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Non-parametric Measures for Yield Stability in Faba Bean (*Vicia faba* L.) Advanced Line in Gangetic Plains of India

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ABSTRACT

Background: Multi environmental trials (MET) is central activity in crop improvement programs for identification of superior genotype across environment before release as a variety. The aim of the present study was to select faba bean genotypes having high seed yield and most stable performance across different environments in gangetic plains of India.

Methods: The material for the study consisted of set of 11 genotype of faba bean subjected to multi-locational seed yield trials for three years (2015-2018) at four locations. The test of significance for genotype x environment (GE) interaction and eight non-parametric measures of stability analysis were used to identify high yield stable genotype across the five environments. A new approach Combined Stability Index based on yield stability performance calculated based on the ranking of the used stability measures of all the genotypes.

Result: Based on low value of Combined Stability Index, HB-12-37, ($CSI_{(i)} = 10$) HB-11-15, ($CSI_{(i)} = 11$), HB-11-32 ($CSI_{(i)} = 14$) were identified as the most stable genotypes with high yield potential. These non-parametric measures were observed to be associated with high mean seed yield. The simple rank correlation coefficient, calculated using the ranks was used to measure the association among the eight stability statistics and mean seed yield. The nature of relationships among the non-parametric measures was assessed and these stability measures are categorized in three groups. The genotype HB-12-37 (G3) fall in section 1 were the most favourable genotype due to high seed yield as well as high stability performance according to plot of all non-parametric measures with seed yield. HB-12-37 (G3) which had higher seed yield (25.19 q / ha) and high protein content (24.85%) with better stability across the environments could be used in further breeding programmes of faba bean and recommended for release as variety for plains of India.

Key words: Combined stability index, Faba bean (*Vicia faba* L.), Genotype x environment interaction, Non-parametric stability methods.

INTRODUCTION

Faba bean (*Vicia faba* L.) is among the oldest crops in the world. Globally, it is fourth most important pulse crops of the world after dry beans, drypea and chickpea. Currently, 58 countries produce this bean on large scale. The major faba bean growing countries are China, Egypt, United Kingdom and Syria. About 70% of total global production is contributed by China alone. Probably faba beans are one of the best performing crops under global warming and climate change scenario because of its unique ability to excel under all most all type of climatic conditions coupled with its wide adoptability to range of soil environment. Faba bean being incredible and crop complete food, unfortunately some part of world including India, it is still underutilized crops and not fully exploited so far, though it is seen as an agronomically viable alternative crop to cereal, with a potential of fixing free nitrogen upto 300 kg N ha^{-1}. It is a good source of lysine rich protein and good source of levadopa (L-dopa), a precursor of dopamine, can be potentially used as medicine for the treatment of Parkinson's disease. The quick varietal improvement is being used as one of the important criteria in increasing the yield potential of this crop. In this context there is a need to evaluate and identify the stable genotype that could give standard performance when tested under diverse environment. The status of this crop could be changed as a Potential Crops

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instead of the underutilized by adopting improved, stable and high in nutritive value of genotypes in cultivation.

The major goal of crop improvement program is to increase stability and stabilize crop yield over average of environments. An important step in multi-environmental Trials (MLTs) is to assess the performance of improved genotypes for identifying promising varieties for large-scale propagation. The farmer would like variety which show high performance for yield and desired traits over as a wide range of environmental conditions. Hardly any work has been taken up on genetic improvement of this species so far in India. At a global level information on genetic improvement, adaptability and genotype environment interaction of faba bean is restricted to few publications. The aims of present study were: (i) to identify genotype that has high seed yield as well as most stable performance across different environment; (ii) to investigate the nature of relationship among non-parametric stability measures. To increase and stabilize the production and productivity, identification of suitable variety with high yielding potential are of the paramount importance stability analysis helps in understanding the varietal adaptation under variable environments. Thus the use of highly adaptable variety is important in stabilizing productivity of over a seasons and region.

