Stability analyses of pearl millet genotypes (Pennisetum glaucum) and its related traits using the Freeman and Perkins model

Abstract

In the present study, twenty-nine genotypes were carried out to determine the stability of morphological characters viz., dry fodder yield, Days to 50% flowering, and Days to maturity of pearl millet in eight different environments viz., ARS Mandor, Bikaner, RARI Jaipur, Jamnagar, Hisar, Gwalior, Ranchi and Jammu Kashmir using Freeman and Perkins model. Data was collected from ICAR- All India Coordinated Research Projects (AICRP) of pearl millet, Agricultural University, Mandor, Rajasthan, India for one year (2019). The combined analysis of variance showed significant differences among genotypes, environments and G x E interaction for all morphological characters under study. The genotypes G10, G14, G22, G23 and G29 were found stable for dry fodder yield, G6, G10, G12, G15, G17, G20, G23, G24 and G29 genotypes were stable for days to 50% flowering and G1, G2, G4, G5, G7, G9, G22 and G23 genotypes were found stable for days to maturity in all environments.

Introduction

Pearl millet (Pennisetum glaucum) is a vital cereal crop known for its adaptability to harsh growing conditions. It is cultivated globally, particularly in arid and semi-arid regions. Pearl millet ranks as the sixth most important cereal crop worldwide, due to its ability to thrive in hot and dry climates. In India, pearl millet holds great significance and is grown extensively in states such as Rajasthan, Gujarat, Haryana, and Uttar Pradesh. This crop is not only a staple food source but also serves as livestock fodder. With its high nutritional content and gluten-free nature, pearl millet has gained attention for its suitability in addressing nutritional challenges and dietary restrictions. Ongoing research and breeding programs aim to enhance pearl millet's productivity, nutritional value, and stress tolerance. These efforts contribute to achieving food security and sustainable agriculture in regions facing climate variability and resource constraints.

Stability analysis plays a crucial role in agricultural research, particularly in crop improvement programs. It involves assessing the performance and adaptability of different genotypes under varying environmental conditions. This analysis helps researchers and farmers identify genotypes that exhibit consistent performance across diverse environments, ensuring reliable crop production and minimizing yield fluctuations. “The stability is the consistency in the performance of genotypes over a wide range of environments” (Singh and Chaudhary, 1985). For farmers, stability analysis provides valuable insights into the performance of crop genotypes across different agro-climatic conditions. It helps them make informed decisions regarding genotype selection, thereby increasing their chances of obtaining stable and high-yielding crops. In such circumstances, the identification of genotypes that exhibit stable performance across diverse environments or locations becomes crucial. The genotypes x environment interaction, as defined by Allard and Bradshaw in 1964, plays a significant role in genotype development and evaluation. This interaction is particularly important as diverse environments can pose challenges and potentially decrease the stability of genotypes (Eberhart and Russell, 1966). It is widely observed that the performance of different genotypes varies across different environments, indicating the presence of genotype-environment interaction. Several studies, such as those conducted by Yates and Cochran (1938), Finlay and Wilkinson (1963), Rowe and Andrew (1964), Eberhart and Russell (1966), Perkins and Jinks (1968), Breese (1969), and Baker

(1969), have further noted that the relationship between genotype performance and environmental factors often exhibits linearity or near-linearity. However, there are two fundamental statistical concerns raised regarding the aforementioned studies. These concerns include the selection of appropriate sums of squares and degrees of freedom to account for regression components, as well as the choice of the environmental measurement used for regression analysis. To address these issues, Freeman and Perkins (1971) developed a model that resolves these statistical challenges.

The aim of this study was to assess the stability for Dry fodder yield (kg/net plot), Days to 50% flowering (days) and Days to maturity (days) of pearl millet genotypes across different environments using the Freeman and Perkins model. Mean, regression coefficient and deviation from regression were used as stability measures.

Material and Methods

Data set:

