International Journal of Plant & Soil Science



33(21): 14-23, 2021; Article no.IJPSS.72728 ISSN: 2320-7035

Characterization of Identified Distinct Tamarind (Tamarindus indica L.) Genotypes for Yield-related Morphological Traits in Karnataka

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Authors' contributions

This work was carried out in collaboration among all authors. Author MNM data collection, data analysis and interpretation, wrote original draft, critical revision of the article and final approval of the version to be published. Authors BGP and BF conceptualization, methodology & formal data interpretation, review & editing the article and final approval of the version to be published. Authors UJ, MKH and APM managed the literature searches. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/IJPSS/2021/v33i2130653 Editor(s): (1) Prof. Marco Trevisan, Catholic University of the Sacred Heart, Italy. Reviewers: (1) Gaurav Sharma, lovely Professional University, India. (2) Chongtham Allaylay Devi, Sharda University, India. Complete Peer review History: https://www.sdiarticle4.com/review-history/72728

> Received 15 June 2021 Accepted 23 August 2021 Published 12 October 2021

Original Research Article

ABSTRACT

A monotypic genus crop tamarind is one of the important grown in India. The multipurpose tree comprises multiuse in cuisine preparation to medicine. All the parts of the tree have been used in many industries. The present study was conducted to assess the quantum of diversity in seventeen morphological traits of identified distinct 96 tamarind genotypes collected from 30 districts of Karnataka during 2018-19 at College of Horticulture, Bengaluru. The morphological traits including fruit yield/plant were observed. Among major yield attributing morphological traits viz., fruit weight ranged from 4.27-32.45 g, pulp weight ranged from 2.10-15.00 g and fruit vield/plant ranged from 49.50 to 298.50 kg. The genetic variation components viz., PCV ranged from 13.93 to 48.25 while

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GCV ranged from 12.22 to 47.28. The high heritability coupled with high genetic advance as per cent over mean was observed in the traits such as fruit weight (96%, 91.20%) and seed weight (96%, 95.45%) while moderate heritability and genetic advance as per cent over mean was revealed in fruit yield/plant (78.00 %, 55.83 %). Present study brought out and identified three top best performing tamarind genotypes TAM_KOL4, TAM_BEN(U)3 and TAM_BEN(U)4 expressed higher yield over the check GKVK17 recorded third highest fruit yield/plant but however it was not significant. The selection based on yield related traits and best performing genotypes in terms of fruit yield/plant could be effectively used in tamarind breeding programme.

Keywords: Tamarind; genetic variations; morphological; fruits; seeds; yield-related traits.

1. INTRODUCTION

A multipurpose tropical fruit tree tamarind, *Tamarindus indica* (L.) with chromosome number 2n=24 is one of the monotypic genus belonging to the subfamily *Detarioideae* of the family *Leguminosae* (*Fabaceae*). Tamarind is a Persian word "Tamar-I-hind," meaning date of India [1]. The multipurpose tree tamarind has a wide geographical distribution in the subtropics and semiarid tropics and the species have been grown in numerous regions. Tamarind is one of the most important tropical fruit tree species in the Indian subcontinent and several geographical areas have been proposed for the origin of tamarind varying from India or Far East or Africa, but the consensus of opinion is in Africa.

Tamarind has been recognized as one of the common and most prevalent and essential trees of India. India is one of the top leading producer in the world's, exporting several thousands of tons of seed, seed powder and fruit pulp each year. As it is a minor tree so often grown in gardens and along roadsides and are usually cultivated commercially as plantation crop. India is the only producer of tamarind on a commercial scale [2]. India is the major producer of sour tamarind in Asia and its annual production is about 300,000T [3]. As with perishables like fruits and vegetables, tamarind production has also had its own set of issues. The pulp constitutes 30-50 per cent of the ripe fruit, the shell and fiber account for 11-30 per cent and the seed about 25-40 per cent [4].

Tamarind being a highly cross-pollinated crop, wide variability is common in this species. Individual variation among trees within a population is crucial, and it may be desirable to pick the finest trees in comparison to neighboring ones within ecological zones in order to increase their frequency [5]. Though tamarind is an ancient cultivated, a very few efforts were directed towards its genetic improvement. It has a lot of phenotypic variation both in morphological and horticultural traits, which can be used to improve its genetic. There is a large amount of tamarind germplasm that has not been characterized over the world. As a result, the current study aims to better understand the morphological variability seen in tamarind genotypes, which would benefit in the identification of elite tamarind genotypes for tree crop improvement in the future.

