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Multi-trait evaluation of tamarind (*Tamarindus indica* L) clones using MGIDI and classical selection indices

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Abstract

Tamarind (*Tamarindus indica* L.) is a climate resilient and versatile multipurpose fruit tree used in food and medicinal industry. An unexplored and underutilized tree, instinct that to develop a high productive Tamarind tree with superior nutritional quality requires unfeigned selection on multiple traits of Tamarind. In this study, sixty diverse tamarind genetic resources representing sour, red, and sweet Tamarind clones were evaluated for morphological and biochemical traits. The classical selection method, Smith-Hazel index (Selection Index I) computed with equal weightage and Selection index I, shortlisted the clones of IFGTBST 2, IFGTBST 7, IFGTBRT 18, IFGTBST 1, IFGTBST 3. The selection index II followed the unequal weight-based method, Tamarind clones *viz*., IFGTBTI 14, IFGTBTI 2, IFGTBTI 1, IFGTBRT 5, IFGTBTI 5 were selected. This contrasting result raised through immense of multicollinearity among the different characters studied in the selection index I. Multi-Trait Genotype-Ideotype Distance Index (MGIDI) were used against traditional selection indices in identifying superior tamarind clones. In MGIDI, high productive clones *viz*., IFGTBTI-2, IFGTBTI-15, IFGTBTI-1, IFGBTST-3, IFGTBST-1 and IFGTBTI-14 were identified and also deliver the strengths and weaknesses of clones by six different factors (FA). Top ranked selected clones by MGIDI were differed from selection index I, while the common clones of IFGTBTI 14, IFGTBTI 2 and IFGTBTI 1 observed in both selection index II and MGIDI. However, MGIDI proved superior to classical indices for multi-trait selection, offering a robust and accurate tool for breeding programs to select high-yielding, nutritionally superior Tamarind clones.

Keywords: Tamarind, Classical selection index, multicollinearity, MGIDI

INTRODUCTION

Tamarind is tropical and sub-tropical tree belongs to the family of Fabaceae and it is highly cross-pollinated diploid tree species with the chromosome number of 2n=2x=24. Tamarind tree, versatile tree has multipurpose utilization in food, wood and medicinal industry. Tamarind fruit pulp is an appetizing nature, used as multiciliate flavour and preserver in cuisine such as sauces and curries, syrups, tamarind pulp powder, tamarind juice and concentrate (Manjula *et al*., 2017). The Tamarind fruits are rich in nutritional value included dietary fiber (5 g), tartaric acid (19.69 %), ascorbic acid (7.10 %), total soluble solid (16.04 Brix^o), calcium (74 mg/100 g), magnesium (92 mg/100 g), phosphorus (113 mg/ 100 g), potassium (628/ per 100 g), and iron (2.8 mg/ 100 g), as well as vitamins including thiamin (0.428 mg/ 100 g), riboflavin (0.152 mg/ 100 g), and niacin (1.94 mg/ 100 g), makes it one of the most affordable sources of multivitamins and minerals (Mayavel *et al*., 2024). It is also used to cure fever, malaria, ulcers, diarrhoea, dysentery and wounds. The commercial value of tamarind continues to rise, particularly with the increasing demand for value-added products and natural ingredients in the global market. Thailand, a major exporter of sweet tamarind, has successfully capitalized on the international demand, particularly from China, the United States, and Europe (Tridge, 2020). India is the largest producer, mainly exports tamarind in processed forms such as pulp, concentrate, and desiccated tamarind, with annual exports estimated at around 96,652 tonnes (Bharathi, 2022). The global tamarind extract market was valued at USD 408 million in 2022 and is projected to grow annually by 6.5 %, indicating its substantial market potential (FreshPlaza, 2023). Despite its economic significance, tamarind remains underutilized as a commercial crop, primarily due to limited research on genetic improvement and value addition.

Presence of tremendous genetic diversity in Tamarind tree based on through cross pollination nature and geographical distribution of Tamarind tree classified into sour, red and sweet Tamarind tree categorized

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by morphological characters such as fruit and biochemical traits total soluble solid, tartaric acid, ascorbic acid, anthocyanin, total sugar and protein (Vijayalakshmi *et al*., 2021; Mayavel *et al*., 2024). Rich diversity in Tamarind tree enlightens amelioration of tree improvement by tree breeding program for economic value of Tamarind.