MATERIALS AND METHODS

Plant materials

The material for the study consisted of set of 11 genotype of faba bean subjected to multi-locational seed yield trials for three years (2015-2018) at four locations viz., Faizabad, Hisar, Ludhiana and Ranchi. In each environment, eleven genotypes were tested in advance varietal trial promoted from initial varietal trial of Crop Improvement Programme of AICRN on Potential Crops. These genotypes (Table 1) were developed by various breeders at different research centre of AICRN on Potential Crops in India.

Experimental detail

At each environment a randomized complete block design was used with three replications. The experimental plot consisted of three row with 4 m. Row to row and plant to plant distances was kept at 30 cm and 10 cm, respectively at all environments. Seed yield was estimated by plot basis and converted into q/ha for each genotype at each tested location.

Statistical analysis

Test of significance of genotype environment interaction

When Bartlett's test shows that the experiments have different error structure, the combined analysis requires a weighted analysis of variance taking $W_j = \frac{r}{S_j^2}$ The different steps involved in this case are:

(i) Using the G x E data on mean yields form the column totals $P_{j=}\sum_i Y_{ij}$ and determine W_jP_j values.

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

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

(iv) Obtain the correction factor $C = \frac{(\Sigma_i \Sigma_i w_j y_{ij})}{t\Sigma_j w_j}$

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

$$\text{Total (T): } \Sigma_j w_j S_j - C$$

$$\text{Genotypes (G): } \frac{\Sigma_i G_j^2}{\Sigma_j w_j} - C$$

$$\text{Environments (E): } \frac{1}{t}\Sigma w_j P_j^2 - C$$

The interaction sum of squares I (I=T-G-E) has to be obtained.

Following Cochran (1937), $\frac{[n-4(n-2)]}{n(n+t-3)}$ I may be approximated as $\times^2$ 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 $\times^2$ value with the significant point of Chi-squre 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 genotypes were those proposed by Huehn (1979), Nassar and Huehn (1987) and Thennarasu (1995). Huehn (1979) proposed the two measures: These are based on ranks of phenotypes in each environment. The phenotypic values of k genotypes are ranked within each environment (j = 1,2……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.

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

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

Nassar and Huehn (1987) proposed the two measures: The genotypic stability, which is measured independently of genotypic effects. The actual ranks (r_{ij}) have to be based on the corrected $y_{ij} = Y_{ij} - Y_i$ values. Rank r_{ij} and r_i have been determined from these corrected (y_{ij}) values only. Nassar and Huhn (1987) proposed two other stability measures. 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:

$$S_i^{(3)} = \frac{\Sigma_j (r_{ij} - \bar{r}_i)^2}{\bar{r}_i}$$

$$S_i^{(4)} = \frac{\Sigma_j |r_{ij} - \bar{r}_i|}{\bar{r}_i}$$

Thennarasu's (1995) non-parametric stability measures

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. The statistics based on yield ranks of genotypes in each environment are expressed as follows:

$$NP_i^{(1)} = \frac{1}{N} \sum_{j=1}^{N} \left| r^*_{ij} - M^*_{di} \right|$$

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

$$NP_i^{(3)} = \frac{\sum (r_{ij}^{*} - \overline{r^*}_i)^2 / N}{\overline{r}_i}$$

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

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

Combined stability index of genotype

A new approach based on yield stability performance calculated based on the ranking of the used stability measures of all the genotypes is recommended. t Genotypes having performance of stability measure K are ranked. $CSI_{(i)}$ of ith genotype is the sum of rank of mean yield of i^{th} genotype (RY_i), rank of mean rank of stability measures of ith genotype and rank of standard deviation ($RSd_{(i)}$) of stability measures. The low value of combined stability index are considered for most stable and high yielding potential genotypes.

$$Sd_{(i)} = \sqrt{\frac{\sum_{j=1}^{k} (R_{ij} - \overline{R}_i)^2}{k-1}}$$

$$CSI_{(I)} = RY_i + Ri + RSd_{(i)}$$

Correlation analysis

The stability parameters were compared using rank correlation in order to understand better the relationship among stability measures.

