



Non-Parametric Stability Approach for Horticultural Crop Varietal Release

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SUMMARY

An attempt has been made to propose a non-parametric stability index for crop varietal release based on the performance of a line for multiple traits coupled with stability. Efficacy of this index has been demonstrated with real time data. It is evident from the results that the rank based non-parametric measures computed based on the relative performance of a genotype as compared to others, may be more practically meaningful to come out with stable lines either for release as variety or as a promising line in the ensuing crop hybridization trails. Measure of importance of the traits worked out may also serve as a selection criterion for the breeders in their future hybridization trails. It is suggested to make use of this method in varietal release program and can be extended for Multi-location trail (MLT) based release of crop varieties.

Keywords: Non-parametric stability, Okra, R- codes, Ranks, Varietal release.

1. INTRODUCTION

Horticultural crop improvement research is mainly aimed to exploit the genetic diversity available in the germplasm by employing various biometrical analysis techniques and culminate with identifying stable lines for release as variety either at institute level or across locations. In doing so, the presence of genotype X environment (GXE) interaction makes it difficult to assess the genetic potential of a variety. Due to this, it may so happen that a particular line may be high yielding but may lack in quality and other important crop protection traits (at least to the bench mark values of several traits, as set by the check variety, upon which improvement being attempted). Further, breeders too may be interested to suggest the farmers, a line which performs consistently well in all the evaluated traits over all the years/seasons/locations, including the trait(s) for which improvement was attempted, instead of recommending a line which performs only in few traits. This calls for employing comprehensive stability analysis in crop improvement research.

The conventional parametric approach of stability analysis is based on various stability measures developed since 1966 and used extensively in various horticultural crop improvement research (Onion: Venugopalan and Veere Gowda (2005); Watermelon (Venugopalan and Pitchaimuthu (2009); Chilli: Venugopalan and Madhavi Reddy (2010)). It may be noticed that through this parametric approach contribution of each genotype to GXE interaction was assessed solely based on their performance and stability over years, and most importantly, for each trait individually. However breeders are interested in assessing the contribution of each genotype to GE interaction based on their relative performance coupled with stability over years and to give recommendation based on collective performance across traits. This calls for employing suitable non-parametric method. Accordingly in this communication, by discussing various non-parametric methods, a new index is proposed with case studies in real time experiments carried out in Okra at ICAR-IIHR, Bengaluru, which

could be potentially used in any crop varietal release. R-codes were built up for ease of analysis.

2. MATERIALS AND METHODS

Non-Parametric approach of stability analysis:

A number of nonparametric measures for assessing yield stability have been proposed (Thennarasu, 1995; Nassar and Huhn, 1987). These statistical measures are based on the ranks of the genotypes in each environment tested. The ranking is based on values of Y_{ij} with lowest Y_{ij} value receiving the rank 1, the next higher value 2 and so on. The nonparametric measures based on yield ranks of the genotypes in each environment are worked out are below:

$$NP_i^{(1)} = \frac{1}{n} \sum_{j=1}^n |r_{ij}^* - Md_i^*|$$

$$NP_i^{(2)} = \frac{1}{n} \left[\sum_{j=1}^n |r_{ij}^* - Md_i^*| / Md_i^* \right]$$

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

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

$$S_i^{(1)} = 2 \sum_j \sum_{j'=j+1}^n |r_{ij} - r_{ij'}| / [n(n-1)]$$

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

$$S_i^{(3)} = \sum_{j=1}^n (r_{ij} - \bar{r}_i)^2 / \bar{r}_i$$

$$S_i^{(6)} = \frac{\sum_{j=1}^n |r_{ij} - \bar{r}_i|}{\bar{r}_i}$$

The rank r_{ij} is determined based on the rank of i^{th} genotype in j^{th} environment (Y_{ij}). The uncorrected Y_{ij} has the drawback that they may show significance even when there is no GE interaction. Hence, rank r_{ij}^* is determined based on corrected phenotypic values $Y_{ij}^* = [Y_{ij} - \bar{Y}_i]$, \bar{Y}_i being the mean performance of i^{th} genotype. The corrected values depend only on the GE interaction and error components. Md_i^* is the median ranks for adjusted values. These measures are widely used to assess the stability for different characters

individually in crop improvement research. A detailed study from practical point of view is discussed in Ravi *et al.*, 2013.

