected ones. The statistics based on yield ranks of genotypes in each environment are expressed as follows:

$$S_i^{(3)} = \frac{\sum_j (r_{ij} - r_i)^2}{r_i}$$

$$S_i^{(4)} = \frac{\sum_i |r_{ij} - r_i|}{r_i}$$

Four non-parametric stability measures [16] were improved by considering the rank median instead of rank mean in mean deviation formula, because mean deviation is minimum taken from the median. Here the denominators are based on uncorrected ranks while the numerators on corrected ones. The statistics based on yield ranks of genotypes in each environment are expressed as follows:

$$NP_i^{(1)} = \frac{1}{N} \sum_{j=1}^{N} |r_{ij}^{*} - M_{di}^{*}|$$

$$NP_i^{(2)} = \frac{1}{N} \left(\sum_{j=1}^{N} |r_{ij}^{*} - M_{di}^{*}| / M_{di} \right)$$

$$NP_i^{(3)} = \frac{\sqrt{\sum (r_{ij}^{*} - r_i^{*})^2 / N}}{r_i}$$

$$NP_i^{(4)} = \frac{2}{N(N-1)} \left[\sum_{j=1}^{N-1} \sum_{j=j+1}^{N} |r_{ij}^{*} - r_{ij}^{*}| / \bar{r}_i \right]$$

In the above formulas, r_{ij}^* is the rank of x_{ij}^* and M_{di}^* are the mean and median ranks for adjusted values, while $\bar{r}_i$ and M_{di} are the same parameters computed from the original (unadjusted) values.

Correlation Analysis:

The stability parameters were compared using rank correlation. To understand better the relationship among stability measures, the hierarchical cluster analysis based on the ranks of seed yield and genotype x environment measures was performed by Ward's method [18]. The based on non-weighted values of 11 job's tear genotypes was perform. The squared Euclidean distance was use as dissimilarity measure required in Ward's method.

III. RESULT

The test for Significance of Genotype x Environment Interaction:

In our study, error mean square of the seven experiments were mentioned in Table 1. A mere look at this figures in table makes one suspect hetero-scedasticity. However, this was confirmed by Bartlett's test, which gave a highly significant value for the Chi-square. Accordingly, the weighted analysis as explained above was undertaken and the results of this exercise are summarized in Table 4.

Table 4. Weighted ANOVA for genotype-environment data of job's tear

Source	**Sum of squares**
Genotypes (*G*)	162.98
Environment (*E*)	3251.32
Interaction (*I*)	404.53
Total (*T*)	**3818.83**
χ^2 (*df* 34)=208.04*	

* Significant at the 0.01 probability level

Thus the parametric analysis shows the presence of GE interaction. As said earlier, not every interaction of this sort causes rank changes among the genotypes (rank interaction), from the stand point of a breeder interaction might be tolerable so long as it does not affect rank orders. If the interaction is so large as to cause rank changes among genotypes, then one can speak of rank interaction, which is also termed qualitative or cross-over interaction. In this type of interaction the true treatment differences vary not only in magnitude but also in direction. In contrast in quantitative or non-crossover interaction the treatment differences vary only in magnitude. Following this concept, we now try to assess the intensity of the interaction and draw suitable conclusions from a strictly non-parametric approach.

Stability Analysis:

