



## **Development of Composite Stability Measure using Multi Criteria Decisions Making (MCDM) Techniques**

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### **SUMMARY**

One of the most important challenges facing Indian agriculture is to provide food & nutritional security for rural resource-poor communities in the wake of decreasing land holdings. Hence, selection of suitable cultivar or variety for specific environment is very much essential. The farmer's risk can be minimized and it may improve their economic condition through selection of stable genotypes by using a suitable stability measure. Evaluation of genotypes on the basis of stability measure is essential for yield trials in different environments. Though, large numbers of stability measures are available in literature, but deciding the proper stability measure for selecting stable genotypes is problematic. Multiple Criteria Decision-Making (MCDM) technique or Technique for Order Preference by Similarity to Ideal Solution (TOPSIS) has been employed to develop the proposed measure. In the present study, a suitable composite measure is developed by combining several methods into a single aggregate method by using MCDM technique, for selecting suitable genotypes which would be stable to environmental variations.

*Keywords:* Genotype  $\times$  Environment interaction, Huehn's nonparametric measures, MCDM technique, Multi-Environment trial, Randomized complete block design, Stability measures, TOPSIS, Wricke's ecovalence.

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### **1. INTRODUCTION**

Decision-making is primarily a process that involves different methods and criteria. Work on multi-criteria decision-making has been started since 1950s, when foundations of modern multi-criteria decision-making methods have been laid (Zionts and Wallenius, 1976). Till now, many researchers devoted their time for development of new multi-criteria decision-making models and techniques.

In the past decades, research and development in the field of multi-criteria decision-making have been accelerated and seem to continue growing exponentially (Zavadskas *et al.*, 2014).

Though there are various methods available in the literature, an attempt has been made to systematically present theoretical basis of multi-criteria decision-making methods for developing a composite stability measure.

Identification of both high yielding and stable genotypes across the different environments is a on-going challenge to the plant breeders (Alwala *et al.*, 2010; Kang (1991, 1993). Resistance or tolerance to biotic or abiotic stress is essential for stable performance (Duvick, 1996). To enhance the potential yield or performance of certain variety, it is required to use improved stable varieties which may perform well in varying environmental conditions (Khush, 1993). Hence, it is required to identify the factors that are responsible for Genotype  $\times$  Environment Interaction (GEI). Wricke (1962) worked on stability measure with GEI for each genotype and his stability procedure is known as *Wricke's ecovalence* ( $W_i$ ). Francis and Kannenberg (1978) used the environmental variance ( $S_i^2$ ) and the coefficient of variance ( $CV_i$ ) to define stable genotypes. Shukla (1972) suggested an unbiased estimated using stability variance of genotypes ( $\sigma^2$ ), which is constructed by linear combination of Wricke's ecovalence ( $W_i$ ).

Eberhart and Russell (1966) used linear regression model and suggested that a genotype would be considered as stable if the genotype has average stability and low variance due to deviations from regression and high mean yield. Huehn (1979), Thennarasu (1995) and Nassar and Huehn (1987) had proposed different nonparametric stability measures to study and interpret the GEI. Nonparametric procedures of stability  $S_i^{(1)}$ ,  $S_i^{(2)}$ ,  $S_i^{(3)}$  and  $S_i^{(6)}$  were based on the classification of the cultivars in different environments (Huehn, 1979; Nassar and Huehn, 1987). Thennarasu (1995) also introduced four nonparametric measures  $NP_i^{(1)}$ ,  $NP_i^{(2)}$ ,  $NP_i^{(3)}$  and  $NP_i^{(4)}$  based on ranks of corrected means of the cultivars in each environment. Nonparametric procedures have been used based on the ranks of cultivars in different environments and cultivars with similar rankings in environments are categorized as stable genotypes. In this paper, a composite measure has been proposed by using MCDM or TOPSIS techniques, which is very simple and easy to implement (Hwang and Yoon, 1981). According to this technique, the best genotype would be the one that has the least deviation from the negative ideal parameter and the most deviation from the positive ideal parameter.

This composite measure has various properties as follows: It helps to select stable genotypes using parametric and nonparametric methods both or we can use either parametric measure or nonparametric measures alone. For selection of stable genotypes, researchers can use several stability methods simultaneously; presumably will increase the efficiency of selection. It can be used as simultaneous selection index for selection of genotypes for both yield and stability. Each stability measures can be examined according to its importance. The proposed new composite measure is a method that can select stable genotypes using parametric and nonparametric stability measures simultaneously.

