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Comparison of Different Stability Parameters in Greengram [*Vigna radiata* (L.) Wilczek]

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ABSTRACT

The study of different stability parameters involving twelve mungbean genotypes in six environments indicated that stability parameters like Wricke's (1962) ecovalence, mean variance due to genotype-environment interaction of Plaisted and Peterson (1959) and variance of ranks over environments gave similar results to that of the deviation from regression (S^2d) of Eberhart and Russell (1966) and Shukla's stability variance whose calculation is cumbersome. All these methods indicated more stable genotypes like LGG 407, LGG 450 and MGG 295 for number of clusters per plant; PDM 54, MGG 351 and MGG 295 for number of pods per plant; LGG 407, MGG 347 and LGG 450 for seed yield per plant; LGG 460, ML 267 and MGG 341 for protein content over environments.

Key words : Greengram, Mugbean, Stability .

Mungbean is an important pulse crop cultivated round the year in almost all parts of India in different climatic conditions and in different cropping systems. Identification of widely adapted genotypes to be used as parents in the hybridization programme is an integral programme aiming to evolve high yielding and stable genotypes and ultimately to stabilize the crop production. The present study was undertaken to evaluate different stability parameters for the stability of yield and its components in elite mungbean genotypes.

MATERIAL AND METHODS

The present experiment was conducted during *rabi,* 2006-07 at Agricultural Research Station (ARS) Madhira, Khammam (district) in Andhra Pradesh to assess the stability of the twelve genotypes of greengram over six environments. The six environments were three dates of sowing *i.e* 15-09-2006, 30-09-2006 and 15-10-2006; two fertility levels *i.e* 20 Kg N: 50 Kg P per ha (only basal) and 20 Kg N: 50 Kg per ha (basal) + 20 Kg N per ha (top dressing at 30 DAS) in each date of sowing. Each genotype was replicated three times in all the six environments with inter- and intra-row spacing of 30X10 cm. Recommended package of practices and plant protection measures were followed. Data were recorded on four characters *viz.,* number of clusters per plant, number of pods per plant, seed yield per plant and protein content from each genotype in each replication and subjected to stability analysis as per the procedure outlined by Eberhart and Russell (1966), stability factor (Lewis, 1954), ecovalence (Wricke, 1962) method, Pairwise analysis (Plaisted and Peterson 1959), genotypic stability (Hanson, 1970), stability variance (Shukla, 1972), mean, variance of each genotype over environments, mean of ranks of each genotype over environments and variance of ranks of each genotype over environments.

The mean values of genotypes over environments were ranked in order of superiority such that the genotype with 1st rank was the one with maximum mean and the one with 12th rank with minimum mean. Similarly another parameter mean of ranks over environments was calculated. Genotypes in each environment were ranked and mean and variance of ranks over environments for a genotype was calculated. The mean of ranks were ranked such that the genotypes with 1st and 12th rank were the one with lower and higher values, respectively. The variance values of the ranks over environments were ranked such that the genotype with 1st rank a least variance may prove desirable compared to the one with 12th rank and with maximum variance. The stability factor (Lewis, 1954) is a ratio between the means of high yielding and low yielding environments and it defines the stable genotype as the one with unit stability factor value and was given first rank.

For ecovalence (Wricke, 1962) over environments and mean variance due to genotype-environment interaction (Plaisted and Peterson, 1959) genotype with lesser value ranked 1st and genotype with higher value ranked 12th. According to Shukla's (s^2_i) stability variance the genotype with 1st rank or least variance and non-significance may prove stable to fluctuations in environments compared to the genotype with 12th rank or maximum variance and significant. Hanson (D^2_i) genotypic stability is a measure which combines the information from equivalence and regression into a simple useful measure of yield stability, in this model the genotypes with least variance over environments were considered to be stable and were ranked as 1st and vice versa. However, these differ from the earlier parameters *viz.,*mean, mean of ranks, variance of genotype over environments, variance of ranks and stability factor such that these models take care of the replication and error effects. The high mean ($\overline{X}$),unit regression coefficients (b) and non-significant deviation from regression (S^2d) proposed by Eberhart and Russell (1966) define a stable genotype. Rank correlation (Spearman, 1904) was used to compare the stability parameters.

