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Research Article

Identification of plus trees through morpho-biochemical characterization in tamarind (*Tamarindus indica* L.)

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Abstract
Morpho-biochemical characterization was conducted to identify superior genotypes (plus trees) of *Tamarindus indica* L. across diverse agro-climatic zones in Palakkad, Kerala. Thirty seedling-origin trees were evaluated for 28 morphological traits and five biochemical parameters. Significant phenotypic variation was observed across all assessed traits, indicating substantial genetic diversity within the population. Correlation analysis revealed strong positive associations between pod weight, pod length, and seed weight per pod and fibre percentage ($p < 0.05$), while spread of corolla exhibited significant correlation with fibre percentage and TSS. Hierarchical cluster analysis categorized the genotypes into four distinct groups, with Cluster I demonstrating superior yield and quality attributes. Five elite genotypes (KTJ 166, KTJ 164, KTJ 162, KTJ 174, and KTJ 165) were identified as plus trees based on comprehensive trait evaluation. KTJ 166 exhibited exceptional pod characteristics, including maximum pod weight (42.17 g), pod length (24.08 cm), seed weight per pod (13.82 g), and seeds per pod (10.13). KTJ 162 demonstrated superior pulp percentage (55.8%) and total antioxidant capacity (55.78 mg AAE/g), while KTJ 48 recorded the highest total soluble solids (85.97°Brix) and total sugar content (41%). These identified elite genotypes represent valuable germplasm for breeding programs, offering significant potential for genetic improvement of yield, nutritional quality, and commercial traits in tamarind.

Keywords: Tamarind, correlation, floral characters, hierarchical clustering, morpho-biochemical characters, pod weight

INTRODUCTION

Tamarind (*Tamarindus indica* L.), a multipurpose species within the Leguminosae (Fabaceae) family and Caesalpinioideae subfamily, is primarily valued for its fruit, consumed both in fresh and processed forms. This resilient tree flourishes across various climatic conditions, including tropical, subtropical, and arid regions, with origin traced back to Madagascar or tropical Africa (Von Maydell, 1986). It is now widely cultivated in many countries, including India, Myanmar, Bangladesh, Malaysia, Sri Lanka, Thailand, and several African, Central American, and South American countries. India is the world's largest producer of tamarind with an estimated production of 300,000 tons annually (Reddy *et al.*, 2024). In India, tamarind is predominantly cultivated in Karnataka, Kerala, Madhya Pradesh, Bihar, Chhattisgarh, Andhra Pradesh, and Tamil Nadu.

Kerala offers a significant contribution to India's tamarind production with 9,434 hectares under cultivation and an annual production of 30,471 MT (Spice Board of India, 2023). In Kerala, there are some recognized primitive cultivars, such as the long-fruited, extremely sour variety known as "valanpuli," and sweet varieties like "madhurapuli" and "thenpuli." Despite not being a significant commercial crop in Kerala, the need for tamarind's fruits, seeds, timber and leaves makes it an essential source of revenue for rural populations. Exhibiting significant genetic diversity and cultural relevance in Kerala, tamarind is recognized for its antibacterial, antifungal, and antioxidant qualities (Graf *et al*., 2016), as well as its use as a building material, fuel, and fodder (Tapia *et al*., 2012). Its acidic pulp is widely used as a souring agent, and processed products like jams, squashes, blended drinks, and ready-to-serve (RTS) beverages having significant global market potential are also produced. The pulp's composition and nutritional quality have been extensively studied (Lumen *et al*., 1986; Mateo *et al*., 1992). Additionally, products derived from tamarind seeds, such as seed gum, polysaccharides, seed powder, tamarind kernel powder (TKP), kernel oil, and decorticated seed meal, find applications in diverse industries (Kumar and Bhattacharya, 2008; Vijayalakshmi *et al*., 2021).