The present communication is organized as follows. Section 2 describes the required materials and methods. The development of the methodology is given in Section 3. An illustration is made to describe the methodology and showed the efficacy of the procedure for selecting stable groundnut genotypes evaluated during the period (1998-2000) in different agro climatic zones in Andhra Pradesh. Finally conclusion is given in the Section Conclusion.

## 2. MATERIALS AND METHODS

### 2.1 Data description

The data used in this study were collected from the multi-location year trials of released and pre-release varieties of ground nut conducted at research stations situated in different agro-climatic zones of Andhra Pradesh, India (erstwhile) during the period (1998-2000). Experimental layout was a randomized complete block design (RCBD) with 3 replications. The data were provided by Regional Agricultural Research Station (RARS), Palem, ANGRAU, Andhra Pradesh (currently PJTSAU, Telangana, India). The data consist of 9 environments and 15 genotypes. The pod yields were expressed as kg/ha. The ranking mean data over the replicates for the 15 genotypes and 9 environments are given in Table 1.

The lesser rank is given to higher yield.

**Table 1.** Ranks of mean yield of 15 groundnut genotypes across each of 9 environment

Variety\ Environments	E1	E2	E3	E4	E5	E6	E7	E8	E9
G1	13	5	12	4	5	11	13	4	4
G2	10	4	4	4	3	5	6	2	10
G3	2	1	14	1	10	9	5	1	1
G4	5	6	13	12	13	13	11	11	8
G5	1	15	15	3	6	12	1	15	2
G6	15	13	9	15	11	14	14	13	12
G7	14	11	5	12	6	8	12	7	14
G8	3	7	1	2	1	2	8	2	11
G9	12	3	2	10	8	6	2	6	13
G10	4	2	11	6	9	15	2	10	15
G11	10	8	10	5	4	12	12	8	11
G12	7	4	6	2	2	6	9	7	13
G13	9	7	8	7	1	9	6	4	10
G14	8	2	9	7	12	13	6	2	9
G15	5	6	13	7	14	15	1	11	7

### 2.2 Model description

The basic model including replication for two-way crossed classification with interaction is as follows

$$Y_{ijr} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + e_{ijr}, \quad i = 1, 2, \dots, G; j = 1, 2, \dots, E; r = 1, 2, \dots, R. \quad (3)$$

where,  $Y_{ijr}$  is the yield of  $r^{\text{th}}$  replicate of  $i^{\text{th}}$  variety in  $j^{\text{th}}$  environment,  $\mu$  is the overall mean,  $\alpha_i$  is the fixed effect of  $i^{\text{th}}$  variety,  $\beta_j$  is the random effect of  $j^{\text{th}}$

environment,  $(\alpha\beta)_{ij}$  is the random interaction effect of  $i^{\text{th}}$  fixed variety in  $j^{\text{th}}$  environment and  $e_{ijr}$  is the error associated with  $Y_{ijr}$ .

### 3. METHODOLOGY

The statistical method to quantify the magnitude of  $G \times E$  interaction is important in applied statistics as well as for the analysis of experiments in plant/animal breeding and crop production. Conventionally, the magnitude of  $G \times E$  interaction is calculated by using analysis of variance (ANOVA) (Fisher, 1925). Combined analysis is used to find the magnitude of  $G \times E$  interaction present in the given data set. If the interaction between genotypes and environments are significant then there needs to use the stability measures to select the stable genotypes.

**Table 2.** Combined analysis of variance of 15 genotype across 20 environments

Source of Variation	Degrees of freedom	Type III SS	Mean Square	F Value	Pr > F
GEN	14	6450005.3	460714.7	10.03	<.0001
ENV	8	157339555.2	19667444.4	428.30	<.0001
REP(ENV)	18	2394049.8	133002.8	2.90	0.0001
GEN*ENV	112	22460806.5	200542.9	4.37	<.0001
Error	252	11571654.8	45919.3		
Corrected Total	404	200216071.7			

**Table 3.** Seven different methods of stability measures are indicated with Method  $M_1$  to  $M_7$ , respectively. Methods  $M_1$ - $M_5$  are parametric measures and  $M_6$  &  $M_7$  are non-parametric measures