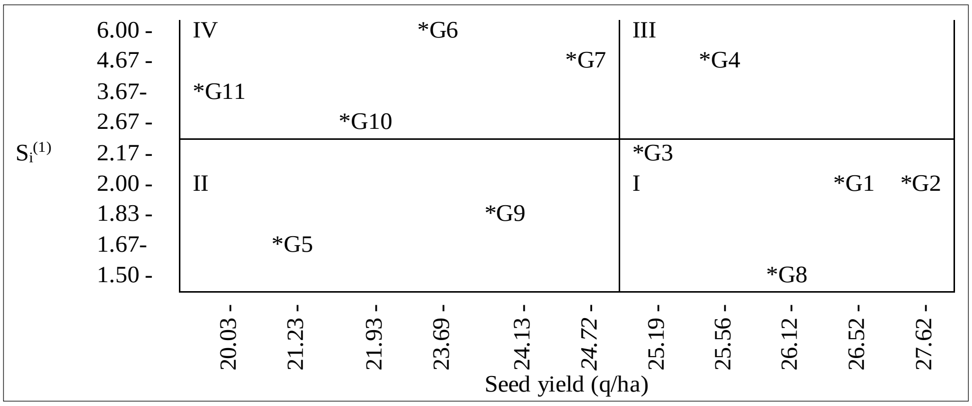

Fig 1: The plot $S_i^{(1)}$ against mean seed yield (q/ha) of faba bean genotype over environment.

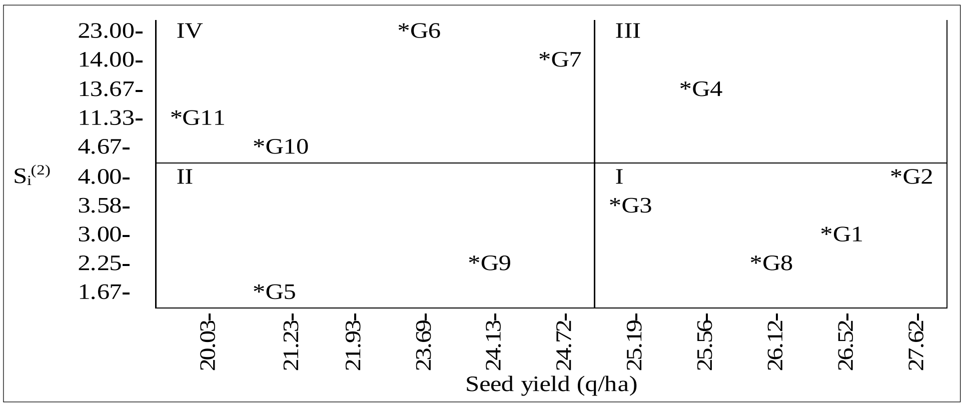

Fig 2: The plot $S_i^{(1)}$ against mean seed yield of faba bean genotype over environment.

Statistical packages

All statistical analysis was done using MS-excel (2007), R, SPSS and SAS packages.

RESULTS AND DISCUSSION

The test for significance of genotype x environment interaction

In our study, error mean square of the four experiments were heteroscedastic. This was confirmed by Bartlett's test, which gave a highly significant value for the Chi-square. Accordingly, the weighted analysis Cochran (1937), $\times^2$ value with the significant point for test for GE interaction had been calculated. Thus the parametric analysis ($\times^2$, df19 = 266.75*) shows the presence of GE interaction. 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 quan-

