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Research Article

Utilizing selection indices to enhance genetic gain in turmeric (*Curcuma longa* L.)

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Abstract

Turmeric, known as "The golden spice" in India, is prized for its curcumin pigment, offering various uses as a food preservative, spice, and coloring agent. Its medicinal potential is gaining global recognition. A total of 24 turmeric genotypes were evaluated at Medicinal and Aromatic Plants Research Station, Anand Agricultural University, Anand, Gujarat. Significant genetic diversity among the genotypes was revealed through multivariate analysis of variance (MANOVA). Discriminant function analysis and selection indices were employed to improve grain yield and other important traits in turmeric. The results showed that selecting multiple traits simultaneously through a selection index yields higher genetic gain compared to selecting single traits. The comparison of selection efficiency for different trait combinations demonstrated an increase in selection efficiency with an increasing number of traits. The highest selection efficiency was observed when all six attributes were considered. The study identified the most effective four trait combination, comprising curing percentage, leaf oil percentage, rhizome oil percentage and fresh rhizome yield per plant, for enhancing grain yield in turmeric. The best-performing genotype, ATG-17, showed promise for future breeding activities.

Keywords: *Curcuma longa* L., Discriminant factor analysis, Multivariate analysis of variance, Selection indices.

INTRODUCTION

India is renowned as "The spice bowl of the world" and celebrated for its exceptional production of high-quality spices. For centuries, India has been esteemed for its expertise in cultivating of various herbs. Among these treasures, Turmeric (*Curcuma longa* L.) stands out as the "golden spice" and "spice of life" cherished both for its medicinal properties and its sacred significance throughout the ages (Ravindran *et al*., 2007). The bright yellow hue of Turmeric has earned it the moniker "Indian Saffron". Belonging to the family *Zingiberaceae*, it is believed to have originated from South East Asia and can be found across South and South East Asia, with a few species even extending their reach to China, Australia, and the South Pacific

(Chickarmane *et al.*, 2003). Turmeric cultivation is prevalent globally, with major producers including India, Sri Lanka, Taiwan and China (Sahoo *et al.*, 2019). However, India stands out as a significant consumer and producer of this cherished spice, ranking first in global production and contributing over 80% to the world's total turmeric yield. Furthermore, India leads the world in producing value-added turmeric products and plays a dominant role in its export (1.71 lakh tons) (Anon., 2021). Turmeric boasts a composition rich in essential elements, with minerals making up 3.5%, fats - 5.1%, volatile oil ranging from 5.0% to 6.0%, carbohydrates - 6.3%, protein - 6.3%, and oleoresin comprising 7.9% to 10.4%. Its distinctive pigment imparts unique chemical and physical properties, making it highly versatile. Across Asian countries, it finds multifaceted applications as a food preservative, spice, additive, coloring agent, and traditional medicine (Sasikumar, 2005). However, its significance extends far beyond its regional use. Globally, Turmeric is gaining recognition as a promising source of new drugs for combating various ailments, marking its potential impact in the field of medicine.

The yellow pigment found in turmeric, scientifically known as curcumin, encompasses a wide range of beneficial properties. These include hypocholesterolemic, choleretic, anti-inflammatory, insect repellent, antirheumatic, antifibrotic, antiaging, antiallergic, antimicrobial, antiviral, antifungal, antidiabetic, anti-venomous, antihepatotoxic, and anticancerous effects (Singh *et al.*, 2012). Furthermore, biomedical investigations have reinforced the therapeutic significance of turmeric in addressing various diseases, as evidenced by studies conducted by (Siju *et al.*, 2010). For generations, turmeric has been recognized in traditional Indian Ayurvedic and Chinese medicine for its medicinal properties in its natural, unprocessed form. Its biologically active components including curcumin, demethoxycurcumin, and bisdemethoxycurcumin, hold promise in regulating carcinogenesis, alleviating rheumatism, and countering pathogenesis related to oxidative stress. Notably, turmeric oil also finds practical applications in the perfume industry and aromatherapy, as substantiated by (Sasikumar, 2005).

The ever-increasing demand from various industries necessitates a continuous effort to enhance turmeric productivity. However, achieving further improvements in productivity requires a comprehensive understanding of genetic variability (Nass, 2001). Turmeric poses a challenge for hybrid breeding due to its status as a cross-pollinated triploid species (2n = 3x = 63) and exclusive propagation through rhizomes (Sasikumar, 2005). In such circumstances, the most feasible option for genetic improvement lies in the introduction, mutation and clonal selection. As turmeric is a crop propagated vegetatively, the scope for variability in various morphological traits is limited. Consequently, genotype selection based on leaf and rhizome characteristics yields less rewarding results, and identifying superior turmeric genotypes through insufficient morphological descriptors and biochemical parameters like curcumin and essential oil proves to be challenging.