Parametric stability measures	References	Method Name
$W_i = \sum_j (Y_{ij} - \bar{Y}_i - \bar{Y}_j + \bar{Y})^2$	Wricke (1962)	$M_1$
$b_i = \sum_j Y_{ij}(\bar{Y}_j - \bar{Y}) / \sum_j (\bar{Y}_j - \bar{Y})^2$ ; where, $Y_{ij} = \mu + \alpha_i + b_i\beta_j + \bar{e}_{ij}$	Finlay and Wilkinson (1963)	$M_2$
$S_{di}^2 = \frac{1}{E-1} [E \sum_j (Y_{ij} - \bar{Y}_i - \bar{Y}_j + \bar{Y})^2 - (b_i - 1)^2 E \sum_j (\bar{Y}_j - \bar{Y})^2]$	Eberhart and Russell (1966)	$M_3$
$CV_i = 100(s_i/\bar{Y}_i)$ ; where, $s_i^2 = \sum_{j=1}^E (Y_{ij} - \bar{Y}_i)^2 / (E-1)$	Francis and Kannenberg (1978)	$M_4$
$L_i = \sum_{j=1}^E  V_{ij} $	Piepho and Lotito (1992)	$M_5$
Non-parametric stability measures		
$S_i^{(2)} = \frac{\sum_{j=1}^E (r_{ij} - \bar{r}_i)^2}{(E-1)}$	Nassar and Huhn (1987)	$M_6$
$NP_i^{(1)} = \frac{\sum_{j=1}^E  r_{ij} - M_{di} }{E}$	Thennarasu (1995)	$M_7$

Composite index is developed by using five parametric Stability measures *i.e.* Wricke (1962) ( $W_i$ ) [1], Finlay and Wilkinson (1963) ( $b_i$ ) [2], Eberhart and Russell(1966)( $S_{di}^2$ ) [3], Francis and Kennenberg (1978) ( $CV_i$ ) [4] and Piepho and Lotito(1992) ( $L_i$ ) [5] and Two non-parametric Stability measures *i.e.* Nassar and huhn (1987)( $S_i^{(2)}$ ) [6] and Thennarasu (1995) ( $NP^{(1)}$ ) [7].

**Table 4.** Rank score of 10 high-yielding genotypes by above mentioned stability measures

Rank based on yield	Genotype\ methods	$M_1$	$M_2$	$M_3$	$M_4$	$M_5$	$M_6$	$M_7$
3	G1	3	12	7	7	5	11	9
6	G4	8	10	1	1	10	5	7
1	G5	15	14	15	15	15	15	15
5	G6	1	8	11	11	1	1	1
7	G7	4	5	5	5	8	6	8
2	G10	13	2	13	13	12	12	12
4	G11	2	6	6	6	2	4	6
8	G12	9	7	8	8	7	7	2
9	G13	10	13	9	9	9	3	3
10	G14	7	9	4	4	4	9	5

In present study, 10 high yielding genotypes are used; generally selection of genotype is based on the objective of the experimenter *i.e.* select the most stable genotype comparative to high yielding genotypes. One can also use all the available genotypes.

Genotypes are selected based on existing measures by using Multiple Criteria Decision-Making (MCDM) technique *i.e.*, the Entropy and TOPSIS Techniques (Pakpouret *al.*, 2013). A typical decision matrix, X is used in MCDM is given by

Genotypes	$G_1$	$G_2$	...	$G_n$
Weights	$w_1$	$w_2$	...	$w_n$
$M_1$	$x_{11}$	$x_{12}$	...	$x_{1n}$
$M_2$	$x_{21}$	$x_{22}$	...	$x_{2n}$
$\vdots$	$\vdots$	$\vdots$	$\ddots$	$\vdots$
$M_m$	$x_{m1}$	$x_{m2}$	...	$x_{mn}$

Where,  $M_i$  represent the methods ( $i = 1, \dots, m$ );  $G_j$  represent the different genotypes ( $j = 1, \dots, n$ ); and  $x_{ij}$  represent the score assigned by different measures of the  $j^{th}$  selected genotypes under the  $i^{th}$  methods.  $w_j$  ( $j = 1, \dots, n$ ) are the weights given on the basis of yield. In order to adjust the entropy measure for the  $i^{th}$  methods, related values in the decision matrix are first normalized and the normalized values are given as  $r_{ij}$ . On the basis of entropy, weight of  $j^{th}$  genotype ( $w_j$ ) is calculated.