Although tamarind is one of the oldest domesticated crops, little is known about its genetic characteristics and population biology to enhance the conservation and utilization of this species (Gunasena and Hughes, 2000). Tamarind has a relatively long generation time and reproduces primarily by outcrossing, so any conventional breeding approaches would require considerable investment in time and money. Since valuable germplasm is slowly vanishing due to urbanization, it is high time to conserve all rare tamarind accessions available in the state. *In-situ* characterization of tamarind genotypes in their natural habitats is crucial for capturing the full range of genetic diversity and understanding the species adaptability to local environments. Determination of genetic variation is important for the development of a high yielding variety (Kumar *et al*., 2015). Given limited information on genetic improvement, this study focused on the identification of plus trees of tamarind based on morpho-biochemical characterization. Morphological evaluation ensures the identification of trees with desirable physical attributes, while biochemical analysis highlights nutritional quality and commercial value. By integrating these criteria, genetically superior tamarind trees can be identified, which can serve as valuable resources for breeding programs and sustainable cultivation practices.

MATERIALS AND METHODS

Palakkad, located at the central region of Kerala, is known for its unique geographical and climatic features, making it an ideal region for studying the genetic diversity of tamarind. The tamarind trees were found scattered from homestead garden in semi wild state to forest areas in wild state. During the fruiting seasons of 2022–2023, a survey of tamarind trees was carried out in order to identify the elite germplasm within the natural population. The study sites are spread across the district, with approximate coordinates as follows: Thenkurissi (10.6574° N, 76.6278° E), Alathur (10.6681° N, 76.4602° E), Nellipathy (10.9456° N, 76.7435° E), and Attappady (11.1155° N, 76.6517° E). These locations were chosen for their diverse agro-climatic conditions, which are representative of the broader environmental variability within the district. Thirty regular bearing tamarind trees of seedling origin surveyed from these locations of Palakkad district formed the material for the study. These genotypes were consistent in flowering and fruiting, with flowering initiated between March and April, and fruits maturing for harvest from April to May. Morphological observations were recorded for 11 qualitative and 17 quantitative characters (PPVFRA, 2017; Singh *et al.,* 2010) and evaluated in completely randomized block design with three replications at the Department of Plant Breeding and Genetics, College of Agriculture, Kerala Agricultural University. All the traits were recorded over two consecutive years (2023 and 2024).

Observations on floral characters were made during the peak flowering period. Thirty healthy panicles were randomly selected from each tree and length of panicle was recorded. Other floral characters like spread of corolla, length and width of petal and sepal, length of filament, ovary and pistil were measured in 30 freshly opened flowers using digital vernier calliper. In addition to this, the colour of new flush, bract of immature bud, buds, sepal, corolla and filaments, number of stamens and staminodes were also recorded.

During the fruiting season, 30 matured and fully ripened pods were harvested using a random sampling method from all four crown directions of each tree to assess the pod and seed characters. The data on pod morphology *viz.,* pod weight, pod colour, pulp colour, fibre percentage, pod length was recorded. The pulp separated from the pods was weighed, and the average pulp weight per pod was recorded as pulp percentage. Similarly, seeds were separated from the pulp, weighed, and their average weight per pod was documented.

The collected genotypes were evaluated for five biochemical parameters in three replications using standard procedures: total soluble solids (TSS), titratable acidity, vitamin C, total antioxidant capacity, total sugar content. TSS was estimated following the FSSAI (2016) protocol. The vitamin C content and titratable acidity of the fruits of tamarind genotypes were estimated by the method suggested by Sadasivam and Manickam (1996). The total antioxidant capacity of the pulp, expressed in mg ascorbic acid equivalents (AAE) per gram, was measured using the phosphomolybdate method proposed by Prieto *et al*. (1999). Additionally, the total sugar content was quantified using the Lane and Eynon titration method.

Analysis of variance was done for 20 quantitative characters including 15 morphological and five biochemical characters using the R based statistical