The stability analysis result for 8 non-parametric statistical parameters are presented in Table 5. Accordingly, the $S_i^{(1)}$ and $S_i^{(2)}$ of the evaluated genotypes showed that genotype H-2279, Mayeun Local, H-0626, H-3768 and H-2902 had the lowest value. The genotype stability tested by $S_i^{(1)}$ the values conceded with the grouping of the genotype stability given by $S_i^{(2)}$. The unstable genotype based on the statistics $S_i^{(1)}$ and $S_i^{(2)}$ were H-2215, H-2287 and Pollin Local, because these genotypes had highest values of $S_i^{(1)}$ and $S_i^{(2)}$. Based on $S_i^{(3)}$ and $S_i^{(6)}$ genotype Mayeun Local, H-2279, H-0626 and DKH-07 were stable but the genotype H-2279 had 2nd rank in seed yield and stability, whereas the genotype AAH-33, Pollin Local, H-2215, H-3768 were the least stable ones. $S_i^{(3)}$ and $S_i^{(6)}$ had positive correlated with seed yield, the results showed that using $S_i^{(3)}$ and $S_i^{(6)}$, it is possible to select stable and high yielding genotype. However, such stable genotypes selected on the basis of those stability measure turn out to have high seed yield. This makes the parameters has so useful for identification of high yielding as well as stable genotype. According to [16] stability statistics [$NP_i(1)$, $NP_i(2)$, $NP_i(3)$, $NP_i(4)$], genotypes with low values are considered as more stable. According the first measure $NP_i(1)$, the genotype H-3768, H-2279, H-2215 and H-0732 having relatively lower values of the measure, were considered stable in comparison to other genotypes. However, the genotype H-2902, H-2287, Mayeun Local and AAH-33 having highest value of the $NP_i(1)$. Based on values of $NP_i(2)$ and $NP_i(4)$, H-3768, H-2279 and Mayeun Local had the lowest value and was therefore considered high stable followed. $NP_i(2)$ and $NP_i(4)$ gave the similar results. These parameters $NP_i(2)$ and $NP_i(4)$ was positively association with seed yield which help for selecting high yielding stable genotype. According to $NP_i(3)$ value, genotypes H-3768, Mayeun Local and H-0732 were considered high stable because of low values of $NP_i(3)$. The genotypes AAH-33, H-2902, H-2215 and Pollin Local with high values were unstable. The result showed that $S_i^{(3)}$, $S_i^{(6)}$, $NP_i(2)$ and $NP_i(4)$ were similar because all had positive relationship with mean seed yield. They were closure associated with seed yield and stability parameter. This parameters were so useful for identification of high yielding stable genotypes.

Table 5. Mean seed yields and stability parameter for 11 genotypes of job's tear tested in 7 environments.

Genotype name	**Mean (kg ha^{-1})**	$S_i^{(1)}$	$S_i^{(2)}$	$S_i^{(3)}$	$S_i^{(6)}$	**$NP_i(1)$**	**$NP_i(2)$**	**$NP_i(3)$**	**$NP_i(4)$**
AAH-33	599.0	4.29	12.95	17.55	4.84	2.71	0.73	0.75	0.95
DKH-07	654.0	3.81	9.62	8.98	2.71	2.71	0.44	0.48	0.62
H-0626	568.0	3.24	6.95	6.35	2.35	2.57	0.38	0.45	0.58
H-0732	619.0	4.29	12.29	11.47	3.20	2.43	0.36	0.44	0.56
H-2215	590.0	4.48	13.90	15.78	4.22	2.29	0.49	0.52	0.68
H-2279	679.0	1.90	2.81	3.28	1.72	1.57	0.28	0.47	0.54
H-2287	723.0	4.29	14.24	11.73	2.90	3.00	0.35	0.45	0.59
H-2902	494.0	3.62	9.14	10.67	3.33	3.00	0.66	0.69	0.87
H-3738	540.0	3.52	8.95	11.75	3.38	1.14	0.24	0.30	0.40

Genotype name	Mean (kg ha^{-1})	$S_i^{(1)}$	$S_i^{(2)}$	$S_i^{(3)}$	$S_i^{(6)}$	NP$_i$(1)	NP$_i$(2)	NP$_i$(3)	NP$_i$(4)
Mayeun Local	649.0	2.19	3.29	2.34	1.25	2.86	0.33	0.41	0.52
Pollin Local	588.0	4.95	16.90	16.14	3.86	2.57	0.46	0.49	0.64

Table 6. Rank correlation for the mean seed yield and 8 non-parametric stability measures.