These weights are then incorporated into the so-called TOPSIS MCDM technique to calculate an overall score for each genotype. The TOPSIS technique is used because of its high speed, accuracy, and compatibility. The algorithm of this technique is summarized as follows:

**1. Transfer the decision matrix to the normalized mode**

$$r_{ij} = \frac{x_{ij}}{\sqrt{\sum_{i=1}^m x_{ij}^2}}, (i = 1, \dots, m), (j = 1, \dots, n)$$

**2. Weights of the normalized decision matrix**

$$v_{ij} = w_j \times r_{ij} (i = 1, \dots, m), (j = 1, \dots, n)$$

Where,  $w_j$  is weights calculated on the basis of rank and lesser rank is given to higher yield.

**3. Define the “ideal positive”  $v_j^+$  and “ideal negative  $v_j^-$  solutions**

$$\{V_1^+, V_2^+, \dots, V_n^+\} = v_{ij} | j \in J, (\text{Max}_i v_{ij} | j \in J') | i = 1, 2, \dots, m$$

$$\{V_1^-, V_2^-, \dots, V_n^-\} = v_{ij} | j \in J, (\text{Min}_i v_{ij} | j \in J') | i = 1, 2, \dots, m$$

**4. Measure the distances,  $d_j^+$  and  $d_j^-$ ,  $i = 1, 2, \dots, m$  from the ideal and negative ideal solutions**

$$d_j^+ = \sqrt{\left[ \sum_{i=1}^n (v_{ij} - v_i^+)^2 \right]}$$

$$d_j^- = \sqrt{\left[ \sum_{i=1}^n (v_{ij} - v_i^-)^2 \right]}$$

, ( $j = 1, 2, \dots, m$ )

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**5. TOPSIS technique finally determines the relative closeness value  $C_j^-$  of  $i$ th genotypes as an ideal solution**

$$C_j^- = \frac{d_j^-}{d_j^+ + d_j^-}, (j = 1, 2, \dots, m)$$

Where  $0 \leq C_j^- \leq 1$  Genotypes with lower magnitudes of closeness are more preferred.

**4. RESULT AND DISCUSSION**

According to the methodology, different methods are used for ranking the genotypes and using the above described dataset, the respective ranks of the genotypes are given below in table 5a and 5b:

**Table 5a.** calculated rank of seven different stability measures

Genotypes\ Methods	W	rW	ABS (1-bi)	rabs (1-bi)	s <sup>2</sup> di	rS <sup>2</sup> di
G1	240706.94	3	0.10	12	16923.73	7
G2	313194.72	5	0.04	3	1840.871	3
G3	1054325.37	14	0.29	15	62817.17	14
G4	349122.60	8	0.09	10	500.2517	1
G5	1382317.77	15	0.17	14	137339.2	15
G6	92180.23	1	0.09	8	36713.9	11
G7	282850.13	4	0.06	5	7284.701	5
G8	547170.96	11	0.10	11	27447.51	10
G9	321577.31	6	0.05	4	1043.144	2
G10	685301.04	13	0.02	2	51811.45	13
G11	240348.13	2	0.07	6	13993.45	6
G12	476944.82	9	0.07	7	19793.04	8
G13	542963.16	10	0.14	13	22321.19	9
G14	327023.93	7	0.09	9	3358.792	4
G15	628500.57	12	0.01	1	43756.38	12