Pros and cons of Non-Parametric approach of stability analysis:

There is an ample justification for the use of non-parametric measures in the assessment of yield stability of crop varieties. Chief advantages are: (i) No assumptions about the phenotypic observations are needed, (ii) Sensitivity to measurement errors or to outliers is much less compared to parametric measures, (iii) Additions or deletions of one or a few genotypes do not cause distortions to non-parametric measures. (iv) Most of the time, the breeder, is concerned with crossover interaction, an estimate of stability based on rank-information, therefore, seems more relevant, (v) These measures are particularly useful in situations where parametric measures fail due to the presence of large non-linear GEI. For these reasons, non-parametric measures are widely employed in the selection of crop varieties especially when the interest lies in cross over interaction (Raiger and Prabhakaran, 2001). It is a known fact that the non-parametric methods are less powerful than their parametric counterparts. Simulation studies conducted against this background by Raiger and Prabhakaran (2001) have shown that when the number of genotypes in the trial is fairly large, the power efficiency of the nonparametric measures will be quite close to those of the parametric measures.

Non-Parametric approach for crop varietal release developed at ICAR-IIHR

In the foregoing non-parametric approaches discussed for crop stability analysis, it may be pertinent to observe that these statistical measures are based on the ranks of the genotypes in each environment tested, either deduced from the average rank or median rank. Further, all these measures are computed individually for all the traits based on the rank performance of each genotype. However, it is obvious for any researchers to attach more weight a group of traits, which were lacking in the released varieties, as compared to other traits. Further, arbitrarily assigning weights to the evaluated traits may favour the researchers in the final recommendation. Also, from practical point of view, crop breeders may be interested to suggest the farmers, a line which performs consistently well in all the evaluated traits over all the years/seasons/locations, instead of a line which performs only in

few traits. Hence, by taking into these considerations, positive and negative traits, an approach was adopted wherein based on the stability over replications in a year/location coupled with consistency over years/locations, suitable weights were worked for the traits. To this end, an attempt has been made to suggest a non-parametric based index (termed as Venugopalan index) by assessing the contribution of each genotype to GE interaction based on their relative performance (performance of a genotype compared to others) and stability over years, simultaneously based on various traits in Okra crop improvement research. The step-by-step procedure is described as a flow chart.

Objective: Selection of best line over different traits across different environments (years).

Data requirement:

- Data of minimum 3 years/seasons of a location (or over location) with 3 replications each for all traits.
- Pre-defined objective of the data (to be decided based on the objective of the research envisaged by the breeder) to decide the positive or negative traits among the evaluated traits to be studied. For example, disease/pest incidence trait/days to flowering, dwarf cultivar (if aimed at), should take reverse ranking (negative trait) as compared to yield, fruit weight, plant spread, no of nodes. This has to be solely decided by the crop breeders. However, weightage of the traits would be decided based on the approach envisaged as below.

Okra: Eight hybrids of okra were evaluated over three continuous periods 2014-15, 2015-16 and 2016-17 for eight different traits *viz.*, Days to 1st flowering, Fruit Length (cm), Fruit Diameter (cm); No of branches, Plant height (cm); Fruit weight (g); Yield (t/h); Incidences of Yellow Vein Mosaic Virus, YVMV (%) at the experimental plot of Division of Vegetable Crops, ICAR-IIHR was considered for this present study.

Steps

- Standardization of data: It is required as characters are measured in different scales.
- $$Z = \frac{(x - \bar{x})}{\sigma}$$
- GLM without interaction: Run univariate ANOVA for all characters by taking different environments

as replication (average of replication in every year is pre-considered).

- Precision factor: Take $y_i = \frac{1}{\sqrt{MSE}}$ so that trait with least error will get highest importance.

$$MSE = \frac{1}{n} \sum_{i=1}^n (Y_i - \hat{Y}_i)^2$$

- Weightage: Proportion of individual y_i is taken over total Y (given as pie chart)

$$Y = \sum y_i, w_i = \frac{y_i}{Y} \times 100$$

- Difference: Take the difference of individual value (\bar{x}_i) and the check (\bar{x}_c)

Positive character: Individual value - check value, $d = \bar{x}_i - \bar{x}_c$

Negative character: Check value - Individual value, $d = \bar{x}_c - \bar{x}_i$

- Superiority %: This is calculated by dividing the differenced value by check value and multiplying by 100, $S = \frac{d}{\bar{x}_c} \times 100$