In this context, supersede of yield with rich nutrition in tamarind clones' emphasis by ambiguous selection program in breeding method. Selection indices play a vital role in breeding programs by facilitating the identification of high-yielding Tamarind clones based on yield and yield contributing traits. Selecting the multiple traits enhances breeding efficiency, as reliance solely on yield may result in genotypes with desirable characteristics. However, yield is significantly influenced by environmental factors that stimulant comprehend of selection approach. The Smith index has been widely used for selecting genotypes based on multi-trait performance, utilizing phenotypic and genotypic variance and covariance matrices. Whilst, impaired of this selection index by multicollinearity issues when focus on multiple traits, which affect the accuracy of genetic gain estimation. The Smith-Hazel (SH) index has challenges in assigning economic weights to different traits, making its computation complex for breeders. To mitigate these challenges, methods that suppress multicollinearity through integrate path coefficients have been proposed. However, a comparative assessment of these methods with the classical index is necessary. In response to these limitations, Olivoto and Nardino (2020) introduced the Multi-Trait Genotype-Ideotype Distance Index (MGIDI), a novel multivariate selection approach that limiting the multicollinearity through predetermined trait weightage. The MGIDI index is more effective than the traditional Smith index in identifying superior genotypes, particularly by resolving challenges related to the multicollinearity which impact genetic gain estimation. In contrast of Smith index, MGIDI simplifies the selection process by addressing these statistical complexities and providing a more reliable method for genotype evaluation. Further, MGIDI enables the assessment of genotypes through a strengths and weaknesses plot, facilitating a comprehensive evaluation of all studied traits. MGIDI were applied to cereal crops of rice (Pallavi *et al*., 2024) and sorghum (Behera *et al*., 2024); fibre crop of cotton (Raj *et al*., 2024); pulses crop of blackgram (Anbazhagan and Palaniyappan, 2025); fodder maize (Subramani *et al*., 2024) but MGIDI are not applied in previous studies in fruit or tree crops to identify the better genotype or clone. The present study aimed to introduce the MGIDI method to Tamarind clones to identify high productive and nutrient rich clones. In this study, Smith index and MGIDI index applied to estimate their efficiency in Tamarind clone selection and providing insights into their effectiveness in breeding programs.

MATERIALS AND METHODS

The experiment was conducted at Tamarind germplasm assemblage, ICFRE-Field Research Station, Kurumbampatty, Salem (11º 45.140 N and 78º 09.417E) during 2019-2021 at ICFRE-IFGTB, Coimbatore. Tamarind germplasm consisting of 60 diverse Tamarind clones representing sour, red and sweet Tamarind collected from over different region of India **(Table 1)** and assembled with the design of Randomized complete Block Design at spacing of 5 x 5 m with four replications. In each replication single tree were selected and 50 fruits were collected in different direction of the trees for the morphological and biochemical characterizations of Tamarind genetic resources.

The data on tree height (m), girth at breast height (m), crown cover area (m^2), number of primary branches, number of secondary branches, fruit weight (g), pulp weight (g), seed weight (g), shell weight (g), vein weight (g), fruit length (cm), fruit width (cm), fruit thickness (cm) was collected. Biochemical traits of Tamarind fruit pulp were assessed at laboratory situated at ICFRE-Institute of Forest Genetics and Tree Breeding. Biochemical traits of tamarind fruit pulp was quantified for following attributes *viz*., Total soluble solid (AOAC (1984)), Tartaric acid (%), (Roopa and Kasiviswanatham (2013)), Total acidity (%) (Anon, (1975)), Ascorbic acid (mg/g) (Ranganna, 1979), Total sugar (%) (Miller, 1972), Reducing sugar (%) (Miller, 1972), Non-reducing sugar (%) (Miller, 1972), Protein (mg/g) (Sadasivam and Manickam, 1996), Carbohydrate (mg/g) (AOAC, 2010).

Statistical analysis

The Smith-Hazel (SH) selection index (Smith, 1936) was used to identify superior genotypes by computing index values as a weighted linear combination of trait means with regression coefficients derived from phenotypic and genotypic variance and covariance matrices and assigned economic weights. Here, two approaches were followed: Selection Index I used equal genetic weights for all traits, while Selection Index II assigned differential weights based on path direct effects (2.00 for high, 1.00 for moderate, 0.50 for low, and −0.50 for negative effects), with annual yield per tree weighted as 2.00. However, the Multi-Trait Genotype-Ideotype Distance Index (MGIDI) was calculated (Olivoto and Nardino, 2021) with concerning trait rescaling, factor analysis, ideotype construction and Euclidean distance, where genotypes with lower MGIDI values were considered superior. The selection intensity was 15 % maintained for discover the ideal genotypes of Tamairnd. The analyses were performed in R program with "metan" package.