The analysis of the multi-environment experiment of twenty-nine pearl millet genotypes namely, HHB272 (G_1), MPMH21(G_2), RHB177(G_3), HHB197(G_4), GHB538(G_5), HHB67(G_6), AHB1269(G_7), HHB299(G_8), AHB1200(G_9), PB1705(G_{10}), XMT1497(G_{11}), 86M01(G_{12}), GHB905(G_{13}), MPMH17(G_{14}), RHB173(G_{15}), HHB223(G_{16}), GHB744(G_{17}), GHB732(G_{18}), KBH108(G_{19}), 86M86(G_{20}), Kaveri Super Boss(G_{21}), MP-7792(G_{22}), Proagro9444(G_{23}), GHB558(G_{24}), Dhanshakti(G_{25}), ICMV221(G_{26}), PusaComposite701(G_{27}), Posa Composite383(G_{28}), JBV 2(G_{29}) conducted at eight different locations of India viz, ARS Mandor, Bikaner, RARI Jaipur, Jamnagar, Hisar, Gwalior, Ranchi, Jammu Kashmir for one year (2019). The Randomized Block Design (RBD) with three replication was used. The data were recorded on Dry fodder yield (kg/net plot), Days to 50% flowering (days) and Days to maturity (days). The net plot size was 14.4 m^2 in four locations viz., ARS Mandor, Bikaner, Jamnagar, Jammu Kashmir and 12 m^2 in other four locations viz., RARI Jaipur, Hisar, Gwalior, Ranchi. Freeman and Perkins model (1971) was used to determine the stability of pearl millet genotypes.

Freeman and Perkins model:

This method ensures that the sum of squares resulting from various components must be correctly divided where environment taken as independent component.

The statistical analysis was based on the model as follows,

$$Y_{ij} = \mu + d_i + \bar{B}Z_j + \bar{\delta}_{ij} + B_{di}Z_j + \delta_{dij} + e_{ij}$$

Z_j is the environmental index of j^{th} environment, μ is the grand mean, B_i is regression coefficient of i^{th} genotype for regression of Y_{ij} on Z_j, $\bar{B}$ is the combined regression coefficient, B_{di} is the difference between regression coefficient of i^{th} genotype and combined regression coefficient, δ_{ij} is the Deviation of i^{th} genotype from its linear regression on j^{th} environment, $\bar{\delta}_j$ is the Deviation from the combined regression line of the mean of all genotypes in the j^{th} environment (i.e., $(e_{ij} - \bar{B}Z_j)$, δ_{dij} is the deviation of the i^{th} genotype from each linear regression on Z_j in the j^{th} environment minus $\bar{\delta}_j$ (*i.e.*, $\delta_{ij} - \bar{\delta}_j$), Such that, $\sum d_i = \sum Z_j = \sum B_{di} = \sum \bar{\delta}_j = \sum \delta_{dij} = 0$; (i = 1, 2, ... , g and j = 1, 2, ... , e). The regression stability parameters of model (b^{Fi}) and $[\bar{S}^2_{di\,(F)}]$ were calculated as

$$b^{Fi} = \sum_i \sum_j \bar{y}_{ij} / \sum_i \sum_j Z_{ij}^2 \text{ and } Z_j = \bar{y}_{.j} - \bar{y}_{..}$$

Where, $\bar{y}_{.j}$ is the mean of genotypes in j^{th} environment

$$[\bar{S}^2_{di\,(F)}] = \left[\sum_j \delta_{ij}^2/(E-2)\right] - (S_e^2/r)s$$

$$\sum_{j} \delta_{ij}^2 = \sigma_{vi}^2 - b^{Fi} \sum \bar{y}_{ij} Z_j$$

$$\widehat{\sigma_{vi}^2} = \sum_{j} y_{ij}^2 = \sum_{j} y_{i.}^2 / E$$

Where, $\bar{y}_{..}$ is the general mean, $\bar{S}_e^2$ is the Pooled EMS, $\widehat{\sigma_{vi}^2}$ is the S.S due to i^{th} genotype

Result and Discussion

The pooled analysis of variance (Table 1) based on eight different environments showed significant differences ($p \leq 0.01$) among genotypes, environments for dry fodder yield (kg/net plot), days to 50% flowering (days) and days to maturity (days). The genotype x environment interaction also showed highly significant differences for all studied characters under study. That indicates genotypes differed not only genetically, but also that some of them displayed diverse reactions to the dynamic environments. Then, various stability measures may be used to find stable genotypes. Similar results of significant differences among genotypes and environments were also reported by Alemu *et al.* (2018) and Haydar *et al.* (2018).

Table 1:- Pooled analysis of variance of different attributes of Pearl millet.

Sources	df	Mean sum of square		
		Dry fodder yield	Day to 50% flowering	Days to maturity
Genotypes	28	21.77**	240.04**	139.36**
Environments	7	999.34**	1774.63**	5185.92**
Rep. in Env.	16	3.75	8.49	4.56
Gen. x Env.	196	8.86**	11.46**	17.10**
Error	464	0.83	2.46	4.27

*,** significant at 5% and 1% prob. level, resp.