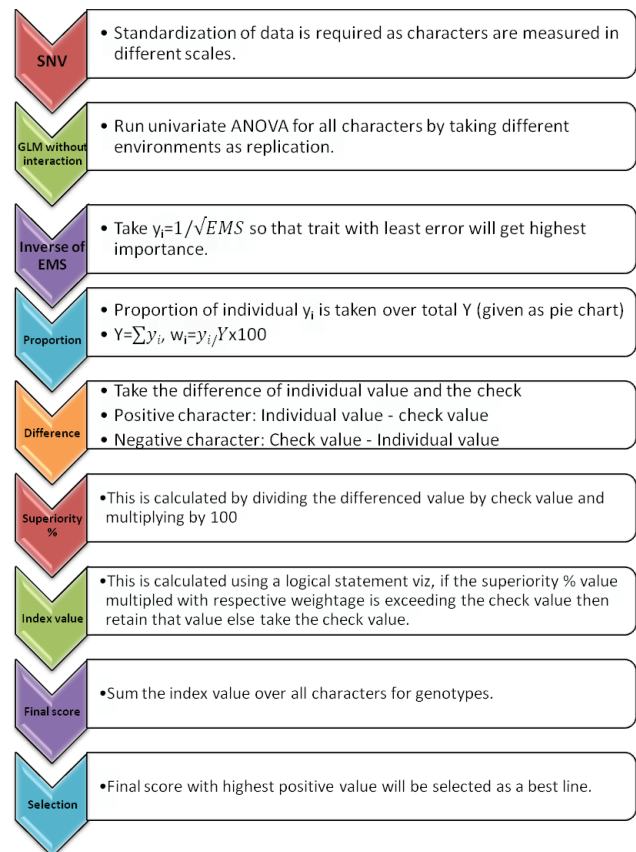


Fig. 1. Flow chart of Non-Parametric approach for crop varietal release developed at ICAR-IIHR

- Index value: This is calculated using a logical statement viz, if the superiority % value multiplied with respective weightage is exceeding the check value then retain that value else take the check value, $I = \text{if}(S * W_i > \bar{x}_c, S * W_i, \bar{x}_c)$
- Final score: Sum the index value over all characters for genotypes. $F = \sum_{j=1}^n I_j$
- Selection: Final score with highest positive value will be selected as a best line.

R code

```
data=read.table(file.choose(), header=TRUE,
row.names=1) # data file name stability test- folder R
stability
```

```
install.packages("phenability")
```

```
library(phenability)
```

```
thsu(data, interaction=TRUE)
```

```
nahu(data, interaction=TRUE)
```

3. RESULTS AND DISCUSSION

Results of various non-parametric measures worked for several traits are presented as below.

i) Days to flowering

>thsu(data, interaction=TRUE)						
\$ThSu	Hybrid	Mean	N1	N2	N3	N4
1	OKMSH-3	36.89	0.67	0.08	0.11	0.04
2	OKMSH-1	39.00	1.33	0.27	0.34	0.27
3	OKMSH-2	37.77	1.33	0.21	0.31	0.00
4	OKMSH-4	38.42	2.00	0.31	0.51	0.39
5	OKMSH-7	39.09	0.33	0.08	0.12	0.08
6	OKMSH-9	42.50	2.00	1.00	1.07	0.57
7	Shakthi(CC*)	45.00	2.33	1.17	1.85	1.40
8	AC-1685	41.67	2.33	0.47	0.74	0.08

```
*Commercial Check
>nahu(data, interaction=TRUE)
```

	Hybrid	Mean	S1	S2	S3	S6
1	OKMSH-3	36.89	0.33	1.00	1.00	1.33
2	OKMSH-1	39.00	1.33	4.33	0.50	0.50
3	OKMSH-2	37.77	0.00	5.33	2.88	1.53
4	OKMSH-4	38.42	2.00	10.33	3.96	1.65
5	OKMSH-7	39.09	0.33	0.33	0.40	0.40
6	OKMSH-9	42.50	1.33	9.33	0.10	0.20
7	Shakthi	45.00	2.33	14.33	0.09	0.18
8	AC-1685	41.67	0.33	14.33	3.34	1.31