2. MATERIALS AND METHODS

2.1 Study Material

The ninety-six tamarind genotypes those were distinct and popular were identified from niche areas of thirty districts of Karnataka during 2017-2018 and studied at College of Horticulture, Bengaluru. The niche areas were identified using key informants and random sampling was carried out. The Randomized Complete Block Design (RCBD) experimental design was followed in the study and seventeen morphological traits were observed and recorded (Table 1) in all the genotypes. The observations were recorded for morphological traits as per the method described for the respective traits in the tamarind descriptor [6].

2.2 Statistical Analysis

The data of all the traits were subjected to Fischer's method of analysis of variance which is used for understanding the variations were significant or not. Critical differences were worked out when the 'F' test was significant. The within and between morphological variability was evaluated using Variance Component Analysis [7]. The various components of genetic variation such as the Genotypic coefficient of variation (GCV %), Phenotypic coefficient of variation (PCV %) and Environmental coefficient of variation (ECV %) were analyzed. Heritability in a broad sense (h2 bs) is the ratio of genotypic variance to phenotypic variance was calculated and by following Burton and DeVane [8] and Johnson et al [9] the expected genetic advance (GA) resulting from the selection of 5 % superior individuals was computed. Cluster analysis was conducted on SPSS software to group the genotypes based on the morphological traits variations. The main parameter that guided the joining (tree clustering) process linkage rule was UPGMA and the distance was computed from raw data using Euclidean distance to depict the morphological variations in genotypes.

3. RESULT

The morphological traits from each of 96 tamarind genotypes indicated a considerable amount of variation in all the traits with highly significant difference among the tamarind genotypes. However, the total variability in different characters does not give information on the identification of the characters showing the highest degree of variability. As a result, estimates of GCV and PCV are required for determining the degree of variability in various features in terms of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean (GAM) are presented in Table 2. Leaf length was found to have a wide ranged varying from 3.05 to 5.20 cm. The higher leaf length was found in genotype TAM BEN (U)4 (5.20 cm) and the lower leaf length was found in the genotypes TAM CHM2 (3.05 cm). The variation observed for leaf width ranged from 0.35 to 0.90 cm. The higher leaf width was found in genotype TAM KOL1 (0.90 cm). The number of leaflets ranged from 7.00 to 15.00. A higher number of leaflets (15.00) were found in genotypes TAM_BAG1, TAM_BEN(U)1, TAM_BEN(U)2, TAM_GUL3, TAM_HAS1 and genotype TAM KOL5. All the 96 genotypes of tamarind genotypes showed 0.25 cm length of flower peduncle (Table 1).

The variation observed for pod length ranged from 4.40 to 19.69 cm. The pod width ranged from 2.20 to 8.80 cm. The higher pod length was found in genotype TAM_BEN(U)4 (19.69 cm). The variation observed for pod width ranged from 2.20 to 8.80 cm. The higher pod width was found in genotypes TAM KOL2 (8.80 cm). The variation observed for fruit length ranged from 3.19 to 18.45 cm. The higher fruit length was found in genotype TAM_BEN(U)4 (18.45 cm). The higher fruit width was found in genotype TAM_CHT1 (7.70 cm). The variation observed for fruit weight ranged from 4.27 to 32.45 g. The higher fruit weight was found in genotype TAM HAS2 (32.45 g). The variation exhibited for

curved nature ranged from 1.80 to 10.50. The higher curved nature was found in genotype TAM_HAS1 (10.50). The fiber cord ranged from 5.00 to 3.00. The higher fiber cord (5.00) was found in most of the genotypes. The variation for peel weight ranged from 1.04 to 6.70 g. The higher peel weight was found in genotypes TAM_HAS2 and TAM_HAS3 with 6.70 g (Table 1).