Discriminant function analysis, proposed by Fisher (1936), aids in formulating an efficient selection strategy for high grain yield and yield-attributing traits (Fisher, 1936; Smith, 1936). The selection index allows for the simultaneous selection of multiple traits, optimizing complex attributes like yield (Hazel, 1943). Choosing yield-contributing traits based on the selection index is more effective than direct yield selection (Islam *et al.*, 2016; Anshori *et al.*, 2019; Antony *et al.*, 2023). A study was undertaken to identify selection indices to enhance rhizome yield in turmeric and to assess their efficiency in the selection process.

MATERIALS AND METHODS

Rhizomes of 24 turmeric genotypes were planted in randomised block design with three replications during *kharif* season of the year 2020-21, at the Medicinal and Aromatic Plants Research Station, Anand Agricultural University, Anand. The spacing between plants was maintained at 45×20 cm throughout the cultivation, the recommended package of practices was followed to ensure the growth of a healthy crop. Five plants were randomly tagged for recording the observations from every experimental unit in each replication. Observations on five distinct characteristics, namely, fresh rhizome yield per plant (g), curing percentage (%), curcumin content (%), crude fiber content (%), leaf oil percentage (%) and rhizome oil percentage (%) were recorded. The Multivariate Analysis of Variance (MANOVA) was executed as per Antony *et al.* (2023). The method proposed by Robinson and Comstock was used to construct selection indices and to develop the discriminant function. Based on six characters, a total of 63 selection indices were developed. R package was used to work selection index for assessing discriminant factors.

RESULTS AND DISCUSSION

Selection indices: Discriminant function analysis was used to determine the relative importance of component attributes and establish effective selection indices for improving complex traits such as grain yield. Multivariate analysis of variance (MANOVA) demonstrated a significant variation among the genotypes (**Table 1**). The comparison of selection efficiency for different trait combinations showed an increase in selection efficiency with an increasing number of traits (**Table 2**). The highest selection efficiency was observed when all six attributes were considered. The genetic gain under selection for a single trait, curcumin (%), showed a genetic advance of 21.44%, which was significantly lower compared to the combinations of traits. The combination of curing (%) (X2) and the fresh rhizome yield per plant (X6) resulted in the highest genetic advance (53.50%) under

Table 1. Multivariate analysis of variance (MANOVA) for 24 turmeric genotypes

Source of variation	df	Approx. F	p value
Genotypes	23	2.32	0.04**
Replication	1	0.1767	0.53
Eror	70		

**- Significance at 1% level of probability

Table 2 Average selection efficiency of various combinations of traits of *curcuma longa*

Number of traits in the index	Percent Relative efficiency
One	21.44
Two	40.67
Three	58.74
Four	41.80
Five	92.56
Six	108.69

simultaneous selection with two discriminants, while the combination of leaf oil (%) (X4) and fresh rhizome yield per plant (X6) produced the second-highest genetic advance (53.14%). Three traits curing (%) (X2), leaf oil (%) (X4) and fresh rhizome yield per plant (X6) resulted in the highest genetic advance (53.97%) under simultaneous selection with three discriminants, while the combination of curing (%) (X2), rhizome oil (%) (X5) and fresh rhizome yield per plant (X6) produced the second-highest genetic advance (53.73%). The combination of curing (%) (X2), leaf oil (%) (X4), rhizome oil (%) (X5) and fresh rhizome yield per plant (X6) resulted in the highest genetic advance (54.19 %) under simultaneous selection with four discriminants, while the combination of curcumin (%) (X1), curing (%) (X2), leaf oil (%) (X4) and fresh rhizome yield per plant (X6) produced the second-highest genetic advance (54.18%). The combination of all six traits showed a high expected genetic advance of 54.39%, which is almost equal to the estimated genetic advance of five traits, including curcumin (%) (X1), curing (%) (X2), leaf oil (%) (X4), rhizome oil (%) (X5) and fresh rhizome yield per plant (X6) showing a 54.36 % expected genetic advance. Considering all attributes, the average selection efficiency increased from 21.44 % to 108.69 % (**Table 2**). As shown in **Table 3**, an increase in the number of traits, along with curcumin percentage, enhanced the relative selection efficiency. The relative efficiency of selection based solely on curcumin percentage was 105.17 %. When practicing concurrent selection on five traits (X1, X2, X3, X5, and X6) or all six traits, the relative efficiency was 108.64% and 108.69%, respectively. Breeding programs aim to maximize genetic gain through selection while suggesting the consideration of a smaller number of traits to reduce the effort and time required for trait improvement. Overall, the four-trait combination of curing (%) (X2), leaf oil (%) (X4), rhizome oil (%) (X5) and fresh rhizome yield per plant (X6) demonstrated a 54.19

Table 3. Highest relative efficiency and genetic advance of trait combinations (*curcuma longa* L.)