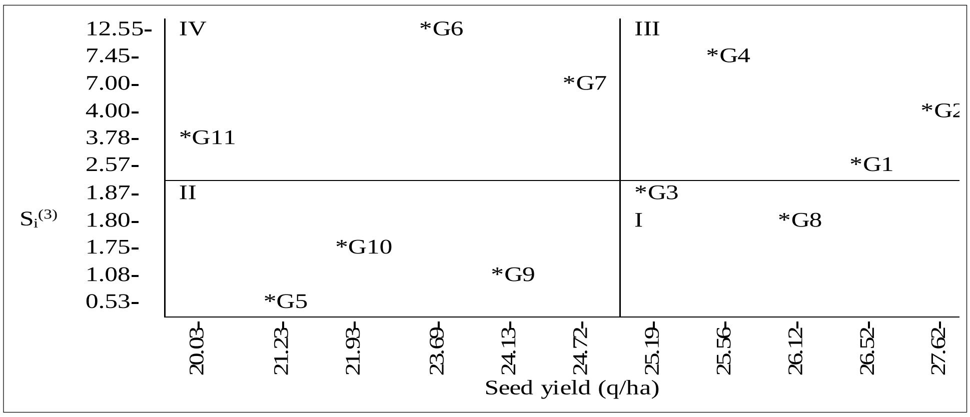

Fig 3: The plot $S_i^{(3)}$ against mean seed yield of faba bean genotype over environment.

Table 1: Genotype code, name and origin of 11 Faba bean genotypes.

Genotype code	Name	Origin	Status	Mean seed yield (q/ha)	Protein (%)
G1	HB 12-8	CCS, HAU, Hisar	Breeding line	26.52	24.50
G2	HB 12-34	CCS, HAU, Hisar	Breeding line	27.62	19.95
G3	HB 12-37	CCS, HAU, Hisar	Breeding line	25.19	24.85
G4	HB 12-42	CCS, HAU, Hisar	Breeding line	25.56	20.30
G5	NDFB 16	NDAUT, Faizabad	Breeding line	21.23	19.25
G6	NDFB 16-2	NDAUT, Faizabad	Breeding line	23.69	21.00
G7	HB 11-12	CCS, HAU, Hisar	Breeding line	24.72	24.50
G8	HB 11-15	CCS, HAU, Hisar	Breeding line	26.12	24.50
G9	HB 11-32	CCS, HAU, Hisar	Breeding line	24.13	23.10
G10	HFB-1 (C)	CCS, HAU, Hisar	Release variety	21.93	22.40
G11	Vikrant (C)	CCS, HAU, Hisar	Release variety	20.03	24.55

Table 2: Mean seed yields and stability parameter for 11 genotypes of Faba bean tested in 4 environments.

Genotype name	Mean (q ha^{-1})	$S_i^{(1)}$	$S_i^{(2)}$	$S_i^{(3)}$	$S_i^{(6)}$	$NP_i(1)$	$NP_i(2)$	$NP_i(3)$	$NP_i(4)$
HB 12-8	26.52	2.00	3.00	2.57	1.43	2.75	0.69	0.82	1.19
HB 12-34	27.62	2.00	4.00	4.00	2.00	2.50	1.25	1.12	1.56
HB 12-37	25.19	2.17	3.58	1.87	0.96	1.25	0.19	0.29	0.38
HB 12-42	25.56	4.67	13.67	7.45	2.18	3.75	0.63	0.73	1.06
NDFB 16	21.23	1.67	1.67	0.53	0.42	2.75	0.29	0.33	0.47
NDFB 16-2	23.69	6.00	23.00	12.55	2.91	4.75	0.95	0.87	1.18
HB 11-12	24.72	4.67	14.00	7.00	1.67	2.50	0.38	0.53	0.78
HB 11-15	*26.12*	1.50	2.25	1.80	1.20	2.00	0.67	0.60	0.89
HB 11-32	*24.13*	1.83	2.25	1.08	0.80	1.00	0.17	0.23	0.32
HFB-1 (C)	*21.93*	2.67	4.67	1.75	0.75	2.75	0.32	0.36	0.52
Vikrant (C)	20.03	3.67	11.33	3.78	1.11	3.00	0.29	0.36	0.52

titative 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 non-parametric measures are based on the rank of the cultivars across the environment / locations. They give equal weight to each location environments. The variety with less change in ranks are expected to be more stable. For simultaneous selection of most suitable genotypes (high yielding and stable), the calculated value of each non-parametric measures were plotted against mean seed yield performance separately (Table 2).