**Table 5b.** Calculated rank of seven different stability measures

Genotypes\ Methods	Si2	Si	C.V.	rC.V.	Li	rLi	N.Si2	rN.Si2	NP1	rNP1
G1	557913.9	746.94	53.01	10	1375.48	5	16.75	11	3.67	9
G2	508028	712.76	55.67	13	1272.28	3	7.50	2	3.00	4
G3	821909.5	906.59	74.41	15	2613.84	14	24.36	14	4.89	14
G4	563211.7	750.47	48.50	8	1471.67	10	10.25	5	3.33	7
G5	757263.8	870.21	58.51	14	3113.84	15	40.36	15	5.67	15
G6	370681.4	608.84	37.15	1	661.02	1	3.86	1	1.44	1
G7	420304.3	648.31	43.57	4	1432.43	8	11.61	6	3.56	8
G8	419724.9	647.86	55.52	12	1717.67	11	12.69	8	3.67	9
G9	436883.3	660.97	48.90	9	1402.46	6	16.19	10	3.78	11
G10	506583.3	711.75	48.20	7	1895.38	12	21.94	12	4.44	12
G11	406351.8	637.46	45.21	6	1188.24	2	8.36	4	3.22	6
G12	435762.4	660.12	42.56	3	1403.24	7	11.94	7	2.22	2
G13	385455.2	620.85	41.12	2	1444.21	9	7.94	3	2.56	3
G14	398154.2	630.99	44.00	5	1300.44	4	14.78	9	3.11	5
G15	502602.3	708.94	53.61	11	2087.10	13	22.19	13	4.67	13

**Table 6.** Standardize value of the decision matrix

	G1	G4	G5	G6	G7	G10	G11	G12	G13	G14	$\sigma_2$	$\sigma$
$r_{W(M1)}$	3	8	15	1	4	13	2	9	10	7	718	26.795
$R_{b(M2)}$	12	10	14	8	5	2	6	7	13	9	868	29.461
$r_{S2d(M3)}$	7	1	15	11	5	13	6	8	9	4	787	28.053
$r_{C.V.(M4)}$	7	8	14	1	4	7	6	3	2	5	449	21.189
$r_{Li(M5)}$	5	10	15	1	8	12	2	7	9	4	709	26.627
$r_{N.Si2(M6)}$	11	5	15	1	6	12	4	7	3	9	707	26.589
$r_{NP1(M7)}$	9	7	15	1	8	12	6	2	3	5	638	25.258

**Table 7.** Rank based on mean yield across the 9 environment

GEN\ENV	E1	E2	E3	E4	E5	E6	E7	E8	E9	Yi.	Rank Yi.
G1	1773	880	2841	2020	856	1382	1458	282	1190	1409.11	10
G2	1715	861	2497	2020	505	1104	1153	275	1394	1280.44	13
G3	1241	424	3266	1717	1148	1225	1130	113	701	1218.33	14
G4	1472	917	3172	2222	1505	1475	1222	632	1308	1547.22	3
G5	1208	1435	3625	1919	903	1432	921	862	1081	1487.33	6
G6	1893	1310	2716	2374	1320	1476	1482	680	1498	1638.78	1
G7	1852	1169	2527	2222	903	1220	1407	455	1637	1488	5
G8	1266	993	2245	1869	292	972	1171	275	1419	1166.89	15
G9	1736	792	2376	2172	981	1113	1051	364	1579	1351.56	11
G10	1442	695	2800	2071	1051	1890	1051	605	1684	1476.56	7
G11	1530	1055	2643	2172	1412	1049	1051	567	1211	1410	9
G12	1697	1222	2770	2273	1759	1343	1153	572	1169	1550.89	2
G13	1637	1097	2715	2071	1806	1158	1199	636	1269	1509.78	4
G14	1641	1403	2712	2071	792	1037	1199	757	1296	1434.22	8
G15	1727	1139	2452	2071	481	883	1519	299	1330	1322.33	12
Y.J	1588.7	1026.1	2757.1	2084.3	1047.6	1250.6	1211.1	491.6	1317.7	1419.43	
rank y <sub>j</sub>	3	8	1	2	7	5	6	9	4		

Out of these 15 genotypes we have selected top ten genotypes with respective score calculated by using different methods.

### Step 1: Standardize the decision matrix

This step transforms various attributes dimension into non-dimension attributes and allows comparisons across methods. For standardizing, each column of decision matrix is divided by square root of sum of square of respective value

### Step 2: Construct weighted standardized decision matrix by multiplying attributes weight to each other

### Step 3: Define ideal positive and ideal negative solutions

### Step 4(b) : Square deviation about maximum value in each row ( $d_j^-$ )

### Step 5: In TOPSIS technique finally determines the relative closeness value $C_i^-$ of $i$ th genotypes as an ideal solution.

Criterion to be followed for arriving at ideal parameter is that genotype which has lowest value of  $C_i^-$  has been considered as stable genotypes.