S.No.	Trait combinations	Genetic Advance	Percent Relative Efficiency
1	X6	52.63	105.17
2	X2,X6	53.50	106.92
3	X4, X6	53.14	106.19
4	X2, X4,X6	53.97	107.86
5	X2, X5, X6	53.73	107.37
6	X2, X4, X5, X6	54.19	108.30
7	X1, X2, X4, X6	54.18	108.27
8	X1, X2, X4, X5,X6	54.36	108.64
9	X2, X3, X4, X5, X6	54.17	108.26
10	X1, X2, X3, X4,X5, X6	54.39	108.69

X1: Curcumin (%), X2: Curing (%), X3: Crude fibre (%), X4: Leaf oil (%), X5: Rhizome oil (%) and X6: Fresh rhizome yield per plant

% genetic advance and 108.30 % relative efficiency, making it the most suitable combination for simultaneous improvement (**Table 4**). Furthermore, the genotypes were ordered (**Table 5**) based on their selection score using the optimal selection index. Genotype ATG-17 had the highest selection score followed by ATG-22, ATG-20 and ATG-21, indicating these genotypes which can be considered for future breeding activities.

Table 4. Selection indices, discriminant function, expected genetic advance and precent relative efficiency for different selection indices in *Curcuma longa*

S.No.	Selection Indices	Discriminant Function	Genetic Advance	Percent Relative Efficiency
1	X1	0.9318	1.32	2.64
2	X2	0.6862	7.74	15.46
3	X3	0.8612	0.99	1.98
4	X4	0.9814	1.24	2.48
5	X5	0.9922	0.46	0.93
6	**X6**	**0.8229**	**52.63**	**105.17**
7	X1, X2	0.3056 X1 + 0.6637 X2	7.37	14.73
8	X1, X3	0.9229 X1 + 0.8588 X3	1.52	3.04
9	X1, X4	0.9328 X1 +1.0046 X4	2.07	4.14
10	X1, X5	0.9247 X1 + 1.0662 X5	1.54	3.09
11	X1. X6	1.602 X1 + 0.8202 X6	52.89	105.71
12	X2, X3	0.692 X2 + 1.2087 X3	7.87	15.72
13	X2, X4	0.6881 X2 + 1.0553 X4	7.84	15.67
14	X2, X5	0.6736 X2 + -0.4913 X5	7.64	15.28
15	**X2,X6**	**1.4117 X2 + 0.8724** X6	**53.50**	**106.92**
16	X3, X4	0.8564 X3 + 1.0238 X4	1.85	3.70
17	X3, X5	0.8548 X3 + 1.0769 X5	1.20	2.40
18	X3, X6	-0.83 X3 + 0.8205 X6	52.55	105.01
19	X4, X5	0.9811 X4 + 0.9956 X5	1.39	2.77
20	X4, X6	3.3167 X4+ 0.8094 X6	53.14	106.19
21	X5, X6	7.6859 X5 + 0.8099 X6	52.87	105.65
22	X1, X2, X3	0.3383 X1 +0.6702 X2 + 1.0961 X3	7.48	14.94
23	X1, X2, X4	0.2381 X1 +0.6639 X2 + 1.286 X4	7.56	15.10
24	X1, X2, X5	0.3994 X1 +0.6589 X2 + 0.0252 X5	7.29	14.56
25	X1, X2, X6	2.3673 X1 +1.4564 X2 + 0.8691 X6	53.71	107.34
26	X1, X3, X4	0.9083 X1 +0.8397 X3 + 1.0591 X4	2.40	4.80
27	X1, X3, X5	0.901 X1 +0.8388 X3 + 1.1831 X5	1.79	3.58
28	X1, X3, X6	1.4208 X1 + -0.7524 X3 + 0.8187 X6	52.80	105.52
29	X1, X4, X5	0.9269 X1 + 1.0028 X4 + 1.059 X5	2.26	4.51
30	X1, X4, X6	1.1321 X1 + 3.289 X4 + 0.8087 X6	53.40	106.72
31	X1, X5, X6	0.9616 X1 + 7.7345 X5 + 0.8096 X6	53.13	106.17
32	X2, X3, X4	0.6938 X2 + 1.2124 X3 + 1.0005 X4	8.03	16.04
33	X2, X3, X5	0.6786 X2 + 1.3565 X3 + -0.6609 X5	7.80	15.59
34	X2, X3, X6	1.4097 X2 + -0.0206 X3 + 0.8708 X6	53.41	106.73
35	X2, X4,X5	0.6753 X2 + 1.1332 X4 + -0.5381 X5	7.76	15.51
36	**X2, X4,X6**	**1.4006 X2 + 2.7807 X4+ 0.8614 X6**	**53.97**	**107.86**
37	X2, X5,X6	1.4552 X2 + 8.2735 X5 + 0.8605 X6	53.73	107.37
38	X3, X4,X5	0.8519 X3 + 1.021 X4 + 1.0665 X5	2.02	4.03
39	X3, X4,X6	-1.994 X3 + 4.281 X4 + 0.8002 X6	53.12	106.16