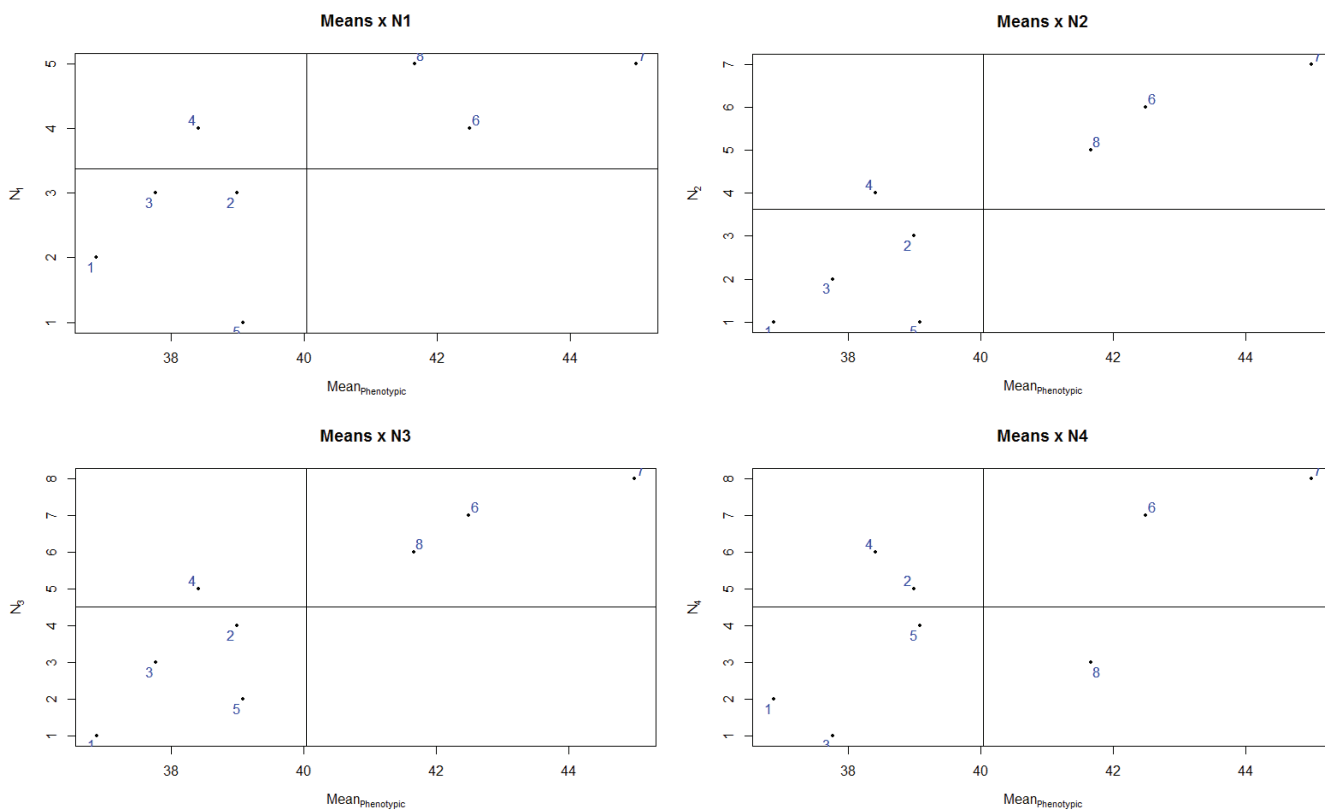


Fig. 2. Performance of N1-N4 measures based on mean phenotypic values for the character days to flowering

Table 1. Ranking of okra genotypes based on Thennarasu NP measure & Nasser and Huehn NP measure for the character days to flowering

	Hybrid	N1	N2	N3	N4	S1	S2	S3	S6
1	OKMSH-3	2	1	1	2	2	2	5	6
2	OKMSH-1	3	4	4	5	5	3	4	4
3	OKMSH-2	3	3	3	1	1	4	6	7
4	OKMSH-4	5	5	5	6	7	6	8	8
5	OKMSH-7	1	1	2	4	2	1	3	3
6	OKMSH-9	5	7	7	7	5	5	2	2
7	Shakthi	7	8	8	8	8	7	1	1
8	AC-1685	7	6	6	3	2	7	7	5

It may be observed that the hybrid OKMSH-3 has performed consistently well across most of the measures, followed by OKMSH-7 for days to flowering. Graphical representation of mean phenotypic value against the ranked measures (Fig. 2) depicted also indicated pictorially the results presented in Table 1 for the measures N1 to N4. Similar pictorial representation for other measure/traits the ranks depicted in Table 1.

ii) Fruit weight

>thsu(data, interaction=TRUE)