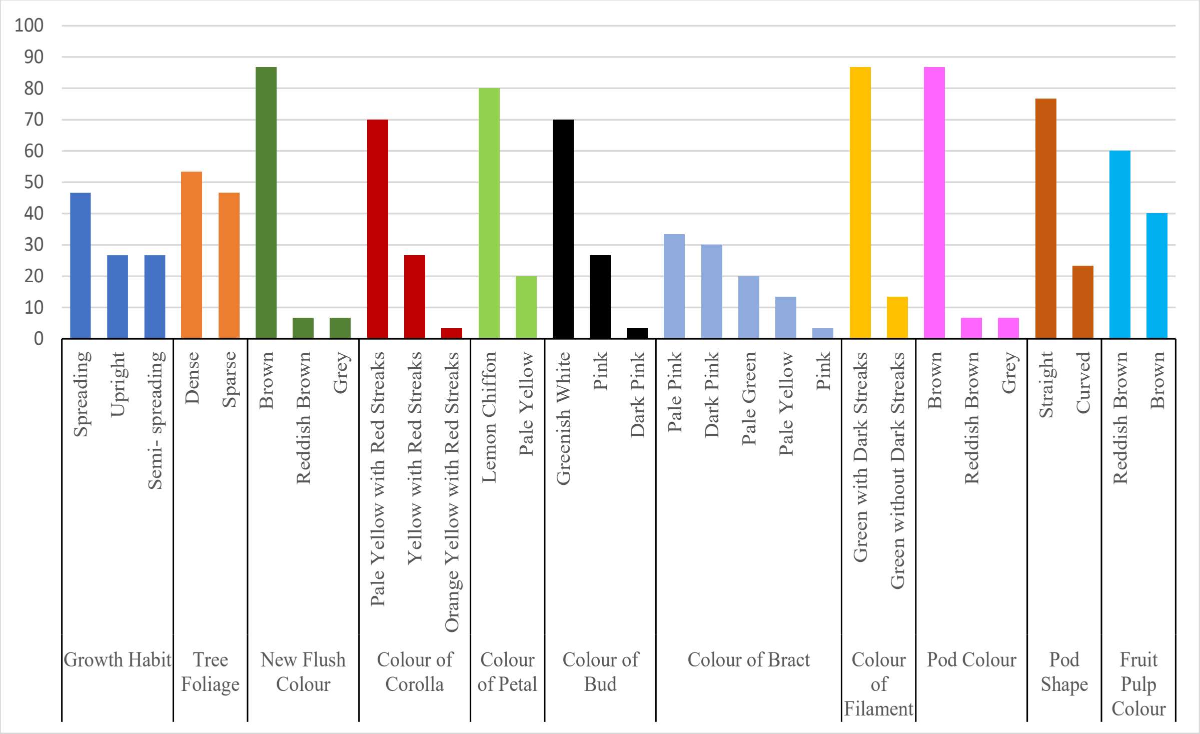


Fig. 1. Variability in qualitative characters of studied genotypes of tamarind

software GRAPES version 1.14.02 (Gopinath, 2020). Descriptive statistics of the studied characteristics of tamarind genotypes were also calculated. Using the ward linkage method in the R program, hierarchical clustering was carried out for the characters with significant critical differences. Dendrogram depicting grouping of genotypes into various clusters at different similarity levels was also drawn using the ‘ggplot2’ and ‘ggdendro’ packages**.** The Pearson’s correlation coefficient was also calculated using the R based statistical software GRAPES version 1.14.02 (Gopinath, 2020) to determine the relationship among morphological and biochemical characters.

RESULTS AND DISCUSSION

Significant phenotypic variability was observed among the tamarind genotypes for all the qualitative traits studied (**Fig. 1**). The growth habit of the experimental population was categorized into three distinct types: spreading (46.67%), semi-spreading (26.66%), and upright (26.67%). Growth habit is a critical morphological trait influencing spatial requirements, with upright growth habits being particularly advantageous for high-density planting systems due to their efficient space utilization. The tamarind accessions exhibited pronounced variation in new flush colouration, an important phenotypic characteristic that can indicate genetic diversity among the genotypes. The new flush colour ranged from green to reddish-green and reddish-brown. Among the evaluated accessions, green flush was the most common, observed in 70.59% of the trees. Notably, accessions KTJ 48 and KTJ 173, displayed a distinctive reddish-brown flush, while KTJ 60 was the sole accession with reddish-green flush (**Fig. 2**). Additionally, foliage density also varied considerably, with dense foliage being the predominant type (53.34%) and sparse foliage observed in 46.66% of the trees. These findings align with earlier reports by Kumar *et al.* (2023), who documented similar variability in foliage density of tamarinds in western parts of Maharashtra . Consistent patterns of variation in new flush colour, foliage density and growth habit have also been reported in tamarind populations from Kerala by Shankarprasad *et al*. (2024), further corroborating the observed phenotypic diversity in the present study.