RESULT AND DISCUSSION

In this study, there are three selection indices were carried out to endorse economic important of trait with 60 Tamarind clones. The pursuant of selection of Tamarind clones with desirable economic attributes, the selection index method able to structure the clones with desired traits which is yield and yield contributing traits and nutritional traits. In this result, classical selection index determined with equal

Table 1. List of Tamarind clones and its geographical details

S.No.	Tree Code	Location	Latitude	Longitude	Altitude
1	IFGTBTI 1	Urigam	N 12°19.04’	E 77°37.47’	619
2	IFGTBTI 2	Kothandapali	N 12°18.08’	E 77°36.39’	609
3	IFGTBTI 3	Kavalur	N 12°34.33’	E 78°48.43’	718
4	IFGTBTI 4	Alangayam	N 12°34.33’	E 78°48.32’ ‘	715
5	IFGTBTI 5	Nandukaran	N 10°37. 25’	E 78°40.420’	360
6	IFGTBTI 6	Oormelagain	N 9° 44.654’	E 77° 37.369’	185
7	IFGTBTI 7	Ilanji	N 8° 95.710’	E77° 27. 365’	214
8	IFGTBTI 8	Mulangadu	N 10°59.136’	E 06° 43.934’	501
9	IFGTBTI 9	Poondi	N 10°59.128’	E 76° 43.944	493
10	IFGTBTI 10	Thanikandi	N 10°59.133’	E 76° 43.955’	483
11	IFGTBTI 11	Kamalapuram	N 12°56.215’	E 78°44.918’	367
12	IFGTBTI 12	Karaikal	N 10°57.017’	E 79°46.524’	20
13	IFGTBTI 13	Eravancheri	N 11°23.162’	E 79°43.528’	26
14	IFGTBTI 14	Komardhapalli	N 12°16.577’	E 77°36.522’	554
15	IFGTBTI 15	Velautampatti	N 10°14.798’	E 78°10.512’	100
16	IFGTBTI 16	Natalam	N 11°00.871’	E 76°56.497’	408
17	IFGTBTI 17	Veerapandipuram	N 09°23.199’	E 77°54.194’	80
18	IFGTBTI 18	Kundal	N 08°05.297’	E 77°32.413’	57
19	IFGTBTI 19	Bodi	N 10°00.333’	E 77°20.474’	342
20	IFGTBTI 20	Cerlapalli	N 12°56.228’	E 78°44.768’	369
21	IFGTBRT 1	Medak	N 18°03.13’	E 78°16.04’	485
22	IFGTBRT 2	Chittampalli	N 13°00.25	E 78°27.32	800
23	IFGTBRT 3	Bodi pudur	N 10°01.191’	E 77°21.128’	352
24	IFGTBRT 4	Karaikal	N 10°57.013’	E 79°46.519’	21
25	IFGTBRT 5	Kuvalapuram	N 09°41.091’	E 77°45.504’	389
26	IFGTBRT 6	Motchampalli	N 12°51.479’	E 78°42.390’	360
27	IFGTBRT 7	Kedampur	N 12°50.248’	E 78°42.548’	413
28	IFGTBRT 8	Nelluvai	N 11°00.885’	E 76°56.655’	419
29	IFGTBRT 9	Shivaraj Nagar	N 12°56.045’	E 78°42.208’	357
30	IFGTBRT 10	Rajapalayam	N 10°06.164’	E 77°36.182’	352
31	IFGTBRT 11	Pudhupatti	N 09°45.154’	E 77°18.207’	388
32	IFGTBRT 12	Bodi	N 10°00.333’	E 77°20.466’	342
33	IFGTBRT 13	Jayamangalam	N 10°06.164’	E 77°36.182’	352
34	IFGTBRT 14	Velauthampatti	N 10°14.677’	E 78°10.367’	356
35	IFGTBRT 15	Natham	N 10°18.241’	E 78°03.677’	348
36	IFGTBRT 16	Peranampet	N 12°55.671’	E 78°42.916’	358
37	IFGTBRT 17	Mukkundram	N 12°56.865’	E 78°48.762’	305
38	IFGTBRT 18	Machempattu	N 12°51.479’	E 78°42.390’	360
39	IFGTBRT 19	Eraiyur	N 12°06.186’	E 78°54.464’	369
40	IFGTBRT 20	Vengalapuram	N 11°45.140’	E 78°09.417’	367
41	IFGTBST 1	Cerlapalli	N 12°56.209’	E 78°44.909’	363
42	IFGTBST 2	Podi	N 10°01.198’	E 77°21.023’	351
43	IFGTBST 3	Kundal	N 08°05.309’	E 77°32.413’	57
44	IFGTBST 4	Oodaipatti	N 09°17.248’	E 77°54.520’	75
45	IFGTBST 5	Veerapandiyapuram	N 09°23.211’	E 77°54.188’	100
46	IFGTBST 6	Pernampet	N 12°56.061’	E 78°42.395’	362
47	IFGTBST 7	Kezhakollai	N 11°38.789’	E 79°32.519’	68
48	IFGTBST 8	Chidambaram	N 11°36.664’	E 79°26.897’	83
49	IFGTBST 9	Natalam	N 08°16.299’	E 77°14.186’	51
50	IFGTBST 10	Velautampatti	N 08°44.786’	E 77°51.409’	36
51	IFGTBST 11	Uluppakudi	N 10°15.880’	E 78°11.805’	354
52	IFGTBST 12	Maniyakarapatti	N 10°18.024’	E 78°08.294’	314
53	IFGTBST 13	Nellukuthi	N 12°27.225’	E 78°53.224’	884
54	IFGTBST 14	Vannathipatti	N 12°26.214’	E 77°53.161’	875
55	IFGTBST 15	Kovalli	N 12°17.507’	E 77°35.566’	592
56	IFGTBST 16	Komardhapalli	N 12°16.591’	E 77°36.443’	554
57	IFGTBST 17	Karaikal	N 10°57.012’	E 79°46.518’	21
58	IFGTBST 18	Eravancheri	N 11°23.158’	E 79°43.521’	28
59	IFGTBST 19	Kamalapuram	N 12°56.213’	E 78°44.912’	365
60	IFGTBST 20	Nattham	N 10°18.244’	E 78°03.679’	347