	Hybrid	Mean	N1	N2	N3	N4
1	OKMSH-3	24.57	2.00	0.29	0.47	0.33
2	OKMSH-1	25.56	0.67	0.11	0.16	0.11
3	OKMSH-2	25.65	1.33	0.27	0.32	0.13
4	OKMSH-4	24.90	2.33	0.67	0.68	0.48
5	OKMSH-7	27.30	1.67	0.83	0.77	0.38
6	OKMSH-9	28.20	1.00	1.00	0.94	0.25
7	Shakthi	26.49	2.33	0.33	0.58	0.38
8	AC-1685	25.76	1.00	0.20	0.26	0.21

>nahu(data, interaction=TRUE)

	Hybrid	Mean	S1	S2	S3	S6
1	OKMSH-3	24.57	2.00	12.00	4.67	2.00
2	OKMSH-1	25.56	0.67	1.33	0.05	0.21
3	OKMSH-2	25.65	0.67	4.00	1.61	0.96
4	OKMSH-4	24.90	2.33	16.33	3.64	1.52
5	OKMSH-7	27.30	1.00	6.33	0.42	0.42
6	OKMSH-9	28.20	0.33	2.33	0.09	0.17
7	Shakthi	26.49	2.00	14.33	7.82	2.36
8	AC-1685	25.76	1.00	2.33	0.28	0.40

It may be observed that the hybrid OKMSH-1 has performed consistently well across most of the measures, followed by AC-1685 for fruit weight.

Table 2. Ranking of okra genotypes based on Thennarasu NP measure & Nasser and Huehn NP measure for the character days to fruit weight

	Hybrid	N1	N2	N3	N4	S1	S2	S3	S6
1	OKMSH-3	6	4	4	5	6	6	7	7
2	OKMSH-1	1	1	1	1	2	1	1	2
3	OKMSH-2	4	3	3	2	2	4	5	5
4	OKMSH-4	7	6	6	8	8	8	6	6
5	OKMSH-7	5	7	7	6	4	5	4	4
6	OKMSH-9	2	8	8	4	1	2	2	1
7	Shakthi	7	5	5	6	6	7	8	8
8	AC-1685	2	2	2	3	4	2	3	3

iii) Yield

>thsu(data, interaction=TRUE)

\$ThSu	Hybrid	Mean	N1	N2	N3	N4
1	OKMSH-3	20.82	1.33	1.33	1.27	1.00
2	OKMSH-1	15.35	0.67	0.11	0.14	0.11
3	OKMSH-2	16.12	2.00	0.29	0.42	0.11
4	OKMSH-4	16.60	1.67	0.33	0.50	0.08
5	OKMSH-7	19.46	2.33	1.17	1.85	1.40
6	OKMSH-9	16.38	2.00	0.50	0.61	0.38
7	Shakthi	15.38	1.33	0.19	0.26	0.15
8	AC-1685	15.50	2.00	0.40	0.44	0.35

>nahu(data, interaction=TRUE)

	Hybrid	Mean	S1	S2	S3	S6
1	OKMSH-3	20.82	1.33	4.33	0.09	0.17
2	OKMSH-1	15.35	0.67	1.00	2.67	1.33
3	OKMSH-2	16.12	0.67	9.33	4.67	2.00
4	OKMSH-4	16.60	0.33	7.00	0.57	0.57
5	OKMSH-7	19.46	2.33	14.33	0.09	0.18
6	OKMSH-9	16.38	1.67	10.33	1.00	0.71
7	Shakthi	15.38	1.00	4.33	0.29	0.57
8	AC-1685	15.50	2.00	9.33	2.60	1.40

Table 3. Ranking of okra genotypes based on Thennarasu NP measure & Nasser and Huehn NP measure for the character yield

	Genotypes	N1	N2	N3	N4	S1	S2	S3	S6
1	OKMSH-3	2	8	7	7	5	2	1	1
2	OKMSH-1	1	1	1	2	2	1	7	6
3	OKMSH-2	5	3	3	2	2	5	8	8
4	OKMSH-4	4	4	5	1	1	4	4	3
5	OKMSH-7	8	7	8	8	8	8	2	2
6	OKMSH-9	5	6	6	6	6	7	5	5
7	Shakthi	2	2	2	4	4	2	3	3
8	AC-1685	5	5	4	5	7	5	6	7

It may be observed that the hybrid OKMSH-1 has performed consistently well across most of the measures for Yield.

iv) Incidence of YVMV

>thsu(data, interaction=TRUE)