Variability in floral qualitative traits, which is frequently documented in temperate trees, is relatively less common in tropical species (Singh *et al.,* 2010). Such phenotypic diversity in floral characteristics can serve as valuable morphological markers for tree identification and progeny testing. In the present study, significant variability was observed in bract coloration among the evaluated tamarind accessions. Immature buds exhibited bract colours ranging from pale pink (33.33% of accessions) to dark pink (30% of accessions). The colour of corolla also demonstrated considerable diversity, with 70% of the accessions displaying pale yellow petals with red streaks, followed by 23.33% exhibiting yellow petals with red streaks. Genotypes KTJ 162 and KTJ 166 were distinguished by their unique orange-yellow petals with red streaks (**Fig. 3**). Bud coloration was predominantly greenish-

Fig. 2. Observed variability in new flush colour of studied tamarind genotypes (Green, reddish green and reddish brown)

white (66.67% of accessions), while pink-coloured buds were observed in 30% of the genotypes. Only KTJ 48 exhibited dark pink buds, further highlighting the extent of variability. Similar variability in bud and bract colouration in tamarind have been reported by Shankarprasad *et al*. (2024). Sepal coloration was primarily lemon chiffon (76.67% of accessions), with the remaining accessions displaying pale yellow sepals. Majority of genotypes (85.19%) exhibited green filaments with dark streaks. The extensive range of coloration observed in reproductive organs underscores their significant breeding potential. These traits can be effectively utilized as morphological markers in progeny testing programs and may confer the added advantage of enhancing fruit set by attracting and increasing pollinator activity, as previously demonstrated by Pooja *et al.* (2022).

Significant variability was observed in pod morphology, with distinct pod shapes from straight to curved,occurring across different canopy regions within the individual genotypes (**Fig. 4**). Consequently, the predominant fruit shape for each accession was systematically recorded, consistent with the methodology described by Algabal *et al.* (2012). Majority of genotypes predominantly produced straight pods, while curved pods were observed in seven genotypes, highlighting notable morphological diversity. Pulp coloration also exhibited variability, ranging from light brown to dark brown, with 12 accessions displaying brown pulp and the remaining 18 accessions characterized by reddish-brown pulp. Reddish-brown pulp is often associated with consumer preferences, as it is frequently perceived as an indicator of freshness and superior quality. With respect to pod coloration, brown pods were the most prevalent, observed in 85.71% of the accessions. However, two accessions, KTJ 60 and KTJ 66, exhibited distinctive reddish-brown pods, while two others, KTJ 84 and KTJ 172, were characterized by grey-coloured pods. These variations in pod shape, pulp colour, and pod coloration underscore the phenotypic diversity within the studied tamarind germplasm, providing valuable insights for breeding programs and market-oriented selection strategies.

Fig. 3. Observed variability in corolla colour of studied genotypes of tamarind (pale yellow with red streaks, yellow with red streaks, and orange yellow with red streaks)

Fig. 4. Observed variability in pod morphology of studied genotypes of tamarind

The genetic analysis conducted on tamarind genotypes based on quantitative traits highlighted substantial variability in different morphological and biochemical traits, demonstrating considerable genetic diversity within the experimental material. Significant differences were observed in the physical attributes of tamarind fruits and flowers, with pronounced variation across all evaluated traits. Descriptive statistics, including mean, range, and variance, for the 20 quantitative traits encompassing 15 morphological and 5 biochemical characteristics are summarized in **Table 1**. Notably, the number of stamens and staminodes remained consistent across all genotypes, with three stamens and four staminodes observed in each accession. The coefficient of variation (CV) was the highest for seed weight per pod (22.52%), followed by panicle length (20.96%), pod weight (19.87%), fibre percentage (19.56%), number of seeds per pod (18.48 %), ovary length (14.54 %), pod length (11.15%), corolla spread (11.09%), and petal width (10.46%). Among biochemical traits, ascorbic acid content exhibited the highest variability (CV = 16.02%), followed by total soluble solids (TSS) (CV = 9.84%), suggesting considerable heterogeneity in these traits. Floral quantitative traits, such as sepal length and width, filament length, and pistil length, along with biochemical parameters including total antioxidant capacity, titratable acidity, and total sugar content, demonstrated moderate range of variability. (**Table 1**)

Among floral traits, significant differences in panicle length were observed across the studied genotypes. All accessions, except KTJ 170 (11.43 cm), exhibited high panicle length (>12 cm) (PPVFRA, 2017). KTJ 162 exhibited the longest panicle length (22.83 cm),