weight (Selection index I) and unequal weight (Selection index II) for assessed traits of Tamarind (**Table 2 and Table 3**). The direct effect of path analysis incurred as unequal weightage to determine the selection index II. Based on the selection index I, the top five ranked Tamarind clones IFGTBST 2, IFGTBST 7, IFGTBRT 18, IFGTBST 1, IFGTBST 3 were identified, whilst selection index II frame the top five Tamarind clones *viz*., IFGTBTI 14, IFGTBTI 2, IFGTBTI 1, IFGTBRT 5, IFGTBTI 5 were selected. The contrasting result of selected Tamarind clones acted by multicollinearity issues conquered in selection index I. Addressing the equal important to all studied traits prone to frame the Tamarind clone with undesired traits leads to ineffective selection of clones. To mitigate this term, placed an unequal weightage based on direct effect of characters in path analysis encompass effective selection of clones with economically wealthy trait. From the result of selection index II, the clones, IFGTBTI 14, IFGTBTI 2, IFGTBTI 1, IFGTBRT 5 and IFGTBTI 5 constitute as top rank better performing clones overall studied traits.

Another selection index method, Multi trait Genotype-Ideotype Distance Index is an existing multivariate method, used to seek the Tamarind clones with substantial attributes. In MGIDI, the principal components used to fix the group of variables declared as factors anchor the Tamarind clones which are aligned with multiple important traits **(Table 4**). Principal component analysis exhibits substantial variation of Tamarind clones, the first six component contribute about 80.20 % variation. The PC1 has highest eigen value (8.80) and contribute variation about 36.90 % in total variation followed by PC2 to PC6 incurred variation of 20.00, 7.64 , 6.18%, 5.03 and 4.40 %, respectively.

In MGIDI, principal component analysis reveal only six components has more than 1 eigen value that forced to create various six factors, each factors incurred the traits which are highly correlated among them. FA1 consist of annual yield per tree, fruit weight, pulp weight, seed weight, shell weight, vein weight and fruit length; FA2 comprises the biochemical traits of Tamarind clones are total soluble solid, tartaric acid, total sugar, reducing sugar and non-reducing sugar; FA3 includes grith at breast height, crown cover area and number of secondary branches; FA4 includes number of secondary branches, fruit thickness and fruit width; FA5 contains

Table 2. Selection index - Weightage of different traits and their regression coefficients

S.No.	Traits	Selection index I		Selection index II	
		Equal weight	Regression (b)	Differential weight	Regression (b)
1	Annual yield/tree	1	-3.50	2.0	1.85
2	Tree height	1	-22.30	-0.5	4.45
3	Girth at breast height	1	3.82	-0.5	-0.59
4	Crown cover area	1	4.11	-0.5	-0.63
5	Number of primary branches	1	12.60	0.5	-2.17
6	Number of primary branches	1	-1.96	-0.5	0.51
7	Fruit weight	1	10.30	2.0	-0.84
8	Pulp weight	1	-5.87	2.0	2.15
9	Seed weight	1	-0.66	-0.5	0.88
10	Shell weight	1	-7.18	1.0	1.61
11	Vein weight	1	79.30	0.5	-14.60
12	Number of seed per fruit	1	15.70	0.5	-2.76
13	Fruit length	1	-0.43	1.0	0.28
14	Fruit thickness	1	43.30	1.0	-7.84
15	Fruit width	1	-67.80	0.5	13.00
16	Total soluble solid	1	17.20	-0.5	-3.11
17	Tartaric acid	1	7.88	2.0	-0.35
18	Ascorbic acid	1	2.57	1.0	0.67
19	Total acidity	1	4.25	1.0	0.39
20	Total sugar	1	-26325.00	0.5	5037.00
21	Reducing sugar	1	26328.00	-0.5	-5037.00
22	Non-Reducing sugar	1	26321.00	-0.5	-5036.00
23	Protein	1	2.61	-0.5	-0.25
24	Carbohydrate	1	-2.10	-0.5	0.30