Each generated plot can be divided into four distinct sections; sections IV had low stability and low yield, section III low stability high seed yield and section II high stability and low seed yield and section I high stability and high seed yield. Therefore, the genotype falling in section I are the most favorable genotype (stable and high yielding). Accordingly genotypes from the section I are to be selected. The advanced lines HB 11-15, NDFB 16, HB 11-32, HB 12-8, HB 12-34 had the lowest value and ranked 3rd, 10th, 7th, 2nd and 1st for seed yield. The highest Si(1) for genotype HB 12-42, NDFB 16-2, HB 11-12, HFB-1 (C) and Vikrant (C) indicated them to be highly unstable genotypes. The Fig 1-8 represent the plots portrayed by mean seed yield (q/ha) and divided in to four sections.

The genotypes HB 12-34, HB 12-8, HB 11-15, having a high seed yield and small $Si^{(1)}$ values can be considered as a stable and well adapted in all environments. $Si^{(2)}$ estimates are simply the variance of the ranks for each genotype across the locations. For the variance of the rank $Si^{(2)}$ estimates may show relative stability. The genotype NDFB 16, HB 11-15, HB 11-32, HB 12-8, HB 12-37 are considered stable due to less value of $Si^{(2)}$. HB 12-8 and HB 11-15, are ranked 2nd and 3rd for mean seed yield. The HB 12-8 and HB 11-15 had highest seed yield with less value of $Si^{(2)}$. Thus HB 12-8 and HB 11-15 are considered most stable as well as high yielding genotype.

The $Si^{(3)}$ and $Si^{(6)}$ non-parametric measures were estimated by using the ranks which are given to genotypes on the basis of original mean data within the environment. The results of $Si^{(3)}$ and $Si^{(6)}$ indicated that genotype NDFB 16, HB 11-32 and HFB-1(C) rank 1st, 2nd and 3rd respectively. They occupied 10th, 7th, 9th and 5th positions in mean seed yield as well.

Therefore, the HB-12-37 genotype was found to be stable and adapted to all environments. Based on estimates of $Si^{(3)}$ and $Si^{(6)}$ the genotype NDFB-16-2 and HB-12-42 were found to be the most unstable genotypes. The plot of $Si^{(3)}$ and $Si^{(6)}$ for mean seed yield for Faba bean genotypes over locations were portrayed and divided in four sections. The genotype HB-12-37 having the high seed yield the small value of $Si^{(3)}$ and $Si^{(6)}$ can be considered as a stable genotype and well adapted to all environments. Section IV exhibits

Table 3: Estimated combined stability index of faba bean genotype.

Genotypes	Rank of yield and stability measures														
	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 $(\overline{R})$	Mean $(\overline{R})$	$sd_{(i)}$	Rank of $sd_{(i)}$	$(CSI_{(1)})$	Frequency
HB 12-8	2	4	4	6	7	6	9	9	10	6.33	6	2.69	8	16.00	3
HB 12-34	1	4	6	8	9	4	11	11	11	7.22	9	3.67	11	21.00	3
HB 12-37	5	6	5	5	4	2	2	2	2	3.67	3	1.66	2	10.00	5
HB 12-42	4	9	9	10	10	10	7	8	8	8.33	10	1.94	4	18.00	1
NDFB 16	10	2	1	1	1	6	4	3	3	3.44	2	2.96	10	22.00	7
NDFB 16-2	8	11	11	11	11	11	10	10	9	10.22	11	1.09	1	20.00	0
HB 11-12	6	9	10	9	8	4	6	6	6	7.11	8	1.96	5	19.00	1
HB 11-15	3	1	2	4	6	3	8	7	7	4.56	4	2.51	7	14.00	5
HB 11-32	7	3	2	2	3	1	1	1	1	2.33	1	1.94	3	11.00	8
HFB-1 (C)	9	7	7	3	2	6	5	5	5	5.44	5	2.13	6	20.00	2
Vikrant (C)	11	8	8	7	5	9	3	4	4	6.56	7	2.70	9	27.00	3
Correlation with rank mean seed yield	1	0.29	0.12	-0.26	-0.50	0.32	-0.58*	-0.56*	-0.62*						

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

that the genotype are low yielding and small value of $Si^{(3)}$ and $Si^{(6)}$ indicate resistance to environmental fluctuations and therefore indicated specificity of adaptability to low yield environment.