RESULTS AND DISCUSSION

A comparison of different stability parameters was made based on rank correlation coefficients between pairs of these parameters (Table1) and by emperically comparing the stable (or) desirable genotypes under each of these parameters (Table 2).

In the present study, the mean and mean of ranks were significantly and positively correlated for all the characters considered in the study as they are similar calculations and have same criteria for defining a stable genotype. The genotypes classified as more or less stable are the same in both these cases. Mean didn't show positive association with all other stability parameters except mean of ranks. Huhn and Leon (1985) reported numerically low (or) intermediate rank correlation coefficients between mean of the lines and different stability parameters like variance, ecovalence, genotypic stability, regression coefficient, sum of squared deviations from the regression and mean rank difference.

The variance over environments showed close positive association with stability factor and Hanson (D^2_i) genotypic stability for all the characters studied. This was confirmed by almost similarity of spotting the more and less stable genotypes by these parameters, for example for protein content genotypes 9, 3, 7 ranked as highly stable and genotypes 4, 6, 11 ranked as less stable according to these parameters (Table 2). Variance positively associated with mean variance due to gxe according to Plaisted and Peterson (1959) for clusters per plant and protein content and with ecovalence, deviation from regression and Shukla's (s^2_i) stability variance for protein content (Table 1).

Variance of ranks and mean variance due to genotype environment interaction (Plaisted and Peterson, 1959) were positively associated for protein content and number of clusters per plant. Variance of ranks also positively associated with deviation from regression for number of clusters per plant, number of pods per plant and seed yield per plant. It is also positively associated with 'bi' for protein content. Variance of ranks was positively associated with ecovalence and Shukla's (s^2_i) stability variance for all the four characters *viz.,* number of clusters per plant, number of pods per plant, seed yield per plant and protein content.

Stability factor had positive association with mean variance due to genotype environment interaction (Plaisted and Peterson, 1959), ecovalence and deviation from regression for protein content. It is also positively associated with Hanson (D^2_i) genotypic stability for all the four characters *viz.,* number of clusters per plant, number of pods per plant, seed yield per plant and protein content.

Mean variance due to genotype environment interaction had positive association with ecovalence and Shukla's (s^2_i) stability variance for all the four characters *viz.,* number of clusters per plant, number of pods per plant, seed yield per plant and protein content, with deviation from regression for protein content and number of clusters per plant, with regression coefficient for protein content and number of pods per plant and with Hanson (D^2_i) genotypic stability for number of clusters per plant.

Ecovalence showed positive association with deviation from regression for number of clusters per plant, number of pods per plant and protein content and with regression values for number of clusters per plant and protein content. It showed significant positive association with Hanson (D^2_i) genotypic stability for number of clusters per plant and with Shukla's (s^2_i) stability variance for all the four characters *viz.,* number of clusters per plant, number of pods per plant, seed yield per plant and protein content. No relationship existed between $\overline{X}$ and b, $\overline{X}$ and S^2d, b and S^2d which are components of Eberhart and Russell (1966) model. It is accordance with earlier report of Yadav and Kumar (1983).

The study indicates similarity of results for spotting stable genotypes according to ecovalence, variance due to genotype-environment interaction of Plaisted and Peterson (1959), S^2di (Eberhart and Russell, 1966), s^2_i, D^2_i and variance of ranks. The study also indicated as far as the spotting of stable genotypes simple methods like ecovalence and variance of ranks shall give similar results like S^2di

Table 1 . Rank correlation between pairs of different stability parameters in greengram [*Vigna radiata* (L.) Wilczek]