Table 3. Selection index score and ranking of 60 tamarind clones

Clones	Selection index I		Clones	Selection index II		Clones	Selection index I		Clones	Selection index II	
	Index score	Rank		Index score	Rank		Index score	Rank		Index score	Rank
IFGTBST 2	1119.48	1	IFGTBTI 14	47.82	1	IFGTBTI 3	824.84	31	IFGTBRT 15	-12.36	31
IFGTBST 7	1105.03	2	IFGTBTI 2	40.99	2	IFGTBST 11	823.34	32	IFGTBTI 18	-12.41	32
IFGTBRT 18	1081.45	3	IFGTBTI 1	40.82	3	IFGTBRT 4	817.35	33	IFGTBRT 4	-14.17	33
IFGTBST 1	1061.15	4	IFGTBRT 5	29.81	4	IFGTBTI 17	800.19	34	IFGTBRT 6	-15.11	34
IFGTBST 3	1059.76	5	IFGTBTI 5	24.99	5	IFGTBRT 20	792.47	35	IFGTBRT 13	-16.12	35
IFGTBST 18	1057.82	6	IFGTBTI 9	17.58	6	IFGTBTI 14	792.35	36	IFGTBRT 8	-19.06	36
IFGTBST 5	1057.62	7	IFGTBTI 15	15.24	7	IFGTBST 14	789.66	37	IFGTBST 14	-22.26	37
IFGTBRT 12	1054.85	8	IFGTBTI 19	14.24	8	IFGTBTI 2	789.07	38	IFGTBRT 18	-37.90	38
IFGTBRT 13	1022.20	9	IFGTBTI 7	13.76	9	IFGTBTI 12	787.02	39	IFGTBST 11	-39.15	39
IFGTBRT 3	1021.52	10	IFGTBTI 17	13.17	10	IFGTBRT 5	786.85	40	IFGTBST 12	-44.70	40
IFGTBST 15	1012.84	11	IFGTBRT 11	13.08	11	IFGTBTI 9	786.13	41	IFGTBST 4	-48.18	41
IFGTBST 19	1012.06	12	IFGTBTI 13	10.92	12	IFGTBST 12	771.76	42	IFGTBST 13	-55.88	42
IFGTBRT 14	1004.28	13	IFGTBTI 10	10.61	13	IFGTBTI 1	766.23	43	IFGTBST 16	-55.99	43
IFGTBST 17	1002.81	14	IFGTBRT 16	10.14	14	IFGTBRT 2	761.02	44	IFGTBRT 14	-57.63	44
IFGTBST 9	1000.66	15	IFGTBRT 7	8.26	15	IFGTBRT 11	755.69	45	IFGTBST 8	-63.39	45
IFGTBST 20	990.34	16	IFGTBRT 19	7.01	16	IFGTBRT 8	749.18	46	IFGTBST 3	-63.75	46
IFGTBRT 17	953.52	17	IFGTBTI 3	6.80	17	IFGTBTI 19	747.52	47	IFGTBRT 17	-64.48	47
IFGTBST 8	926.08	18	IFGTBTI 16	4.69	18	IFGTBRT 10	743.52	48	IFGTBST 17	-67.46	48
IFGTBST 10	922.53	19	IFGTBTI 11	1.88	19	IFGTBTI 8	741.44	49	IFGTBST 10	-67.74	49
IFGTBST 4	885.36	20	IFGTBTI 8	-0.56	20	IFGTBRT 9	739.93	50	IFGTBST 18	-68.10	50
IFGTBST 16	877.05	21	IFGTBRT 20	-1.61	21	IFGTBTI 7	722.89	51	IFGTBRT 12	-68.46	51
IFGTBTI 4	857.49	22	IFGTBTI 12	-2.12	22	IFGTBTI 10	708.74	52	IFGTBRT 3	-72.42	52
IFGTBRT 7	855.88	23	IFGTBRT 2	-4.22	23	IFGTBRT 1	698.77	53	IFGTBST 1	-73.42	53
IFGTBTI 11	848.78	24	IFGTBRT 1	-5.34	24	IFGTBTI 18	697.05	54	IFGTBST 7	-74.25	54
IFGTBTI 5	840.39	25	IFGTBST 6	-5.73	25	IFGTBTI 20	674.23	55	IFGTBST 20	-74.36	55
IFGTBTI 13	835.05	26	IFGTBTI 20	-7.19	26	IFGTBRT 15	667.32	56	IFGTBST 19	-76.16	56
IFGTBTI 6	832.76	27	IFGTBTI 4	-8.86	27	IFGTBRT 19	662.36	57	IFGTBST 15	-79.96	57
IFGTBTI 15	831.61	28	IFGTBTI 6	-10.75	28	IFGTBRT 6	647.66	58	IFGTBST 2	-83.82	58
IFGTBST 13	827.30	29	IFGTBRT 9	-10.76	29	IFGTBTI 16	631.77	59	IFGTBST 9	-84.07	59
IFGTBRT 16	826.45	30	IFGTBRT 10	-10.86	30	IFGTBST 6	621.58	60	IFGTBST 5	-100.29	60