Table 1. Descriptive statistics of morpho-biochemical characters of tamarind genotypes

S. No.	Characters	Mean	Range	SD	SE	CV(%)
1	Pod weight (g)	18.49	6.33 - 42.17	3.67	2.12	19.87
2	Pod length (cm)	13.13	6.93 - 24.08	1.46	0.85	11.15
3	Pulp percentage (%)	42.48	26.23 - 55.80	2.15	1.24	5.06
4	Fibre percentage (%)	3.33	1.09 - 5.91	0.65	0.38	19.56
5	Seed weight per pod (g)	5.43	1.76 - 13.82	1.22	0.71	22.52
6	Number of seeds per pod	5.49	2.40 - 10.13	1.01	0.59	18.48
7	Length of panicle (cm)	16.28	11.43 - 22.83	3.41	1.97	20.96
8	Corolla spread (cm)	2.76	2.28 - 3.40	0.31	0.18	11.09
9	Length of petal (cm)	1.47	1.26 - 1.58	0.08	0.04	5.25
10	Width of petal (cm)	0.63	0.54 - 0.70	0.06	0.04	10.46
11	Length of filament (cm)	1.45	1.33 - 1.55	0.08	0.05	5.51
12	Length of sepal (cm)	1.34	1.14 - 1.51	0.10	0.06	7.49
13	Width of sepal (cm)	0.49	0.45 - 0.53	0.03	0.02	5.27
14	Length of ovary (cm)	0.85	0.72 - 1.17	0.12	0.07	14.54
15	Length of pistil (cm)	1.61	1.48 - 1.77	0.04	0.03	2.83
16	Total soluble solids (Brix)	66.35	46.35-85.97	6.53	3.77	9.84
17	Titratable acidity (%)	10.33	7.59 - 13.27	0.80	0.46	7.71
18	Total sugar content (%)	23.78	13.96 - 41.00	0.96	0.55	4.03
19	Total antioxidant capacity (mg AAE/g)	42.21	26.50 - 58.36	3.32	1.92	7.87
20	Ascorbic acid content (mg/g)	12.77	5.12 - 20.93	2.04	1.18	16.02

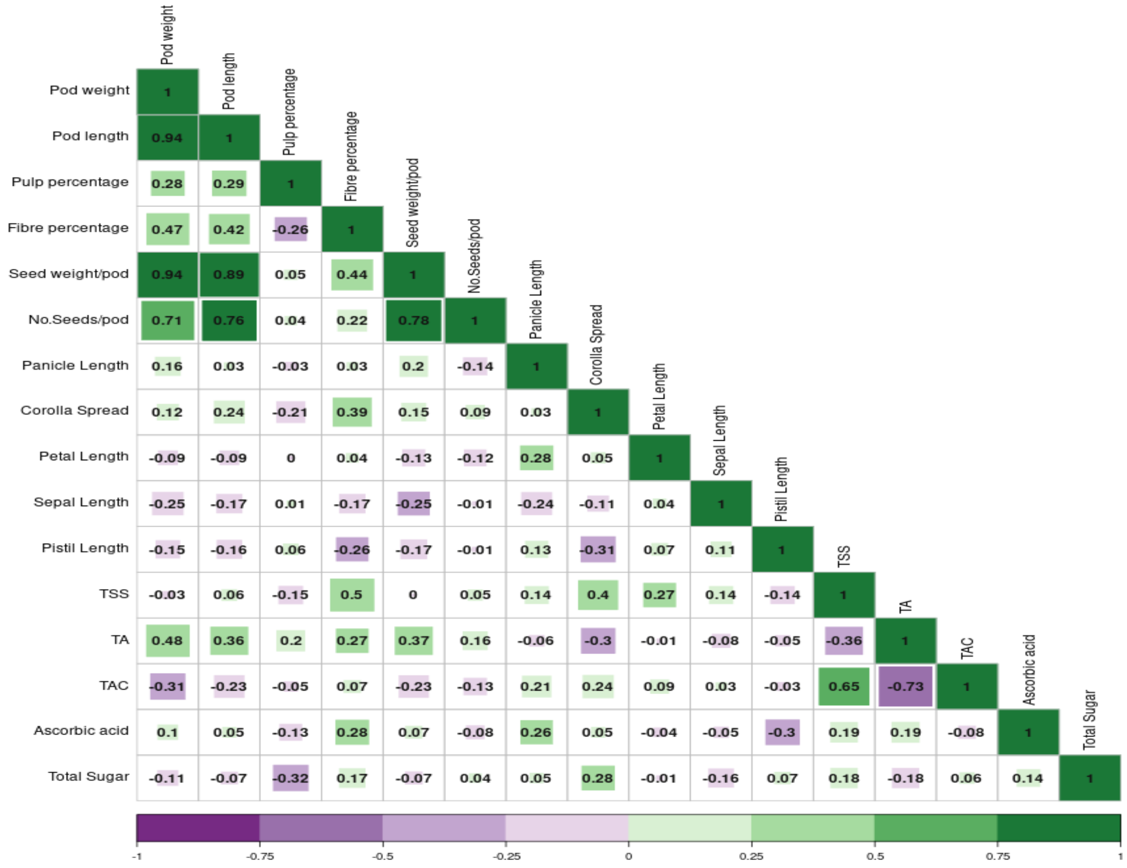
followed by KTJ 84 (22.47 cm) and KTJ 66. Traits like corolla spread (CV = 11.09%), petal width (10.46%), sepal length (7.49%) and ovary length (14.54%) recorded considerable variability. Among the flower traits, petal length, sepal width and filament length had less variability (CV = 5.25–5.51%), the least being the length of pistil (CV = 2.83%). The variations in metric traits of flowers were genetically controlled and varied from genotype to genotype due to its highly cross-pollinated nature (Singh *et al*., 2010). Similar findings regarding variability in floral and fruit traits in tamarind have been reported by Khadivi *et al.* (2024) and Shankarprasad *et al*. (2024).