Parameters	Mean	$S_i^{(1)}$	$S_i^{(2)}$	$S_i^{(3)}$	$S_i^{(6)}$	NP$_i$(1)	NP$_i$(2)	NP$_i$(3)	NP$_i$(4)
Mean	1.00								
$S_i^{(1)}$	0.03	1.00							
$S_i^{(2)}$	-0.02	0.98**	1.00						
$S_i^{(3)}$	0.29	0.78**	0.81**	1.00					
$S_i^{(6)}$	0.46	0.70*	0.70*	0.95**	1.00				
NP$_i$(1)	-0.11	0.13	0.23	-0.07	-0.08	1.00			
NP$_i$(2)	0.34	0.52	0.53	0.50	0.62*	0.44	1.00		
NP$_i$(3)	0.13	0.42	0.45	0.46	0.56	0.35	0.88**	1.00	
NP$_i$(4)	0.21	0.57	0.61*	0.55	0.64*	0.47	0.96**	0.95**	1.00

* Significant at the 0.01 probability level * significant at the 0.05 probability level

Relationship between mean Seed Yield and Stability Measures:

The result of rank correlation between mean seed yield and 8 non-parametric stability measures are presented in Table 6. The correlation between mean seed yield and all non-parametric measures were positively correlated except $S_i^{(2)}$ and NP$_i$(1). The high correlation between mean seed yield and stability measures expected as the values of these measures were higher for high seed yielding genotypes. The stability parameters $S_i^{(1)}$, $S_i^{(2)}$ and $S_i^{(3)}$ were positively significant correlated with each other ($p<0.01$) and NP$_i$(1), NP$_i$(2), NP$_i$(3) and NP$_i$(4) were positively and highly significant correlated with each other. The genotypes and stability measures were classified in different groups on the basis of hierarchical classification.

IV. DISCUSSION

In present study, the clusting based on rank of genotypes by different yield stability measures our 7 environments that the 8 stability measure would be divided into four distinct group (Fig. 1).

We observed four [14] stability measures of cluster together, indicating that the two measures were similar in their capacity of classifying genotypes according to yield stability under different environmental situations. We can use only one of them to select stable genotypes in breeding programmes. In group-II include NP$_i$(2), NP$_i$(3) and NP$_i$(4) for stability measures. The mean and NP$_i$(1) were categorized in group-III and IV. These parameters mean and NP$_i$(1) were entirely different from other stability measures.

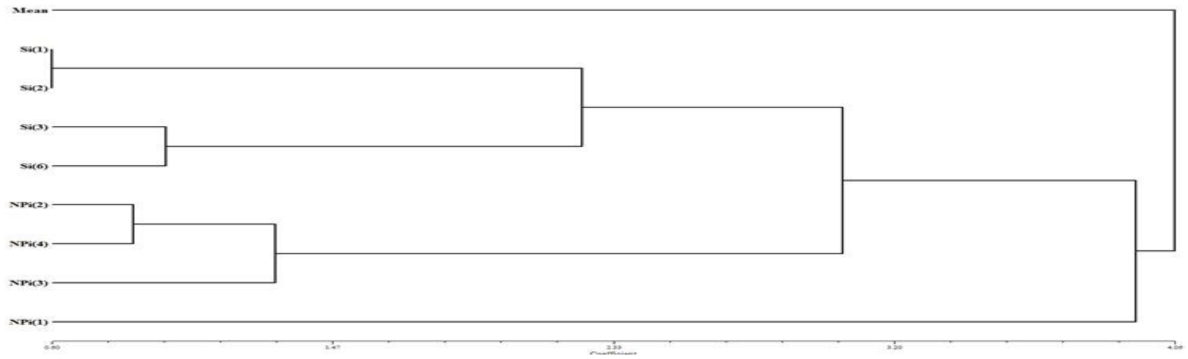

Fig. 1. Hierarchical cluster analysis of the eight non-parametric stability measures based on Ward's method.