Stability param-eters	Characters	Varia-nce	Mean of ranks	Varia-nce of rank	Stability factor	Mean variance due to g*e(+)	Ecovlen-ce	S^2di	bi	Hanson's genotypic stability	Shukla's Variance
	No. of clusters per plant	-0.203	0.993**	-0.208	0.154	-0.140	-0.357	-0.182	-0.531	-0.154	-0.357
Mean	No. of pods per plant	-0.455	0.951**	0.166	0.154	-0.007	-0.014	-0.021	-0.063	-0.308	-0.014
	Seed yield per plant	-0.503	0.956**	0.147	0.042	-0.028	0.014	0.378	-0.392	-0.448	-0.010
	Protein content	0.147	0.977**	-0.175	0.175	0.189	0.196	0.336	0.406	0.238	0.231
	No. of clusters per plant		-0.224	0.236	0.867**	0.622*	0.441	0.364	0.063	0.909**	0.441
Variance	No. of pods per plant		-0.406	-0.047	0.664**	0.189	0.154	0.042	0.196	0.916**	0.154
	Seed yield per plant		-0.379	-0.189	0.776**	0.245	0.105	-0.517	0.126	0.972**	0.122
	Protein content		0.170	0.545	0.972**	0.748**	0.839**	0.769**	0.385	0.867**	0.811
	No. of clusters per plant			-0.215	0.133	-0.161	-0.385	-0.147	-0.538	-0.196	-0.385
Mean	No. of pods per plant			0.040	0.224	-0.196	-0.217	-0.168	-0.182	-0.399	-0.217
of ranks	Seed yield per plant			0.005	0.089	-0.065	-0.096	0.201	-0.495	-0.341	-0.121
	Protein content			0.005	0.170	-0.086	-0.079	0.012	-0.379	0.187	0.180
Variance	No. of clusters per plant				-0.044	0.760**	0.855**	0.747**	0.533	0.404	0.855**
of	No. of pods per plant				-0.117	0.547	0.659*	0.792**	0.320	-0.236	0.659*
rank	Seed yield per plant				0.021	0.490	0.664*	0.587*	0.231	-0.056	0.661*
	Protein content				0.462	0.790**	0.811**	0.301	0.671*	0.147	0.783**
	No. of clusters per plant					0.399	0.168	0.119	-0.203	0.741**	0.168
Stability	No. of pods per plant					0.077	0.007	-0.175	0.161	0.608*	0.007
factor	Seed yield per plant					0.294	0.238	-0.147	-0.126	0.797**	0.248
	Protein content					0.734**	0.797**	0.783**	0.343	0.881**	0.783**
Mean	No. of clusters per plant						0.888**	0.790**	0.434	0.811**	0.888**
variance	No. of pods per plant						0.951**	0.538	0.825**	-0.070	0.951**
due to	Seed yield per plant						0.818**	0.357	0.490	0.448	0.822**
g*e(+)	Protein content						0.965**	0.664*	0.727**	0.378	0.979**
	No. of clusters per plant							0.664*	0.748**	0.678*	1.000**
	No. of pods per plant							0.867**	0.566	-0.112	1.000**
Ecovlence	Seed yield per plant							0.573	0.559	0.287	0.997**
	Protein content							0.664*	0.685*	0.497	0.993**
	No. of clusters per plant								0.350	0.469	0.748**
S^2di	No. of pods per plant								0.140	-0.182	0.566
	Seed yield per plant								0.189	-0.357	0.535
	Protein content								0.515	0.650*	0.650*
	No. of clusters per plant									0.231	0.664*
bi	No. of pods per plant									0.049	0.867**
	Seed yield per plant									0.224	0.570
	Protein content									0.105	0.720**
Hanson's	No. of clusters per plant										0.678*
geno-	No. of pods per plant										-0.112
typic	Seed yield per plant										0.304
stability	Protein content										0.462

* Significant 5% probability level ** Significant 1% probability level

(+) = Mean variance due to $G \times E$ (according to Plaisted and Peterson, 1959)

Table 2 More and less stable genotypes according to different stability parameters of greengram [*Vigna radiata* (L.) Wilczek]