\$ThSu	Hybrid	Mean	N1	N2	N3	N4
1	OKMSH-3	8.94	0.33	0.06	0.08	0.00
2	OKMSH-1	11.11	1.33	0.24	0.38	0.27
3	OKMSH-2	5.44	2.00	0.31	0.39	0.30
4	OKMSH-4	11.20	2.00	0.36	0.61	0.43
5	OKMSH-7	8.26	1.00	0.18	0.29	0.21
6	OKMSH-9	12.86	2.00	0.67	0.87	0.11
7	Shakthi	9.20	0.33	0.07	0.10	0.00
8	AC-1685	81.59	2.33	2.33	3.30	0.00

>nahu(data, interaction=TRUE)

	Hybrid	Mean	S1	S2	S3	S6
1	OKMSH-3	8.94	0.00	0.33	0.17	0.33
2	OKMSH-1	11.11	1.33	5.33	1.63	1.00
3	OKMSH-2	5.44	2.00	10.33	1.36	1.14
4	OKMSH-4	11.20	2.00	12.00	2.58	1.23
5	OKMSH-7	8.26	1.00	3.00	3.16	1.36
6	OKMSH-9	12.86	0.33	10.33	0.33	0.33
7	Shakthi	9.20	0.00	0.33	0.28	0.40
8	AC-1685	81.59	0.00	16.33	0.00	0.00

Table 4. Ranking of okra genotypes based on Thennarasu NP measure & Nasser and Huehn NP measure for the character incidence of YVMV

	Hybrid	N1	N2	N3	N4	S1	S2	S3	S6
1	OKMSH-3	1	1	1	1	1	1	2	2
2	OKMSH-1	4	4	4	6	6	4	6	5
3	OKMSH-2	5	5	5	7	7	5	5	6
4	OKMSH-4	5	6	6	8	7	7	7	7
5	OKMSH-7	3	3	3	5	5	3	8	8
6	OKMSH-9	5	7	7	4	4	5	4	2
7	Shakthi	1	2	2	1	1	1	3	4
8	AC-1685	8	8	8	1	1	8	1	1

It may be observed that the hybrid OKMSH-3 has performed consistently well across most of the measures, for the incidence of YVMV.

Similar analysis was carried out for the remaining 4 traits and it was noted that different hybrids were ranked best across different measures and there was no consistency. Accordingly, new index as discussed was adopted which was based on assigning derived weights

(Fig.10) for all the traits and collective ranking based on all the traits.

Table 5. Results based on combined index for Okra (Non-Parametric approach for crop varietal release developed at ICAR-IIHR)

Name of the hybrid	IIHR NP (Venugopalan’s NP measure)	
	Value	Rank
OKMSH-3	1034.48	2
OKMSH-1	239.52	6
OKMSH-2	1223.67	1
OKMSH-4	353.43	4
OKMSH-7	676.85	3
OKMSH-9	265.59	5
Shakthi	205.00	7
AC-1865	100.00	8

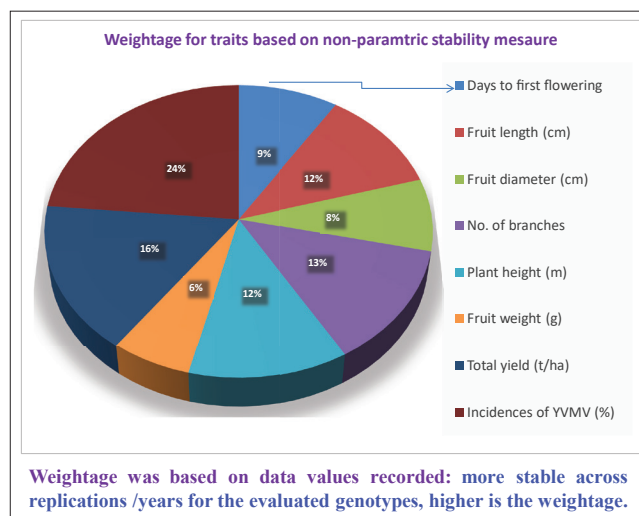


Fig. 10. The weightage of various traits computed (for combined non-parametric index) Okra

Efficiency of combined index over the individual trait based index

Based on combined index, results revealed that the lines OKMSH 2, 3, 7 (in the same order) as superior with highest NP value as **1223.67(OKMSH 2)** over all the evaluated traits. This is probably due to the higher weight assigned to the trait incidence of YVMV, (incidence being least in OKMSH2) in addition to yield. Thus, there is a scope for releasing OKMSH2,3 and 7 as hybrids based on combined performance of all the characters.