Thennarasu's (1995) non-parametric stability measures for seed yield 11 advance lines are presented in Table 3. According to these stability measures ($NP_i(1)$, NPi(2), $NP_i(3)$, $NP_i(4)$ with minimum values were considered more stable. Based on $NP_i(1)$, the genotype HB-11-32, HB-12-37, HB-11-15, HB-12-34 with lower values were identified as stable in comparison to other genotype.

According to the values of $NP_i(2)$, the genotype HB-11-32, HB-12-37 and Vikrant had the lowest values, while genotypes HB-12-34, NDFB-16-2 had the highest values and were considered as relatively unstable in comparison to other genotypes. The genotype HB-11-32, HB-12-37, NDFB-16, Vikrant and HFB-1 had the lowest value of NPi(3) and therefore, were the most stable genotypes. However, the genotypes HB-12-

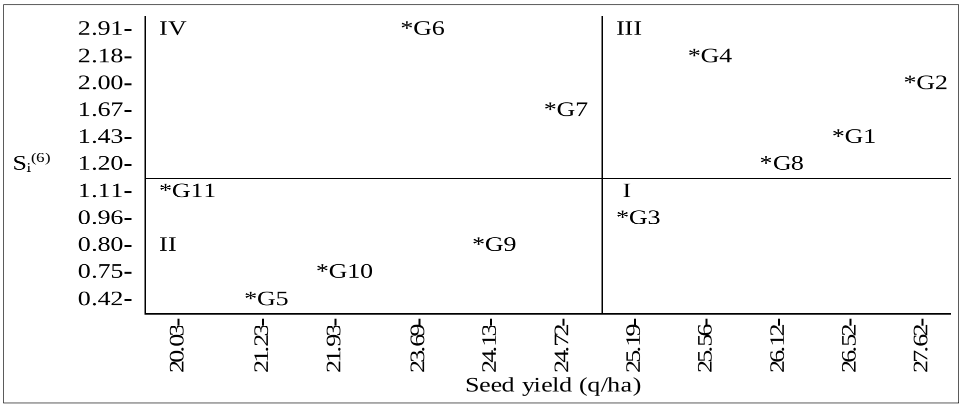

Fig 4: The plot $S_i^{(6)}$ against mean seed yield of faba bean genotype over environment.

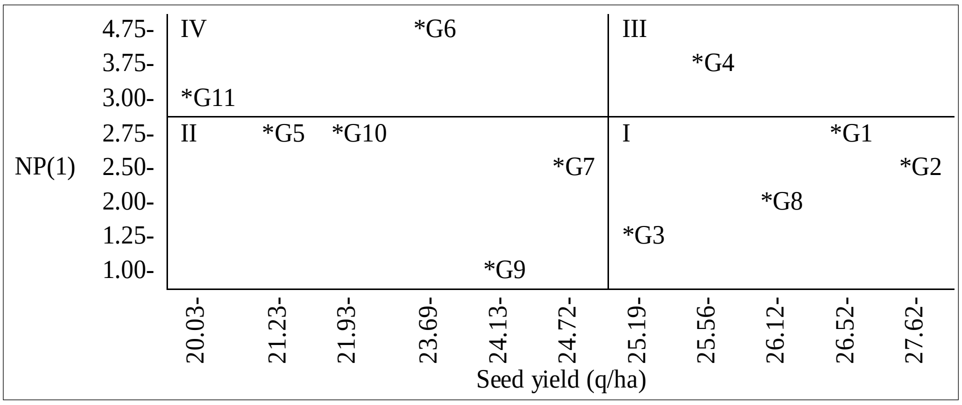

Fig 5: The plot NP(1)against mean seed yield of faba bean genotype over environment.