ascorbic acid, total acidity and protein; FA6 encompass tree height and number of primary branches. MGIDI also provide predicted selection gain but it is not possible while classical selection index method. Selection gain which offers the strength and weakness of individual traits that could be make selection of effective clones. According to Al-Ashkar *et al*. (2023) least MGIDI score calculated by Euclidean distance shows the closer amid clones and ideotypes. In contrast, the Smith and Hazel method is based on genotypic and phenotypic variance and does not include the correlation between variables. The selection of best-performing genotypes by using MGIDI approach was also done earlier in different crops, such as strawberries (Olivoto and Nardino 2021), soybean (Maranna *et al*. 2021), guar (Benakanahalli *et al*. 2021), maize (Uddin *et al*. 2021) barley (Pour-Aboughadareh *et al*. 2021); Pallavi *et al*., (2024). With the selection intensity at 15 % level, the least MGIDI score observed for IFGTBTI-2 (3.58), IFGTBTI-15 (4.01), IFGTBTI-1 (4.02), IFGBTST-3 (4.05), IFGTBST-1 and IFGTBTI-14 (4.08) clones were performed as top ranked clones across the all traits (**Table 5**). The top ranked clones and strength and weakness of Tamarind clones are visualised in graph of **Fig.1.** The maximum contribution of FA1 observed for IFGTBTI-14, IFGTBTI-2 and IFGTBTI-1 were high in yield contributing traits of annual yield per tree, fruit weight,

Table 4. MGIDI selection index - Factor analysis, selection gain on Tamarind clones

S.No	PC	Eigen values	Variance (%)	Cumulative variance (%)	Variables	Factor	SG (%)
1	PC1	8.85	36.90	36.90	Annual yield/tree	FA1	40.80
2	PC2	4.80	20.00	56.90	Fruit weight	FA1	23.40
3	PC3	1.83	7.64	64.50	Pulp weight	FA1	23.90
4	PC4	1.48	6.18	70.70	Seed weight	FA1	24.70
5	PC5	1.21	5.03	75.80	Shell weight	FA1	28.10
6	PC6	1.06	4.40	80.20	Vein weight	FA1	28.40
7	PC7	0.82	3.42	83.60	Fruit length	FA1	40.90
8	PC8	0.75	3.12	86.70	Total soluble solid	FA2	-11.60
9	PC9	0.54	2.23	88.90	Tartaric acid	FA2	-1.33
10	PC10	0.48	2.02	90.90	Total sugar	FA2	-0.28
11	PC11	0.44	1.83	92.80	Reducing sugar	FA2	-2.07
12	PC12	0.38	1.60	94.40	Non-reducing sugar	FA2	4.27
13	PC13	0.37	1.53	95.90	Girth at breast height	FA3	11.00
14	PC14	0.22	0.92	96.80	Crown cover area	FA3	15.30
15	PC15	0.18	0.76	97.60	Number of secondary branches	FA3	40.90
16	PC16	0.15	0.62	98.20	Number of seed/fruit	FA4	17.80
17	PC17	0.12	0.52	98.70	Fruit thickness	FA4	25.20
18	PC18	0.10	0.41	99.10	Fruit width	FA4	28.20
19	PC19	0.08	0.33	99.50	Ascorbic acid	FA5	1.80
20	PC20	0.05	0.19	99.60	Total acidity	FA5	20.20
21	PC21	0.03	0.14	99.80	Protein	FA5	19.80
22	PC22	0.03	0.13	99.90	Carbohydrate	FA5	-9.64
23	PC23	0.02	0.09	100.00	Tree height	FA6	0.48
24	PC24	0.00	0.00	100.00	Number of primary branches	FA6	12.30