Higher fruit weight and pulp recovery are desirable characteristics in tamarind, particularly for processing purposes like pulp extraction. In the present investigation, KTJ 166 and KTJ 164 recorded the highest pod weights of 42.17 g and 41.78 g, respectively, whereas KTJ 48 and KTJ 175 exhibited the lowest pod weights of 6.33 g and 6.34 g. These findings underscore the genetic variability influencing pod weight, suggesting that selective breeding could target specific genotypes to produce larger, more commercially valuable pods. Length of pod also demonstrated a wide range, varying from 6.93 cm to 24.08 cm, further illustrating the genetic diversity in pod size (**Table 2**). Genotypes KTJ 166 (24.08 cm) and KTJ 164 (22.47 cm) had the longest pods, while KTJ 175 (6.93 cm) and KTJ 66 (7.52 cm) recorded the shortest length, aligning with the observed trends in pod weight (**Fig 3**). Mayavel *et al*. (2024) reported significant genetic variation in pod weight, with a phenotypic coefficient of variation (PCV) of 24.41% and a genotypic coefficient of variation (GCV) of 24.23%, alongside high heritability (98.58%). Similarly, pod length exhibited high genetic variability (PCV = 25.70%, GCV = 25.53%) and strong heritability (98.61%), indicating a strong relationship between genotype and pod dimensions, providing insights that could guide breeding strategies aimed at enhancing pod size traits in tamarind. The highest pulp percentage was reported in KTJ 162 (55.8%) and the lowest in KTJ 51 (26.23%). The variation in pulp percentage per pod can be directly attributed to differences in pod dimensions, including length, width, thickness, and pulp content (Pooja *et al*., 2022).

The genetic makeup of a tree plays a significant role in determining seed shape and the number of seeds per fruit, both of which are key factors influencing fruit shape (Kidaha *et al*., 2019). The highest seed weight (13.82 g) and number of seeds per pod (10.13) were recorded in the accession KTJ 166, whereas KTJ 168 exhibited the lowest seed weight (1.76 g), and KTJ 175 had the minimum number of seeds per pod (2.4). The accession KTJ 166 exhibited the highest fiber percentage per pod (5.91%), whereas KTJ 88 showed the lowest fibre percentage (1.09%). Variations in fibre weight among genotypes are likely due to variations in the development rate of vascular tissues within the fruits (Pooja *et al*., 2022). Similarly, differences in seed weight are associated with the number and size of seeds, whereas variations in seed number can be linked to pod length and ovule fertility. Additionally, variations in pod size and the number of seeds per fruit among tamarind trees have been strongly influenced by factors such as cross-pollination, fruit abortion, and resource availability, as previously reported by Diallo *et al*. (2008). Variations in these traits among tamarind genotypes have previously been documented in the Palakkad region (Menon *et al*., 2023). Raut *et al*. 2022 reported similar variability in pod weights, attributing differences to factors such as the number of seeds per fruit, unit seed weight, pulp content, and shell weight—all of which are highly variable traits among trees. Variability in pod-related quantitative traits, including pod length, girth, fruit weight, fibre weight, seed weight, pulp content, and seed content, has also been documented by Kidaha *et al*. (2019), Khadivi *et al.* (2024), Shankarprasad *et al*. (2024) and Mayavel *et al*. (2024).