4. CONCLUSION

In any crop improvement research, unpredictable environmental variation directly results in reduced gain due to selection, as the presence of G X E interaction

would directly reduce the accuracy of prediction of genetic value. Stability solely based on single or 2-3 traits alone may not be sufficient, as the breeders expect that a hybrid /variety should also possess stability in desirable characters of other characters. A rank based non-parametric method has been suggested to identify a line/genotype evaluated over years as the best for varietal release simultaneously based on its superior performance over all traits, instead of one or two traits. Using the desired weights for individual traits arrived at based on its stability over years & within year replications, instead of assigning arbitrary weights, best lines were identified. Traits to be given reverse ranking (based on the improvement sought by the breeders over the existing cultivar) and direct ranking were also taken into consideration. It is suggested to make use of this method in varietal release / identification program and can be extended for MLT based varietal release.

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Annexure: R code for combined Index

```

rbd=read.csv("D:\\1.Chaitra\\R\\np new.csv")# take the standardized value
res1<-aov(A~as.factor(Rep)+as.factor(Trt),data=rbd)
res2<-aov(B~as.factor(Rep)+as.factor(Trt),data=rbd)
res3<-aov(C~as.factor(Rep)+as.factor(Trt),data=rbd)
res4<-aov(D~as.factor(Rep)+as.factor(Trt),data=rbd)
res5<-aov(E~as.factor(Rep)+as.factor(Trt),data=rbd)
res6<-aov(F~as.factor(Rep)+as.factor(Trt),data=rbd)
res7<-aov(G~as.factor(Rep)+as.factor(Trt),data=rbd)
res8<-aov(H~as.factor(Rep)+as.factor(Trt),data=rbd)
summary(res1)
summary(res2)
summary(res3)
summary(res4)
summary(res5)
summary(res6)
summary(res7)
summary(res8)
X<-c(0.479, 0.300, 0.619, 0.234, 0.259, 1.024, 0.146, 0.071)# mse of each
variable
Y<-1/sqrt(X)
Z<-Y/sum(Y)*100
Z# weightage for each variable
CW<-as.matrix(read.table(file.choose(), header=TRUE, row.
names=1))#CW=Check value and weight
MD<-as.matrix(read.table(file.choose(), header=TRUE, row.
names=1))#MD=mean data
D<-cbind((MD[,1]-CW[1,1]), (MD[,2]-CW[2,1]), (MD[,3]-CW[3,1]),
(MD[,4]-CW[4,1]), (MD[,5]-CW[5,1]), (MD[,6]-CW[6,1]), (CW[7,1]-
MD[,7]), (CW[8,1]-MD[,8]))
S<-cbind((D[,1]/CW[1,1])*100, (D[,2]/CW[2,1])*100, (D[,3]/
CW[3,1])*100, (D[,4]/CW[4,1])*100, (D[,5]/CW[5,1])*100, (D[,6]/
CW[6,1])*100, (D[,7]/CW[7,1])*100, (D[,8]/CW[8,1])*100))
W1<-CW[1,2]
W2<-CW[2,2]
W3<-CW[3,2]
W4<-CW[4,2]
W5<-CW[5,2]
W6<-CW[6,2]
W7<-CW[7,2]
W8<-CW[8,2]
I1<-cbind((S[,1]*W1), (S[,2]*W2), (S[,3]*W3), (S[,4]*W4), (S[,5]*W5),
(S[,6]*W6), (S[,7]*W7), (S[,8]*W8))
IA<-rbind((if (I1[1,1]>W1) {(I1[1,1])} else {(W1)}), (if (I1[2,1]>W1)
{(I1[2,1])} else {(W1)}), (if (I1[3,1]>W1) {(I1[3,1])} else {(W1)}), (if