The variation for seed number ranged from 1.80 to 10.00. The higher number of seeds was found in genotype TAM_HAS2 (10.00). The seed size ranged from 2.45 to 5.55 cm. The higher seed size was found in genotype TAM_BID3 (5.55 cm). The variation observed for seed weight ranged from 1.45 to 12.30 g. The higher seed weight was found in genotype TAM CHK4 (12.30 g). The variation observed for pulp weight ranged from 2.10 to 15.00 g. The higher pulp weight was found in genotype TAM HAS1 (15.00 g). The seed/pulp ranged from 0.31 to 1.50. The higher seed/pulp ratio was found in genotype TAM BEL3 (1.50). The variation observed for fruit yield/plant ranged from 49.50 to 298 kg. The higher fruit yield/plant was found in genotype TAM KOL4 (298.50 kg) (Table 1).

4. DISCUSSION

Table 1 indicated that fruit yield/plant, curved nature and seed number expressed high CV%. expressing that the traits had vast differences among all the genotypes studied. Among top five best performing genotypes in terms of yield/plant, and TAM BEN(U)4 GKVK17 genotypes exhibited high yielding with the support of attributing traits such as fruit weight (26.71 and 24.97 g), number of curve nature (9.50 and 10.10), fiber cord (5.00 and 5.00), peel weight (5.25 and 5.41 g), number of seed/pod (9.50 and 9.90), and pulp weight (12.55 and 12.00 g) respectively.

Although, TAM_HAS2 was the sixth top best performing genotype which had high values for pod length (15.80 cm), pod width (8.43 cm), fruit length (14.47 cm), fruit width (7.27 cm), fruit weight (32.45 g), number nature (9.50), fiber cord (5.00), peel weight (6.70 g), number of seed/pod (10.00), seed weight (11.80 g), pulp weight (14.05 g) of which traits attributed to fairly good fruit yield/plant (273 kg). Present study brought out and identified three top best performing tamarind genotypes TAM_KOL4 (298.50 kg/plant), TAM_BEN(U)3 (296.00 kg/plant) and TAM_BEN(U)4 (286.00 kg/plant) expressed higher yield over the check GKVK17 (284.50 kg/plant) but however it was not significant.