PC-Principle component, h^2-heritability, SG (%)-Predicted selection gain.

pulp weight, seed weight, shell weight, vein weight and fruit length. For improving the yield in Tamarind tree, the clones for IFGTBTI-14, IFGTBTI-2 and IFGTBTI-1 would be directly recommended for multilocation evaluation trials to assess the site-specific clones for yield improvement programme. In FA2, the clones IFGTBST-1, IFGTBST-3 and IFGTBTI-14 has contributed maximum for sugar contents, total soluble solid and tartaric acid. The sweet Tamarind clones, IFGTBST-1 and IFGTBST-3 were found to be rich in sugar content, whilst IFGTBTI-14 showed more in tartaric acid content. FA3 governed the traits of girth at breast height, crown cover area and number of secondary branches. The clones IFGTBST-1, IFGTBST-3 and IFGTBTI-1 showed high values for girth at breast height, crown cover area number of secondary branches. All Tamarind clones contributed maximum strength in FA4 which clumps the traits of number of seed per fruit, fruit thickness and fruit width that indicates selected clones showed large size of fruits directly proportional to yield improvement. The traits, ascorbic acid and total acidity tend together in FA5, the peak strength observed for IFGBTI-14, IFGTBTI-15 and IFBGTBTI-2, that deliver the provenance of high yielding clones are that were rich in high acidity content. In FA6, the topmost strength observed in IFGBTI-14, IFGTBTI-15 and IFBGTBTI-2 for tree height and number of primary branches. This strength and weaknesses of genotypes have been highlighted earlier (Benakanahalli *et al*. 2021; Pour Aboughadareh *et al*. 2021; Olivoto and Nardino 2021). The MGIDI method utilizes a comprehensive assessment of multiple characteristics along with an examination of strengths and weaknesses, the treatment ranking proves to be a potent tool for directing researchers toward more effective treatment recommendations. So, comparing the conventional method, MGIDI selection based on multiple traits is more effective for the identification of best performing genotypes.

The study highlights that unequal weightage-based selection index and MGIDI are effective tools for identifying superior *Tamarindus indica* clones. The unequal weightage index improved selection efficiency compared to equal weightage by prioritizing economically important traits. The MGIDI approach further enhanced