The partitioning analysis of variance model of Freeman and Perkins was conducted for traits under study showed in Table 2. It was noticed that the mean squares due to genotype showed significance for dry fodder yield (kg/net plot), days to 50% flowering (days) and days to maturity (days). Moreover, significant variations were observed in all three studied characters. Significant combined regression indicated that environments were well measured. Residual-1 item, when compared to the error was significant. Suggesting that the environmental index adequately captured to the error was significant. Suggesting that the environmental index adequately captured the index of additive environmental effect. G x E interaction was significant for a studied character, indicating that pearl millet genotypes interacted with the environment differently. The significant interaction of genotypes with environments warrants further computations of stability parameters. The heterogeneity of regression was found to be significant. On the other hand, residual-2 was significant, which indicates that the studied characters showed linear performance in the environments in which it was grown. Similar finding were reported by Sowmya *et al.* (2018).

Table 2: - Analysis of variance of pearl millet genotypes using Freeman and Perkins model (1971).

Sources	**df**	**Mean sum of square**		
		Dry fodder yield	**Days to 50% flowering**	**Days to maturity**
Genotypes (G)	28	12.97**	168.70**	94.05**
Environment (E)	7	648.89**	1180.33**	3497.00**
Combined regression	1	4430.86**	8109.88**	24413.07**
Residual (1)	6	18.56**	25.41**	10.99**
G x E interaction	196	6.10**	8.71**	13.63**
Heterogeneity of reg.	28	6.15**	18.26**	15.42**

Residual (2)	168	6.09**	7.12**	13.34**
Error between rep.	232	0.83	2.78	4.32

*,** significant at 5% and 1% probability levels, respectively

Stability analysis

Dry Fodder Yield

Three stability measures viz., mean, regression coefficient and mean square deviation were estimated for all the genotypes and its morphological characters under study for analysis presented in Table 3. Based on Freeman and Perkin's model, a genotype is said to be stable if it has regression coefficient near to unity and mean square deviation near or equal to zero. High value of regression ($b^{Fi} > 1$) indicates that the genotype/ variety is more responsive for input rich (favourable) environment, while low value of regression ($b^{Fi} < 1$), is an indication that the variety may be adopted in poor (unfavourable) environment.

Mean values of dry fodder yield ranged from 5.76 kg/net plot (G_{17}) to 8.93 kg/net plot (G_{10}) and the regression coefficient of both genotypes was quite equal but G_{17} has highest mean square deviation (S_{di}^2) among genotypes after G_9. The genotypes G7, G10, G11, G12, G14, G15, G18, G19, G21, G22, G23, G28 and G29 had higher mean values then the overall mean. G2, G4, G6 and G19 genotypes have unity regression coefficients indicating that these can be adapted to all environments, and G3, G10, G12, G13, G16, G17, G18 and G28 may be adopted in favourable environments, while the remaining may be adopted in unfavourable (poor) environments. Therefore, the genotypes G10, G14, G22, G23 and G29 have high mean value than the overall mean, unity regression coefficient and non-significant deviation from regression. These results agreed with Thakur *at el.*, 2019

Days to 50% flowering

The mean value for days to 50% flowering (days) ranged from 34.83 (G6) to 44.80 (G21) and the regression coefficient of both genotypes have less than unity indicating that they may be responsive to poor environments but the G21 had the highest mean square deviation. The genotypes G7, G8, G10, G11, G12, G15, G18, G19, G20, G21, G22, G23, G27, G28 and G29 had higher mean values than the overall mean. The genotypes G7, G8, G20, G24 and G29 have regression coefficients equal to one indicating that these can be adapted to all environments, and G4, G9, G12, G14, G15, G16, G17, G18, G22, G23, G27 and G28 may be adapted in favourable environments, while the remaining may be adopted in unfavourable (poor) environments. Meanwhile, the genotypes G6, G10, G12, G15, G17, G20, G23, G24 and G29 have high mean values than the overall mean, unity regression coefficient and non-significant deviation from regression.

Days to maturity

The mean value for days to maturity (days) ranged from 61.67 (G6) to 69.37 (G19) and the regression coefficient of both genotypes have unity indicating that these may have adapted to all environments. The genotypes G7, G11, G12, G17, G18, G19, G20, G21, G22, G23, G27 and G29 had higher mean values than overall mean. G1, G4, G5, G9, G24 and G25 genotypes have regression coefficient equal to one indicating that these genotypes adapted to all environments, and genotypes G3, G6, G7, G14, G15, G16, G17, G18, G19, G22, G23 and G26 have ($b^{Fi} > 1$) indicating genotypes may be adapted to favourable environments, while the remaining may be adapted in unfavourable environments. Therefore, the genotypes G1, G2, G4, G5, G7, G9, G22 and G23 found the most stable genotypes among all genotypes with mean square deviation near to zero.