SI. No.	Genotypes	Leaf length (cm)	Leaf width (cm)	Numbe r of leaflets	Pod length (cm)	Pod width (cm)	Fruit length (cm)	Fruit width (cm)	Fruit weight (g)	Numbe r of curves	Fiber cord	Peel weight (g)	Numbe r of seed/p od	Seed size (cm)	Seed weight (g)	Pulp weight (g)	Seed/ Pulp Ratio	Fruit yield/pla nt (kg)
1	TAM KOL4	4.20	0.60	11.00	8.90	5.65	7.66	5.57	9.51	3.50	4.00	2.52	3.50	4.55	3.95	6.15	0.64	298.50
2	TAM BEN(U)3	5.15	0.75	14.00	13.16	6.00	12.29	4.92	15.92	7.50	4.00	3.01	4.15	3.90	4.35	9.10	0.48	296.00
3	TAM_BEN(U)4	5.20	0.70	14.00	19.69	7.20	18.45	6.73	26.71	9.50 c	5.00	5.25	9.50	3.95	9.85	12.55	0.78	286.00
4	GKVK17	4.90	0.70	13.00	13.80	6.93	12.67	5.97	24.97	10.10	5.00	5.41	9.90	3.90	6.95	12.00	0.58	284.50
5	TAM_KOL1	4.60	0.90	13.00	16.90	7.48	14.05	6.20	19.60	8.65	5.00	3.85	8.65	3.75	5.65	10.95	0.51	277.00
6	TAM_HAS2	3.70	0.45	9.00	15.80	8.43	14.47	7.27	32.45	9.50	5.00	6.70	10.00	4.10	11.80	14.05	0.84	273.00
7	TAM_CHK1	3.90	0.70	9.00	13.80	6.95	13.00	5.85	23.70	9.75	5.00	4.50	9.50	4.55	9.60	9.25	1.03	270.00
8	TAM_KOL2	4.45	0.65	11.00	19.45	8.80	17.53	7.55	23.25	9.00	4.50	5.64	8.50	4.75	10.10	7.85	1.29	268.50
9	TAM_BEN(U)2	5.00	0.70	14.00	18.20	8.00	17.45	7.10	19.54	8.50	3.50	2.66	5.30	4.00	4.05	10.15	0.40	260.50
10	TAM_HAS3	3.80	0.55	11.00	15.30	7.29	13.94	6.51	26.02	9.80	5.00	6.70	9.80	3.65	9.10	12.05	0.76	258.00
11	TAM_CHA3	4.20	0.70	10.00	10.80	6.25	9.25	5.31	15.55	7.50	5.00	3.30	7.50	3.30	6.80	5.20	1.31	252.00
12	TAM_MAN4	3.85	0.35	9.00	9.65	6.16	8.22	5.34	11.96	4.00	3.50	2.45	4.00	3.85	4.85	6.95	0.69	252.00
13	TAM_KOL5	4.90	0.85	15.00	13.65	6.75	11.95	5.64	14.95	7.00	4.50	3.10	7.00	4.30	4.15	9.35	0.44	249.50
14	TAM_HAS1	4.50	0.85	15.00	14.50	7.62	13.70	6.75	29.85	10.50	5.00	5.43	9.50	3.75	9.95	15.00	0.66	247.50
15	TAM_THM1	3.40	0.45	9.00	10.35	6.06	8.95	4.70	13.60	7.50	5.00	2.68	7.00	4.10	4.25	8.30	0.51	242.50
16	TAM_CHK3	4.90	0.50	11.00	13.45	7.99	12.36	6.17	23.92	9.00	5.00	5.70	9.00	4.95	8.25	11.15	0.74	219.00
17	TAM_CHK4	4.70	0.50	11.00	17.10	7.95	15.28	7.26	26.83	9.50	5.00	5.09	9.50	4.45	12.30	9.35	1.31	216.50
18	TAM_DAV2	3.90	0.50	11.00	11.98	6.21	11.05	5.18	21.29	4.55	5.00	4.48	4.40	3.50	8.75	9.80	0.86	221.50
19	TAM_HAS4	4.10	0.65	11.00	12.85	7.87	11.75	6.67	21.60	7.75	4.00	4.40	7.50	3.67	6.35	12.55	0.51	232.00
20	TAM_MAN3	4.00	0.50	10.00	9.53	6.04	8.85	4.85	14.27	8.60	5.00	3.65	8.50	4.75 b	4.85	7.10	0.68	199.50
Grai	nd Mean	3.99	0.54	10.64	9.82	5.85	8.77	4.88	12.98	5.20	4.13	2.88	5.03	3.94	4.80	6.28	0.80	191.85
CV		4.38	14.33	9.49	6.54	7.64	7.52	8.30	9.24	11.33	9.96	10.30	11.12	4.65	9.62	10.95	10.42	2 16.05
CD	@ 5%	0.28	0.12	1.62	1.02	1.72	1.06	1.65	1.93	1.94	1.66	0.74	0.90	0.92	0.79	1.10	0.83	19.59
SEn	۱±	0.10	0.04	0.58	0.37	0.25	0.38	0.23	0.69	0.34	0.23	0.17	0.32	0.10	0.26	0.39	0.048	3 17.77

Table 1. The mean values for morphological traits among top best performing tamarind genotypes in terms of fruit yield/plant

X1: Leaf length (cm), X2: Leaf width (cm), X3: Number of leaflets, X4: Pod length (cm), X5: Pod width (cm), X6: Fruit length (cm), X7: Fruit width (cm), X8: Fruit weight (g), X9: Number of curves, X10: Fiber cord, X11: Peel weight (g), X12: Number of seed/pod, X13: Seed size (cm), X14: Seed weight (g), X15: Pulp weight (g), X16: Seed/Pulp Ratio, X17: Fruit yield/Plant (kg), PCV (%) = Phenotypic Co-efficient of Variability, GCV (%) = Genotypic Co-efficient of Variability, GC