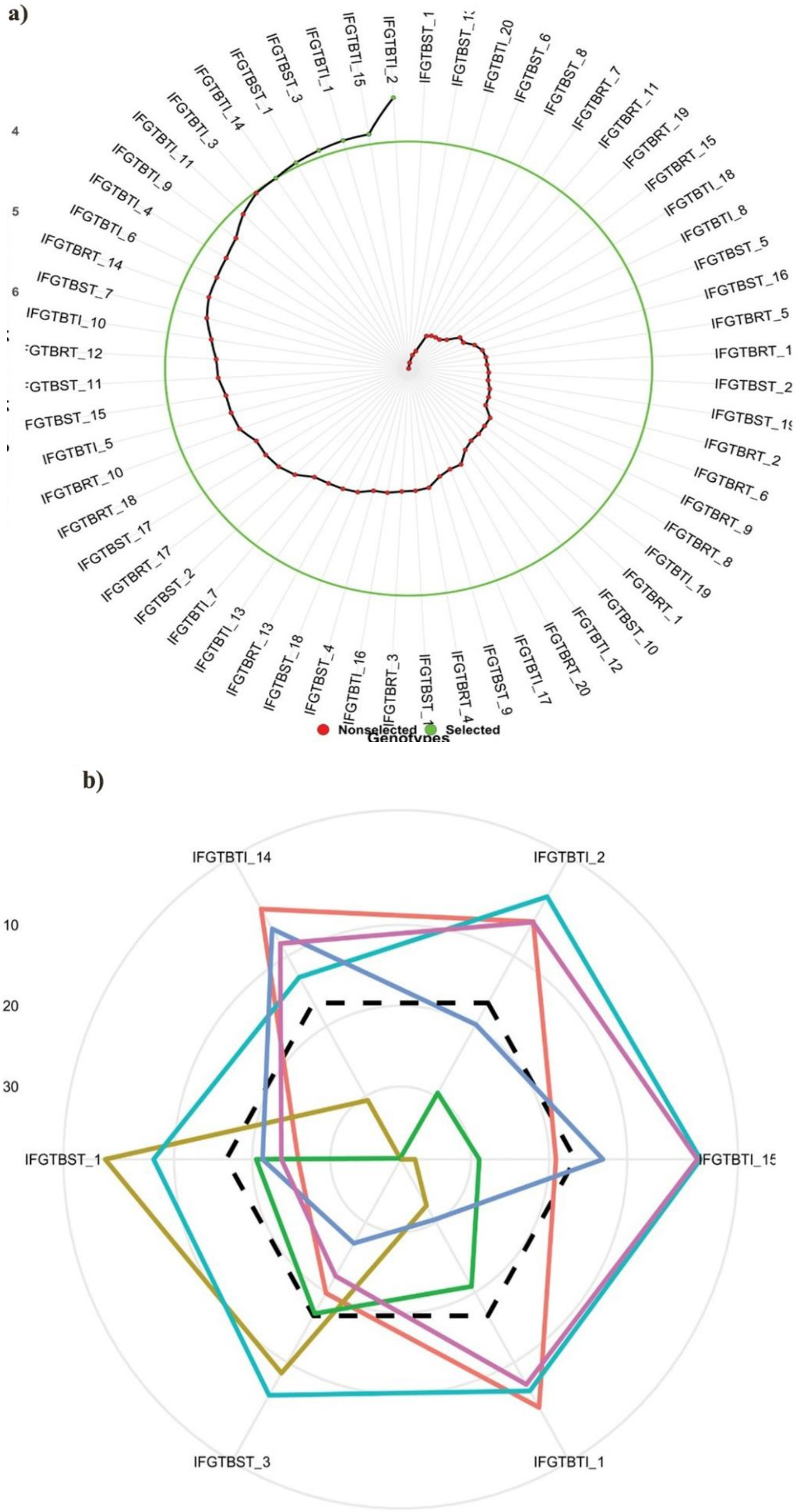

Fig. 1. a) Ranking of Tamarind clone using the multi-trait genotype– ideotype index (MGIDI). The selected clones are shown as green dots, while the unselected clones are shown as red dots. The green circle represents the selection point. **b) The strengths and weaknesses of the selected genotypes.**

Table 5. MGIDI score for 60 Tamarind clones

S.No.	Genotype	MGIDI	S.No	Genotype	MGIDI
1	IFGTBTI 2	3.58	31	IFGTBST 14	5.43
2	IFGTBTI 15	4.01	32	IFGTBRT 4	5.46
3	IFGTBTI 1	4.02	33	IFGTBST 9	5.57
4	IFGTBST 3	4.05	34	IFGTBTI 17	5.62
5	IFGTBST 1	4.08	35	IFGTBRT 20	5.62
6	IFGTBTI 14	4.13	36	IFGTBTI 12	5.75
7	IFGTBTI 3	4.15	37	IFGTBST 10	5.8
8	IFGTBTI 11	4.24	38	IFGTBRT 1	5.81
9	IFGTBTI 9	4.38	39	IFGTBTI 19	5.82
10	IFGTBTI 4	4.43	40	IFGTBRT 8	5.83
11	IFGTBTI 6	4.46	41	IFGTBRT 9	5.95
12	IFGTBRT 14	4.48	42	IFGTBRT 6	5.96
13	IFGTBST 7	4.53	43	IFGTBRT 2	5.98
14	IFGTBTI 10	4.64	44	IFGTBST 19	6.02
15	IFGTBRT 12	4.72	45	IFGTBST 20	6.03
16	IFGTBST 11	4.75	46	IFGTBRT 16	6.05
17	IFGTBST 15	4.81	47	IFGTBRT 5	6.05
18	IFGTBTI 5	4.83	48	IFGTBST 16	6.07
19	IFGTBRT 10	4.86	49	IFGTBST 5	6.14
20	IFGTBRT 18	4.97	50	IFGTBTI 8	6.24
21	IFGTBST 17	4.98	51	IFGTBTI 18	6.25
22	IFGTBRT 17	5.02	52	IFGTBRT 15	6.39
23	IFGTBST 2	5.09	53	IFGTBRT 19	6.45
24	IFGTBTI 7	5.22	54	IFGTBRT 11	6.46
25	IFGTBTI 13	5.25	55	IFGTBRT 7	6.47
26	IFGTBRT 13	5.28	56	IFGTBST 8	6.5
27	IFGTBST 18	5.31	57	IFGTBST 6	6.72
28	IFGTBST 4	5.38	58	IFGTBTI 20	6.78
29	IFGTBTI 16	5.39	59	IFGTBST 13	6.88
30	IFGTBRT 3	5.43	60	IFGTBST 12	6.96

selection by integrating multiple traits and identifying genotype strengths and weaknesses. Clones such as IFGTBTI-14, IFGTBTI-2, IFGTBTI-1 and IFGTBST-3 consistently showed superior performance and can be recommended for multilocation trials and future breeding programs aimed at yield and quality improvement.

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