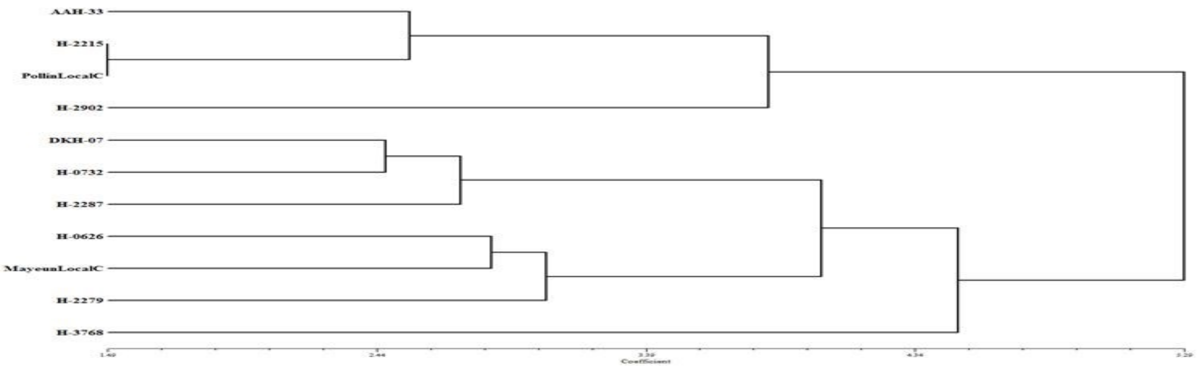

Fig. 2. Hierarchical cluster analysis of the eleven genotypes based on Ward's method.

In our study for example, the genotype H-2279 was assessed as a stable using $S_i^{(1)}$ and $S_i^{(2)}$ but unstable with non-parametric stability measures $NP_i(3)$. This emphasis in this method is to identify and group genotypes, which shows similar pattern of response across the environments. In our study the hierarchy cluster analysis [18] based on non-weighted values of 8 non-parametric stability measures and mean seed yield, was used to classify the genotypes into three major groups (Fig. 2) using the squared eucliden as a dissimilarity measures. The group-I include the five high yielding genotypes H-2287, H-2279, DKH-07, Mayeun Local, H-0732 and one low yielding genotype H-0626, these genotype were identify as a less stable by different non-parametric measures. The group-II most of the genotypes which had low yield clustered in group-II included genotypes AAH-33, H-2215, Pollin Local and H-9202. These genotypes were identified as a moderate stable genotypes by [14] and low stable by [16] stability parameters. The lowest yielding genotypes H-3768 was clustered in group-III. This genotype was identify as a highly stable genotype by [16] stability parameters.

V. CONCLUSION

The stability analysis is very useful for selection of the high yielding genotype for breeding programmes as well as for commercial release variety in future. The eight stability measures have been taken in this study for stable varieties in terms of high yield and stability. Simultaneous selection of genotype for high yield and stability is useful effect of genotype x environment interaction and selection genotype can be selected in refined manner. GxE interaction were highly significant ($p<0.05$), sowed the different response of genotypes to the test location/year. Eight non- parametric measure had been employed, based on low value of non-parametric measures, H-2279 was identified most stable as well as high yielding genotype.

ACKNOWLEDGEMENT

The authors thank the incharges of the CSK HPKV, Palampur (Himachal Pradesh); GBPUAT, Ranichauri (Uttaranchal) and NBPGR Regional Station, Shillong (Meghalaya) for helping in data recording of the experiments conducted at these centres.

REFERENCES

[1] Dua RP, Raiger HL, Phogat BS, Sharma SK (2009) Underutilized Crops: Improved Varieties and Cultivation Practices pp 66.

[2] Freeman, G.H, (1973). Statistical methods for analysis of genotype-environment interactions. Heredity, 31:339-354.