**Table 8.** Weights of 10 selected genotypes based on mean yield of genotypes

GEN\ENV	E1	E2	E3	E4	E5	E6	E7	E8	E9	Weights ( $w_j$ )
G1	3	11	4	11	11	5	3	12	12	8.00
G4	11	10	3	3	3	3	5	5	8	5.67
G5	15	1	1	13	9	4	15	1	14	8.11
G6	1	3	7	1	5	2	2	3	4	3.11
G7	2	5	11	3	9	8	4	9	2	5.89
G10	12	14	5	7	7	1	12	6	1	7.22
G11	10	8	10	5	4	12	12	8	11	8.89
G12	7	4	6	2	2	6	9	7	13	6.22
G13	9	7	8	7	1	9	6	4	10	6.78
G14	8	2	9	7	12	13	6	2	9	7.56

**Table 9.** Ideal positive and ideal negative solutions of different stability measures

Methods/Genotypes	G1	G4	G5	G6	G7	G10	G11	G12	G13	G14
M1	0.896	1.692	4.541	0.116	0.879	3.504	0.663	2.090	2.529	1.974
M2	3.258	1.923	3.854	0.845	0.999	0.490	1.810	1.478	2.991	2.308
M3	1.996	0.202	4.337	1.220	1.050	3.347	1.901	1.774	2.174	1.077
M4	2.643	2.139	5.359	0.147	1.112	2.386	2.517	0.881	0.640	1.783
M5	1.502	2.128	4.569	0.117	1.769	3.255	0.668	1.636	2.291	1.135
M6	3.310	1.066	4.576	0.117	1.329	3.259	1.337	1.638	0.765	2.557
M7	2.851	1.570	4.817	0.123	1.865	3.431	2.111	0.493	0.805	1.496

**Table 10.** Calculated Square deviation about maximum value in each row ( $d_j^+$ )

	G1	G4	G5	G6	G7	G10	G11	G12	G13	G14
M1	0.61	2.48	19.58	0.00	0.58	11.48	0.30	3.90	5.82	3.45
M2	7.66	2.05	11.32	0.13	0.26	0.00	1.74	0.98	6.25	3.30
M3	3.22	0.00	17.10	1.04	0.72	9.89	2.89	2.47	3.89	0.77
M4	6.23	3.97	27.17	0.00	0.93	5.01	5.62	0.54	0.24	2.68
M5	1.92	4.05	19.82	0.00	2.73	9.85	0.30	2.31	4.73	1.04
M6	10.19	0.90	19.88	0.00	1.47	9.87	1.49	2.31	0.42	5.96
M7	7.44	2.09	22.03	0.00	3.03	10.94	3.95	0.14	0.46	1.88
dj-	6.10	3.94	11.70	1.08	3.12	7.55	4.04	3.56	4.67	4.37



**Table 11.** Relative closeness value  $C_i^-$  of  $i^{th}$  genotypes

	G1	G4	G5	G6	G7	G10	G11	G12	G13	G14
dj++dj-	12.537	12.197	11.700	12.358	11.922	12.806	12.176	12.170	12.890	12.067
$C_j = d_j^- / (d_j^+ + d_j^-)$	0.487	0.323	1.000	0.087	0.262	0.590	0.332	0.292	0.362	0.362

A TOPSIS technique is defined as the Technique for Order of Preference by Similarity to Ideal Solution (TOPSIS) is a multi-criteria decision analysis method. Smaller value of relative closeness value  $C_i^-$  gives the genotypes which is more stable as well as high yielding. Here, we can observe the  $C_i^-$  value of G6 genotype is minimum (0.087) indicates G6 genotype is the best genotype among other genotypes.

## 5. CONCLUSION

The objective of the study is to develop a methodology to appraise best genotypes based on parametric and nonparametric stability methods using Multiple Criteria Decision-Making (MCDM) technique. This technique is very simple decision making method and easy to implement. According to this technique, the best genotype (stable genotype) has the largest deviation from the positive ideal parameter and has the least deviation from the negative ideal parameter. In this study, Multiple Criteria Decision-Making (MCDM) technique is illustrated using a real data set. In the present investigation, parametric and nonparametric stability measures have revealed useful implications for plant breeding research towards selection of best genotypes. Finally, results from this study indicates that MCDM technique serve a better platform to identify stable and high yielding genotypes using a set of stability measure, simultaneously.

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