(I1[4,1]>W1) {(I1[4,1])} else {(W1)}), (if (I1[5,1]>W1) {(I1[5,1])} else
{(W1)}), (if (I1[6,1]>W1) {(I1[6,1])} else {(W1)}), (if (I1[7,1]>W1)
{(I1[7,1])} else {(W1)}), (if (I1[8,1]>W1) {(I1[8,1])} else {(W1)}))
IB<-rbind((if (I1[1,2]>W2) {(I1[1,2])} else {(W2)}), (if (I1[2,2]>W1)
{(I1[2,2])} else {(W2)}), (if (I1[3,2]>W1) {(I1[3,2])} else {(W2)}), (if
(I1[4,2]>W1) {(I1[4,2])} else {(W2)}), (if (I1[5,2]>W1) {(I1[5,2])} else
{(W2)}), (if (I1[6,2]>W1) {(I1[6,2])} else {(W2)}), (if (I1[7,2]>W1)
{(I1[7,2])} else {(W2)}), (if (I1[8,2]>W1) {(I1[8,2])} else {(W2)}))
IC<-rbind((if (I1[1,3]>W3) {(I1[1,3])} else {(W3)}), (if (I1[2,3]>W1)
{(I1[2,3])} else {(W3)}), (if (I1[3,3]>W1) {(I1[3,3])} else {(W3)}), (if
(I1[4,3]>W1) {(I1[4,3])} else {(W3)}), (if (I1[5,3]>W1) {(I1[5,3])} else
{(W3)}), (if (I1[6,3]>W1) {(I1[6,3])} else {(W3)}), (if (I1[7,3]>W1)
{(I1[7,3])} else {(W3)}), (if (I1[8,3]>W1) {(I1[8,3])} else {(W3)}))
ID<-rbind((if (I1[1,4]>W4) {(I1[1,4])} else {(W4)}), (if (I1[2,4]>W1)
{(I1[2,4])} else {(W4)}), (if (I1[3,4]>W1) {(I1[3,4])} else {(W4)}), (if
(I1[4,4]>W1) {(I1[4,4])} else {(W4)}), (if (I1[5,4]>W1) {(I1[5,4])} else
{(W4)}), (if (I1[6,4]>W1) {(I1[6,4])} else {(W4)}), (if (I1[7,4]>W1)
{(I1[7,4])} else {(W4)}), (if (I1[8,4]>W1) {(I1[8,4])} else {(W4)}))

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IE<-rbind((if (I1[1,5]>W5) {I1[1,5]} else {(W5)}), (if (I1[2,5]>W1)
{I1[2,5]} else {(W5)}), (if (I1[3,5]>W1) {I1[3,5]} else {(W5)}),(if
(I1[4,5]>W1) {I1[4,5]} else {(W5)}), (if (I1[5,5]>W1) {I1[5,5]} else
{(W5)}), (if (I1[6,5]>W1) {I1[6,5]} else {(W5)}), (if (I1[7,5]>W1)
{I1[7,5]} else {(W5)}), (if (I1[8,5]>W1) {I1[8,5]} else {(W5)}))
IF<-rbind((if (I1[1,6]>W6) {I1[1,6]} else {(W6)}), (if (I1[2,6]>W1)
{I1[2,6]} else {(W6)}), (if (I1[3,6]>W1) {I1[3,6]} else {(W6)}),(if
(I1[4,6]>W1) {I1[4,6]} else {(W6)}), (if (I1[5,6]>W1) {I1[5,6]} else
{(W6)}), (if (I1[6,6]>W1) {I1[6,6]} else {(W6)}), (if (I1[7,6]>W1)
{I1[7,6]} else {(W6)}), (if (I1[8,6]>W1) {I1[8,6]} else {(W6)}))
IG<-rbind((if (I1[1,7]>W7) {I1[1,7]} else {(W7)}), (if (I1[2,7]>W1)
{I1[2,7]} else {(W7)}), (if (I1[3,7]>W1) {I1[3,7]} else {(W7)}),(if

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(I1[4,7]>W1) {I1[4,7]} else {(W7)}), (if (I1[5,7]>W1) {I1[5,7]} else
{(W7)}), (if (I1[6,7]>W1) {I1[6,7]} else {(W7)}), (if (I1[7,7]>W1)
{I1[7,7]} else {(W7)}), (if (I1[8,7]>W1) {I1[8,7]} else {(W7)}))
IH<-rbind((if (I1[1,8]>W8) {I1[1,8]} else {(W8)}), (if (I1[2,8]>W1)
{I1[2,8]} else {(W8)}), (if (I1[3,8]>W1) {I1[3,8]} else {(W8)}),(if
(I1[4,8]>W1) {I1[4,8]} else {(W8)}), (if (I1[5,8]>W1) {I1[5,8]} else
{(W8)}), (if (I1[6,8]>W1) {I1[6,8]} else {(W8)}), (if (I1[7,8]>W1)
{I1[7,8]} else {(W8)}), (if (I1[8,8]>W1) {I1[8,8]} else {(W8)}))
IV<-cbind(IA, IB, IC, ID, IE, IF, IG, IH) #IV= Index value
FS<-c(rowSums(IV)) # FS= final score
rank(-FS)

```