Table 4. Continued..

S.No.	Selection Indices	Discriminant Function	Genetic Advance	Percent Relative Efficiency
40	X3, X5,X6	-1.6603 X3 + 9.409 X5 + 0.8033 X6	52.83	105.57
41	X4, X5 X6	3.149 X4 + 7.275 X5 + 0.7982 X6	53.36	106.64
42	X1, X2, X3, X4	0.2559 X1 + 0.6694 X2 + 0.9885 X3 + 1.2875 X4	7.72	15.42
43	X1, X2, X3, X5	0.4626 X1 + 0.6657 X2 + 1.2195 X3 + -0.1211 X4	7.41	14.81
44	X1, X2, X3, X6	2.287 X1 + 1.4536 X2 + 0.2218 X3 + 0.8681 X5	53.61	107.14
45	X1, X2, X4, X5	0.3311 X1 + 0.6586 X2 + 1.3103 X4 + -0.0331 X5	7.48	14.96
46	X1, X2, X4, X6	2.0255 X1 + 1.4366 X2 + 2.4879 X4 + 0.8607 X6	54.18	108.27
47	X1, X2, X5, X6	1.7742 X1 + 1.4776 X5 + 7.6591 X5 + 0.8595 X6	53.92	107.76
48	X1, X3, X4, X5	0.8859 X1 + 0.8189 X3 + 1.0616 X4 + 1.1812 X5	2.61	5.22
49	X1, X3, X4, X6	0.5626 X1 + -2.1139 X3 + 4.4476 X4 + 0.8004 X6	53.39	106.69
50	X1, X3, X5, X6	0.4495 X1 + -1.7988 X3 + 10.0123 X5 + 0.8037X6	53.09	106.09
51	X1, X4, X5, X6	0.4938 X1 + 3.2842 X4 + 7.7231 X5 + 0.7981 X6	53.64	107.19
52	X2, X3, X4, X5	0.6804 X2 + 1.3449 X3 + 1.0485 X4 + -0.6682 X5	7.97	15.93
53	X2, X3, X4, X6	1.3887 X2 + -0.8825 X3 + 3.397 X4 + 0.8549 X6	53.91	107.74
54	X2, X3, X5, X6	1.4551 X2 + -0.8301 X3 + 9.464 X5 + 0.8558 X6	53.66	107.24
55	**X2, X4, X5, X6**	**1.4436 X2 + 2.5711 X4 + 7.9341 X5 + 0.8513** X6	**54.19**	**108.30**
56	X3, X4,X5, X6	-2.8534 X3 + 4.3275 X4 + 9.5359 X5 + 0.7824 X6	53.40	106.72
57	X1, X2, X3, X4,X5	0.383 X1 +0.6652 X2 + 1.1161 X3 + 1.2698 X4 + -0.0962 X5	7.66	15.31
58	X1, X2, X3, X4,X6	1.6814 X1 + 1.4151 X2 + -0.6529 X3 + 3.1305 X4 + 0.8551 X6	54.11	108.13
59	X1, X2, X3, X5,X6	1.4532 X1 + 1.4692 X2 + -0.6961 X3 + 9.0277 X5 + 0.8554 X6	53.85	107.61
60	**X1, X2, X4, X5,X6**	**1.4432 X1 + 1.4581 X2 + 2.4585 X4 + 7.6155 X5 + 0.8513** X **6**	**54.36**	**108.64**
61	X1, X3, X4,X5, X6	-0.6862 X1 + -3.5244 X3 + 4.9625 X4 + 11.3915 X5 + 0.7805 X6	53.71	107.33
62	X2, X3, X4,X5, X6	1.4341 X2 + -1.6971 X3 + 3.4047 X4 + 9.4876 X5 + 0.8398 X6	54.17	108.26
63	**X1, X2, X3, X4,X5, X6**	0.6393 X1 + 1.4244 X2 + -1.8406 X3 + 3.5533 X4 + 9.8596 X5 + 0.8386 X6	**54.39**	**108.69**