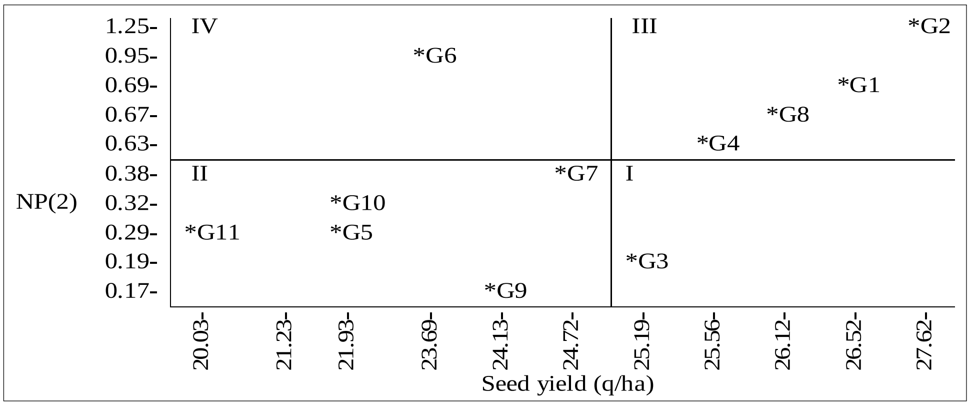

Fig 6: The plot NP(2)against mean seed yield of faba bean genotype over environment.

34 and NDFB-16-2 with maximum values were identified as the unstable genotypes. Also, according to $NP_i(4)$, genotype HB-11-32, HB-12-37 had the lowest value and therefore, were the most stable, but genotype HB-12-34, HB-12-8 had highest value of $NP_i(4)$, were unstable genotype.

Combined stability index of genotype

A new approach known as a genotypic selection index was calculated by ranking the mean seed yield of the genotype across the environment and standard deviation of the rank of eight stability measures. (Sdi), the rank of standard deviation of the rank of eight stability measure were calculated. Genotypic Selection Index is measured in terms of sum of the rank yield, mean rank and the rank of standard deviation of rank stability measure. Low values of this parameter are considered for selection of the stable genotype and high yielding (Table 4). The advanced genotypes HB-12-37 ($CSI_{(i)}$ = 10), HB-11-15 ($CSI_{(i)}$ = 11); HB-11-32 ($CSI_{(i)}$ = 14) were identified as the most stable and high potential yielding genotype on the basis of index. Table 3 shows rank-

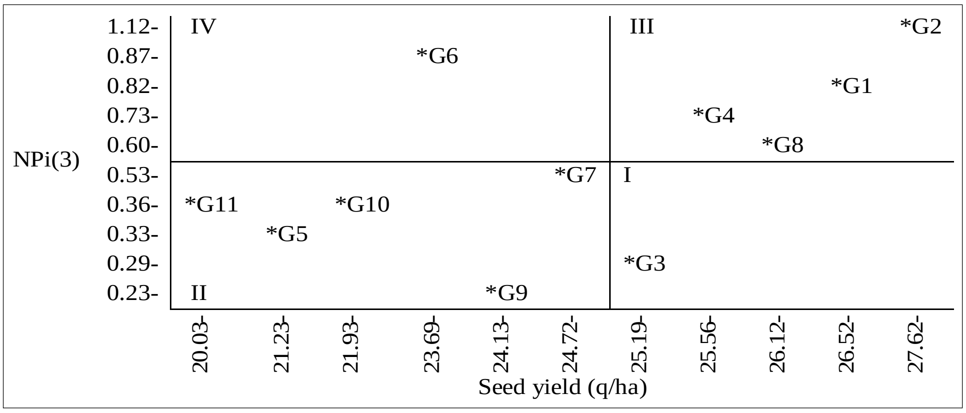

Fig 7: The plot NP(3)against mean seed yield of faba bean genotype over environment.