Table 3: - Estimates of stability measures for pearl millet genotypes in different environments of India.

Varieties	Dry fodder yield			Days to 50% flowering			Days to maturity		
	mean	b^{Fi}	S_{di}^2	mean	b^{Fi}	S_{di}^2	mean	b^{Fi}	S_{di}^2
G_1	6.33	0.89	2.65**	36.33	0.77	-1.51	62.43	1.07	-1.53

G_2	6.38	1.00	2.36**	37.30	0.50	-0.63	63.03	0.84	0.51
G_3	6.46	1.05	0.56	35.10	0.56	-1.38	61.83	1.12	5.85**
G_4	6.72	1.02	1.83**	37.77	1.19	2.15*	62.63	1.00	3.10*
G_5	6.16	0.93	0.73*	36.67	0.67	1.40*	61.93	1.03	1.31
G_6	6.49	1.04	-0.29	34.83	0.79	0.01	61.67	1.09	4.60*
G_7	**7.05**	0.77	3.15**	**41.00**	1.04	2.20*	**65.57**	1.12	0.66
G_8	6.45	0.91	0.92*	**39.70**	1.01	2.84*	**64.40**	0.96	-1.98
G_9	6.41	0.50	5.26**	39.27	1.08	-1.99	64.20	1.01	0.42
G_{10}	**8.93**	1.25	0.37	**40.60**	0.91	0.13	64.00	0.83	0.14
G_{11}	**7.71**	0.90	1.16**	**40.17**	0.56	-0.53	**64.43**	0.67	2.22
G_{12}	**7.80**	1.11	2.21**	**41.50**	1.11	-1.38	**65.10**	0.94	-2.38
G_{13}	6.76	1.18	0.44	38.57	0.82	1.80*	63.97	0.98	-2.25
G_{14}	**7.08**	0.98	0.41	37.77	1.16	-1.78	63.67	1.14	5.11**
G_{15}	**7.11**	0.83	0.65*	**39.50**	1.21	-0.23	64.07	1.12	-0.47
G_{16}	6.39	1.13	2.67**	37.40	1.16	-0.72	62.43	1.09	-2.85
G_{17}	5.76	1.24	3.94**	**41.00**	1.18	0.54	**66.17**	1.14	1.60
G_{18}	**7.16**	1.18	1.42**	**40.57**	1.22	-2.00	**65.20**	1.15	-1.15
G_{19}	**8.44**	1.04	3.44**	**44.47**	0.95	2.10*	**69.37**	1.08	-1.93
G_{20}	6.83	0.57	3.78**	**43.37**	1.00	-1.54	**67.00**	0.90	1.43
G_{21}	**8.23**	0.88	3.39**	**44.80**	0.91	5.79**	**68.73**	0.87	1.76
G_{22}	**7.28**	0.85	0.38	**41.27**	1.19	-2.52	**66.43**	1.24	0.69
G_{23}	**7.04**	0.75	0.50	**40.50**	1.30	-0.01	**65.13**	1.30	-0.09
G_{24}	6.80	0.95	1.31**	39.37	1.05	0.39	**64.70**	1.05	3.17*
G_{25}	5.78	0.91	0.66*	36.77	0.64	4.29**	61.70	1.02	2.44
G_{26}	6.40	0.74	1.66**	36.87	0.70	1.12	63.20	1.10	0.51
G_{27}	6.69	0.84	-0.22	**40.17**	1.27	-1.10	**64.73**	0.89	1.48
G_{28}	**7.84**	1.18	1.07*	**41.63**	1.47	-2.03	**65.13**	0.90	-0.39
G_{29}	**7.46**	0.71	0.43	**40.63**	1.05	-1.84	**64.83**	0.84	-2.99
Average	6.96			39.48			64.40		

*, ** significant at 5% and 1% probability level, respectively

Conclusion

The results were found highly significant among genotypes, environments and genotype x environment interaction for all the morphological characters viz., dry fodder yield, days to 50% flowering and days to maturity. The genotypes G2, G4, G6 and G19 were responsive to all environments for dry fodder yield, G7, G8, G20, G24 and G29 genotypes were responsive to all environments for days to 50% flowering while, G1, G4, G5, G9, G24 and G25 genotypes may be adopted to all environments for days to maturity. The genotypes G10, G14, G22, G23 and G29 were found stable for dry fodder, G6, G10, G12, G15, G17, G20, G23, G24 and G29 genotypes were stable for days to 50% flowering and G1, G2, G4, G5, G7, G9, G22 and G23 genotypes were stable for days to maturity. The genotype G23 was observed stable for all the morphological characters.

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