Character	Mean		Variance		Mena of ranks		Variance of ranks		Stability factor		Mean variance due to GxE(+)		Ecovalence		S^2 di		bi		Hanson's genotypic stability		Shukla's Variance	
	MS	LS	MS	LS	MS	LS	MS	LS	MS	LS	MS	LS	MS	LS	MS	LS	MS	LS	MS	LS	MS	LS
Days to 50% flowering	6,1,4	9,8,7	12,6,4	7,9,1	6,1,4	12,11,8	11,4,6	1,7,2	2, 11, 12	7,1,9	6,12,11	9,7,1	11,6,12	7,9,1	10,3,8	7,9,1	3,4,6	1,5,2	5,2,12	7,1,9	11,6,12	7,9,1
Days to maturity	1,4,6	7,11,3	4,11,2	5,3,9	1,4,6	7,11,8	7,4,1	5,9,8	10,4,7	3,5,8	4,11,7	5,9,8	4,11,7	5,3,8	1,10,6	5,3,4	11,4,12	8,3,2	2,4,8	3,5,9	4,11,7	5,3,8
Plant height	9,6,7	4,3,2	4,8,12	11,9,10	9,6,7	4,2,3	9,4,2	11,10,3	4,8,12	11,10,1	7,4, 12	6,10,11	2,7,4	6, 11,10	12,8,3	10,11,2	2,1,4	6,11,8	6,8,4	11,9,10	2,7,4	6,11,10
No. of primary branches /plant	12,11,7	1,3,5	1,5,10	9,2,4	12,11,7	1,5,3	11,5,12	6,2,9	12,11,7	6,2,5	6,8,5	1,3,9	5,8,10	1,3,9	10,8,5	3,12,7	6,7,12	1,8,4	1,5,10	9,2,12	5,8,10	1,3,9
No. of clusters / plant	12,10,7	3,2,1	7,11,3	4,6,12	12,10,7	3,1,2	8,5,12	10,6,4	7,11,3	6,4,2	7,8,1	6,4,10	1,8,5	6,4,10	5,2,7	6,10,4	9,8,1	3,11,6	7,1,8	6,4,12	1,8,5	6,4,10
No. of pods / plant	9,7,12	6,1,2	4,5,6	10,9,12	9,7,12	1,3,6	9,1,11	2,10,4	4,7,12	10,3,11	11,5,1	6,10,2	1,4,11	5,9,2	11,9,1	2,10,7	8,1,5	6,10,4	6,4,2	10,9,12	1,5,11	6,10,2
No. of seeds / pod	9,8,4	5,11,10	3,4,5	6,9,2	9,8,4	5,11,12	7,12,11	6,2,8	3,4,1	6,2,12	5,1,4	6,12,2	4,3,5	6,2,12	8,9,11	6,2,12	11,10,4	6,9,12	3,4,11	6,9,2	4,3,5	6,2,12
1000 seed weight (gm)	6,1,3	4,12,2	4,6,2	8,10,11	6,1,3	12,4,2	7,1,2	8,9,4	2,6,7	8,9,3	7,11,2	8,4,9	2,7,11	8,4,9	10,2,7	8,4,9	11,1,2	8,10,9	2,6,7	8,4,10	2,7,10	8,4,9
Seed yield / plant (g)	9,7,12	3,1, 11	4,5,1	10,9,12	9,7,12	4,3,1,11	9,1,3	6,11,4	4,5,2	11,10,3	7,3,8	6,10,11	1,8,3	6,11,10	12,8,3	6,11,5	11,3,8	6,10,9	4,5,1	10,9,12	1,8,3	6,11,5
Protein content	1,3,7	4,9,8	9,3,7	4,6,11	1,3,7	2,9,4,5	9,10,5	12,6,11	9,3,7	4,6,11	9,10,2	4,12,8	9,2,10	4,12,6	7,3,10	4,11,1	1,10,9	12,4,6	7,3,9	4,6,11	9,2,10	4,12,6

(+) = Mean variance due to Genotype ×Environment (Plaisted and Peterson, 1959); MS= More stable genotypes, LS= Less stable genotypes

1= MGG 295	3= MGG 347	5= MGG 351	7= LGG 407	9= LGG 460	11= PDM 54
2= MGG 341	4= MGG 348	6= MGG 353	8= LGG 450	10= ML 267	12= TM 96-2

whose calculation is cumbersome. The above simpler techniques may be applied as per suitability and convenience of the experimenter.

The other parameters like mean, stability factor, mean of ranks and variance over environments may not specify the same genotypes as in case of other parameters like genotypic stability (D^2_i), stability variance (s^2_i),bi and S^2di and may not be very useful due to the facts that the first three parameters employ the mean, which is a first order statistics and the partitioning of treatment and error effects was not there in calculation of these parameters *viz,* mean, variance, mean of ranks and stability factor.

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