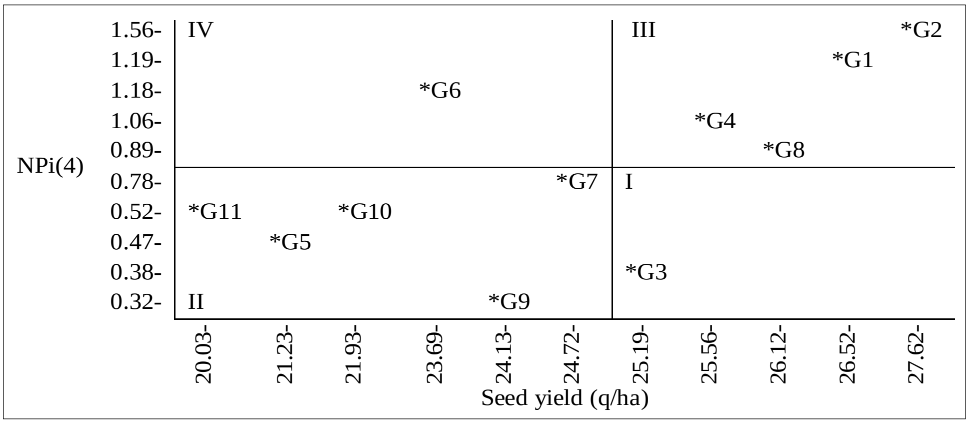

Fig 8: The plot ***NP(3)***against mean seed yield of faba bean genotype over environment.

Table 4: Identify genotype based on stability statistics and high seed yield.

Statistics	Stable genotypes and high yield
Mean (q ha^{-1})	HB 12-34, HB 12-8, HB 11-15, HB 12-42 , HB 12-37
$S_i^{(1)}$	HB 11-15, NDFB 16, HB 11-32, HB 12-8, HB 12-34
$S_i^{(2)}$	NDFB 16, HB 11-15, HB 11-32, HB 12-8, HB 12-37
$S_i^{(3)}$	NDFB 16, HB 11-32, HFB-1 (C) , HB 11-15, HB 12-37
$S_i^{(6)}$	NDFB 16, HFB-1 (C) , HB 11-32, HB 12-37, Vikrant (C)
$NP_i(1)$	HB 11-32, HB 12-37, HB 11-15, HB 12-34, HB 11-12
$NP_i(2)$	HB 11-32, HB 12-37, Vikrant (C) , NDFB 16, HFB-1 (C)
$NP_i(3)$	HB 11-32, HB 12-37, NDFB 16, Vikrant (C) , HFB-1 (C)
$NP_i(4)$	HB 11-32, HB 12-37, NDFB 16, Vikrant (C) , HFB-1 (C)
$(GSI_{(1)})$	HB 12-37, HB-11-15, HB-11-32

ing frequencies for the stability measures and mean yield. The genotypes are divided in three layers (Top, Mid, Low) in each environment. The genotype in the top five ranks from each environment were categorized as the stable and adaptive. The stable genotype based on ranking frequency were HB-12-37 (5), HB-11-15 (7) and HB-11-32.

Relationship between mean seed yield and stability measures

The relationship of different statistical measures with mean seed yields are presented in Table 3. The mean seed yield was significantly and positively correlated with $S_i^{(1)}$,$S_i^{(2)}$ and $NP_i^{(1)}$ (Category I), non-significantly and negative correlated with $S_i^{(3)}$, $S_i^{(6)}$, (Category II) and significant negatively correlated with $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ Category III). As the parameters under category I are most suitable to find out the best genotype, either of these three, ($S_i^{(1)}$, $S_i^{(2)}$ and $NP_i^{(1)}$ can suitably be used to find out best stable genotypes. As per these parameters, the best stable genotype in the present case is HB-11-32 followed by HB-12-37 and HB-11-15).

CONCLUSION

This method of analysis is very useful for the selection of the high potential yielding genotypes for crop improvement programme. The eight stability measures used in this study quantified stability of varieties with respect to yield and stability. Simultaneous selection of genotypes for high yield and stability is useful for selection in refined manner. G x E interaction were highly significant ($p<0.05$), suggesting different response of genotypes to the test location/year. Based on low value of non-parametric measures and combined stability index, HB 12-37 was identified most stable and highest potential yielding genotype (Table 4).

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