[3] Becker, H.C. and Leon, J. (1988). Stability analysis in plant breeding., Plant Breeding, 101:1-23.

[4] Sprague, G.E. and Federer, W.T. (1951). A comparison of variance components in cotton yield trials. II. Year x variety, location x variety and variety components. Agron. J., **43:** 535-541.

[5] Finlay KW, Wilkinson GN (1963) the analysis of adaptation in a plant breeding program. Aust J Agric Res 14: 742-754.

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

[7] Perkins, J.M. and Jinks, J.L. (1968) Environmental and genotype-environmental components of variability. III Multiple lines and crosses. Heredity, **23:** 339-356.

[8] Freeman, G.H. and Perkins, J.M. (1971). Environmental and genotype environmental components of variability VIII. Relations between genotypes grown in different environments and measurement of these environments. Heredity, 27:15-23

[9] Fripp. Y.J. and Caten, C.E. (1971). Genotype-environment interactions in Schizophyllium commune 1. Analysis and character. Heredity, 27:393-407.

[10] Tai, G. C. C. (1971). Genotypic stability analysis and its application to potato regional trials. Crop Sci., **11:** 184-190.

[11] Shukla GK (1972) some aspects of partitioning genotype-environmental components of variability. Heredity 28: 237-245.

[12] Raiger HL, Prabhakaran VT (2000) A statistical comparison between non-parametric and parametric stability measures. Indian J Genet 60(4): 417-432.

[13] Raiger HL, Prabhakaran VT (2001) A study on the performance of a few non-parametric stability measures using pearl-millet data. Indian J Genet 61(1): 7-11.

[14] Huehn VM (1979) Beitrage zur erfassung der phanotypischen stabilitat. EDV Med Biol 10: 112-117.

[15] Nassar, R. and Huhn, M. (1987). Studies on estimation of phenotypic stability: Test of significance for nonparametric measures of phenotypic stability. Biometrics, **43:** 45-53.

[16] Thennarasu, K. 1995. On certain non-parametric procedures for studying genotype-environment interactions and yield stability. Unpublished Ph.D. Thesis, P.G. School, IARI, New Delhi.

[17] Cochran WG (1937) Problems a raising in the analysis of a series of similar experiments. J Roy Stat Soc Supply 4: 102-1118.

[18] Ward JH (1963) Hierarchical grouping to optimize an objective function. J Am Stat Assoc 58: 236-224.

AUTHORS PROFILE'

First Author H.L. RAIGER. Dr. Raiger is a Principal Scientist in National Bureau of Plant Genetics Resources and working on Underutilized Crops since 1998. Dr. Raiger passed B.Sc. (Ag.) from Rajasthan Agricultural University Bikaner in 1991 and passed M.Sc. (Ag.) from Indian Agricultural Research Institute, New Delhi - 110012 in 1994. Co--mpleted Ph.D. with specialization in Biometrics (Statistical Genetics) from IARI in 2000. He has an experience of 21 years of Research, Teaching and Extension Activities of underutilized Crops. He has published more than 50 Research Papers and Editor of Annual Report (30) and Technical Bulletins/ Crop catalogues (50) and Popular Articles on underutilized crops (30) and Author of one book on Underutilized Crops, Three varieties of Potential Crops had been released by Raiger Association. AICRN on Potential Crops, NBPGR, Pusa Campus, New Delhi-110012, India. Tel. (O) +91-11-25841835, Mobile +91 9968271997. Fax: +91-11-25841835; email address: drhanumanlal@yahoo.co.in, hanuman.raiger@icar.gov.in

Second Author: N.K. Jajoriya. He is now research Scholar in Baba Farid Institution Technology HNB Garhwal Central University, Dehradun (Uttarakhand). He passed B.Tech. in Computer Engineering from Rajasthan Technical University Kota and completed M.Sc. (Ag.) in Information and Communication Technology from SKN Agriculture University Jobner (Raj.).