Traits	Minimum	Maximum	Mean	PCV %)	GCV (%)	Heritability(%)	GA	GAM (%)
X1	3.05	5.20	3.99	13.93	12.22	90.00	1.03	25.86
X2	0.35	0.90	0.54	26.98	22.86	71.00	0.21	39.91
X3	7.00	15.00	10.64	20.45	18.12	78.00	3.52	33.07
X4	4.40	19.69	9.82	31.10	30.41	95.00	6.01	61.24
X5	2.20	8.80	5.85	22.04	19.67	88.00	2.33	39.94
X6	3.15	18.45	8.77	34.24	33.40	95.00	5.88	67.13
Х7	1.45	7.70	4.88	24.90	23.47	88.00	2.22	45.59
X8	4.27	32.45	12.98	46.12	45.19	96.00	11.84	91.20
X9	1.80	10.50	5.20	42.34	40.79	92.00	4.21	80.97
X10	3.00	5.00	4.13	18.48	15.56	70.00	1.11	27.00
X11	1.04	6.70	2.88	43.91	42.69	94.00	2.46	85.49
X12	1.80	10.00	5.03	42.76	41.28	93.00	4.13	82.12
X13	2.45	5.55	3.94	15.14	14.41	90.00	1.11	28.25
X14	1.45	12.30	4.80	48.25	47.28	96.00	4.58	95.45
X15	2.10	15.00	6.28	45.07	43.72	94.00	5.49	87.37
X16	0.31	1.51	0.80	34.98	33.40	91.00	0.529	65.67
X17	49.50	298.50	191.85	34.55	30.60	78.00	17.11	55.83

Table 2. Genetic variation for morphological traits among the different genotypes of the tamarind

X1: Leaf length (cm), X2: Leaf width (cm), X3: Number of leaflets, X4: Pod length (cm), X5: Pod width (cm), X6: Fruit length (cm), X7: Fruit width (cm), X8: Fruit weight (g), X9: Number of curves, X10: Fiber cord, X11: Peel weight (g), X12: Number of seed/pod, X13: Seed size (cm), X14: Seed weight (g), X15: Pulp weight (g), X16: Seed/Pulp Ratio, X17: Fruit yield/plant (kg), PCV (%) = Phenotypic Co-efficient of Variability, GCV (%) = Genotypic Co-efficient of Variability, GA = Genetic Advance, GAM = GA as % mean

The estimates of the phenotypic coefficient of variation were higher than the genotypic coefficient of variation for most of the morphological traits of tamarind. The results indicated the influence of the environment on the expression of the characters. The PCV ranged from 13.93 (leaf length) to 48.25 (seed weight) and GCV ranged from 12.22 (leaf length) to 47.28 (seed weight) among all morphological traits of tamarind. GCV does not compute all of the variation in a population as it is the sum of heritable and non-heritable components and higher heritability estimates indicate that the genotype has a considerable influence on the phenotype of the traits (Figs. 2 & 3, Table 2).

The heritability value ranged from 70 per cent (fiber chord) to 96 per cent (fruit and seed weight). In this study, high heritability was found in every morphological traits of the tamarind. genotypes except fiber cord, leaf width, number of leaflets, fruit yield/plant (moderate). The genetic advance as per cent of mean ranged from 25.86 per cent to 95.45 per cent and the higher value of genetic advance as per cent a mean recorded for all the characters expect leaf length, fiber cord and seed size (low). It might be due to the high range of variation among the genotypes. The seed weight has the highest genetic advance as per cent of mean (95.45 per cent) whereas, the lowest value was recorded in leaf length (25.86 per cent). High heritability estimates coupled with high genetic advance as per cent of mean were observed in all the character except leaf length, fiber cord and seed size. It indicates additive gene action, making selection based on these characteristics more reliable [10].

Wide variation in tamarind genotype is expected with a broad genetic base due to its highly crosspollinating nature. The relative values of PCV and GCV give an idea about the magnitude of variability present in the genetic population. An estimate of GCV is lower than PCV for many traits, which implies the role of the environment in the expression of the traits. In the present investigation, higher estimates of phenotypic and genotypic coefficient of variation were obtained for pod length, fruit length, fruit width, fruit weight, curved nature, peel weight, seed number, seed weight, pulp weight, seed/pulp ratio and yield/plant. It indicates that the environment plays an important role in the expression of the characters and these characters were considered for the selection of outstanding genotypes of tamarind. Selections of genotypes with high heritable characters are best for any tree improvement programme and development of new clones in tamarind. The present finding was in accordance with the finding of Divakara, [11], Patilshekar and Hanamashetti, [12], Singh and Nandhini, [13] and Mayavel, et al., [14-15]. This variation noticed in this present study also concurs with the study by Nyadoi, et al. [16] who reported there was a great diversity among the