X1: Curcumin (%), X2: Curing (%), X3: Crude fibre (%), X4: Leaf oil (%), X5: Rhizome oil (%) and X6: Fresh rhizome yield per plant

In almost all crop improvement programs, selection is a commonly used approach primarily aimed at increasing grain yield (Bos and Caligari, 2007). According to Smith (1936), selecting essential yield-contributing traits simultaneously using an index that assigns appropriate weights to each trait, rather than selecting only one trait, increases selection efficiency. Robinson and Comstock (1951) proposed a well-known model of selection indices, and the application of selection indices to enhance selection efficiency has been reported in rice (Venmuhil, 2020). This study aims to identify the best trait combination suitable for selection and identify superior germplasm/ genotypes. The results of MANOVA revealed significant differences among all genotypes, indicating considerable genetic diversity in the genotypes under investigation for the studied traits. The results showed that a selection index comprising multiple traits can significantly enhance genetic progress compared to selecting a single trait, highlighting the potential of utilizing selection indices for the simultaneous improvement of multiple traits (Kalola *et al*., 2018). The highest genetic gain was achieved when selection was based on all six traits. However, the results suggest that selecting curcumin (%) (X1), curing (%) (X2), crude fibre (%), (X3), leaf oil (%) (X4), rhizome oil (%) (X5) and fresh rhizome yield per plant (X6) can yield comparable results. Similar studies in bajra by Venkataramana *et al*. (2021) identified leaf length, flag leaf length, thousand grain weight, and grain yield per plant as efficient trait combinations for selection; maize by Antony *et al*. (2023) observed an ideal discriminant function for grain yield, kernels per row, 100-grain weight, and cob length trait combination; okra by Monpara and Chhatrola (2010) identified fruit yield per plant, plant height, and ten fruit weight as suitable trait combinations; and vegetable cowpea by Jivani *et al*. (2016) noted green pod yield per plant, pod length, and ten pod weight as ideal trait combinations for desirable crop improvement traits. The highest relative efficiency was found for fruit weight, fruits per plant, and yield per plant as an ideal combination, indicating their potential effectiveness (Hasan *et al*., 2016). To determine the combinations that maximize the selection index, it is ideal to explore all possible trait combinations. However, from a practical plant breeding perspective, breeders may be more concerned with maximizing gains and relative efficacy while using the fewest traits feasible in a selection

Table 5. Selection score and genotype ranking based on scores for 24 genotypes of turmeric

S.No.	Genotype	Selection Score	Rank
1	ATG-1	193.95	10
2	ATG-10	164.74	20
3	ATG-11	170.69	19
4	ATG-12	182.46	16
5	ATG-13	188.96	12
6	ATG-14	175.29	18
7	ATG-15	159.45	22
8	ATG-16	186.91	14
9	ATG-17	261.70	1
10	ATG-18	175.66	17
11	ATG-19	187.45	13
12	ATG-2	197.49	6
13	ATG-20	212.56	3
14	ATG-21	211.78	4
15	ATG-22	245.67	2
16	ATG-23	164.30	21
17	ATG-24	194.22	9
18	ATG-3	158.22	23
19	ATG-4	203.07	5
20	ATG-5	194.34	8
21	ATG-6	196.31	7
22	ATG-7	185.81	15
23	ATG-8	191.80	11
24	ATG-9	157.66	24

index. In this regard, the index that includes traits that are relatively easier to measure with greater precision in the field and are routinely recorded in research activities is the most convenient and relatively efficient index (Bos and Caligari, 2007). Additionally, it benefits breeders by reducing the cost of phenotyping (Jivani *et al*., 2016). The current study identified curing (%) (X2), leaf oil (%) (X4), rhizome oil (%) (X5) and fresh rhizome yield per plant (X6) as the best model. Furthermore, these traits are regularly recorded in routine research and do not incur additional costs.

Usage of discriminant function analysis in selection increases the breeding efficiency. In the present study, four key traits, namely, curing percentage, leaf oil percentage, rhizome oil percentage and fresh rhizome yield per plant were observed to be traits of interest for maximising genetic gain in turmeric. The genotypes ATG-17, ATG-22, and ATG-20, having exhibited the most promising performances for the above traits, bode well for future breeding efforts.

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