tamarind populations collected in the Maasai region in Kenya. Similar studies were reported by Soloviev, et al., 2004; [17,18] Abasse, et al., [19] Fandohan, et al., [4] Bilcke, et al., [20] Dadegnon, et al. [21] Mkwezalamba, et al., [22] Shameer, et al., [23] Okwu, et al., [24] Okello, et al., [25] Mayavel, et al., [14-15]. The observed morphological variations are probably attributed to the influence of agro-ecological zones factors, environmental factors, climate, land use types, and farming systems, a reflection of tamarind adaptation to different conditions showing high genetic and phenotypic differences to be exploited.



Fig. 1. Clustering of 96 tamarind genotypes based on morphological traits relationship (Tocher's method)



Fig. 2. Phenotypic and genotypic coefficient of variability for quantitative traits in tamarind

- X1: Leaf length (cm) X2: Leaf width (cm) X3: Number of leaflets X4: Pod length (cm) X5: Pod width (cm)
- X6: Fruit length (cm) X7: Fruit width (cm) X8: Fruit weight (g) X9: Number of curves X10: Fiber cord Fiber cord
- X11: Peel weight (g) X12: number of seed/pod X13: Seed size (cm) X14: Seed weight (g) X15: Pulp weight (g)

X16: Seed/Pulp Ratio X17: Fruit yield/Plant (kg)



Fig. 3. Heritability and genetic advance as per cent mean for morphological traits in tamarind

X1: Leaf length (cm) X2: Leaf width (cm) X3: Number of leaflets X4: Pod length (cm) X5: Pod width (cm)	X6: Fruit length (cm) X7: Fruit width (cm) X8: Fruit weight (g) X9: Number of curves X10: Fiber cord	X11: Peel weight (g) X12: Number of seed/pod X13: Seed size (cm) X14: Seed weight (g) X15: Pulp weight (g)	X16: Seed/Pulp Ratio X17: Fruit yield/Plant (kg)
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Based on the morphological traits, cluster analysis revealed, that there were a total of 6 clusters in the dendrogram and presented in Fig. 1. The 96 tamarind genotypes were presented in 6 clusters of which the maximum number of genotypes were included in cluster I has 83 numbers of genotypes and the minimum number in cluster II, cluster IV and cluster V having only one genotype. The clustering is majorly grouped genotypes according to the variations which indicate the presence of wide diversity in selected populations hence further exploiting this genotypes will help to conserve variations present in the tamarind the The morphological evaluation populations. results and clustering of tamarind would be useful in tamarind cultivar selection and improvement breedina of programmes. Hybridization between intra-cluster genotypes would further enhance gain in breeding of desirable traits.

5. CONCLUSION

Present study on variations in tamarind morphological traits confirmed that huge factors contribute to the relative amounts of variation observed among genotype, particularly when genotypes have been separated for a long period. Among the top five best performing genotypes in terms of yield, TAM_BEN(U)4 and GKVK17 genotypes supported high yielding with attributing traits such as fruit weight (26.71 and 24.97 g), number of curve nature (9.50 and 10.10), fiber cord (5.00 and 5.00), peel weight (5.25 and 5.41 g), number of seed/pod (9.50 and 9.90), and pulp weight (12.55 and 12.00 g) respectively. Present study brought out and identified three top best performing tamarind genotypes TAM KOL4. TAM BEN(U)3 and TAM_BEN(U)4 expressed higher yield over the check GKVK17 but however it was not significant. The observed variations suggest that different factors affect morphological traits, landuse types such as environmental and climatic factors may be possible due to gene flow/genetic drift of gene for a particular trait. The spontaneous mutation possibly occurred in a particular trait over the years which may be expressed in one geographical area and not in the other may also be counted among the reasons for variation in a particular morphological trait. The best performing genotypes could be further exploited in tree improvement program for selecting the elite desirable genotype.

ACKNOWLEDGEMENT

Research in the laboratory of FB is funded by the Dept. of IT, BT and S&T, and RKVY, Government of Karnataka.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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Peer-review history: The peer review history for this paper can be accessed here: https://www.sdiarticle4.com/review-history/72728