The biochemical parameters evaluated, exhibited significant variation among the studied genotypes (**Table 1**). TSS values ranged from 52.10 °Brix in KTJ 88 to 86.71°Brix in KTJ 51. Titratable acidity varied between a minimum of 8.65% in KTJ 48 and a maximum of 13.95% in KTJ 59. The differences observed in titratable acidity might be due to variation in sugar content of the pulp, which is inherited property of genotype as reported by Pooja *et al*. (2022). Total sugar content rangedwidely across genotypes, from 13.96% in KTJ 57 to 40.52% in KTJ 72. Vitamin C (ascorbic acid) content also showed substantial variation, with the highest level of 20.93 mg/100 g recorded in KTJ 44, KTJ 51, KTJ 86, and KTJ 172, while the lowest value of 5.12 mg/100 g was observed in KTJ 169. This wide range in chemical traits is likely attributed to heterozygosity, as many cultivated tamarind forms have traditionally been propagated through seeds. Comparable findings for total soluble solids, titratable acidity, ascorbic acid content, total acidity, and total sugar have also been reported by Khadivi *et al.* (2024), Shankarprasad *et al*. (2024), Chaturvedi *et al.* (2024) and Mayavel *et al.* (2024), further supporting the observed genetic variability in these biochemical traits.

Correlation analysis provided valuable insights into the relationships among traits, offering guidance for improving yield and other characteristics (**Fig. 5**). Pod weight, a crucial determinant of yield, showed a strong positive correlation with pod length (0.94) and seed weight per pod (0.94), suggesting that larger pods are generally associated with heavier seeds. Furthermore, pod weight exhibited a moderate positive correlation with fibre percentage (0.47), indicating its potential role in influencing pod structure. These findings are consistent with the observations of Pooja *et al*. (2022), Raut *et al.* (2022), Chaturvedi *et al.* (2024) and Khadivi *et al.* (2024), who observed similar positive relationship between pod weight and pulp percentage, seed weight and number of seeds. Pulp percentage was not significantly correlated with most pod traits but showed a weak negative



	Pod weight	Pod length	Pulp percentage	Fibre percentage	Seed weight/pod	No.Seeds/pod	Panicle Length	Corolla Spread	Petal Length	Sepal Length	Pistil Length	TSS	TA	TAC	Ascorbic acid	Total Sugar
Pod weight	1															
Pod length	0.94	1														
Pulp percentage	0.28	0.29	1													
Fibre percentage	0.47	0.42	-0.26	1												
Seed weight/pod	0.94	0.89	0.05	0.44	1											
No.Seeds/pod	0.71	0.76	0.04	0.22	0.78	1										
Panicle Length	0.16	0.03	-0.03	0.03	0.2	-0.14	1									
Corolla Spread	0.12	0.24	-0.21	0.39	0.15	0.09	0.03	1								
Petal Length	-0.09	-0.09	0	0.04	-0.13	-0.12	0.28	0.05	1							
Sepal Length	-0.25	-0.17	0.01	-0.17	-0.25	-0.01	-0.24	-0.11	0.04	1						
Pistil Length	-0.15	-0.16	0.06	-0.26	-0.17	-0.01	0.13	-0.31	0.07	0.11	1					
TSS	-0.03	0.06	-0.15	0.5	0	0.05	0.14	0.4	0.27	0.14	-0.14	1				
TA	0.48	0.36	0.2	0.27	0.37	0.16	-0.06	-0.3	-0.01	-0.08	-0.05	-0.36	1			
TAC	-0.31	-0.23	-0.05	0.07	-0.23	-0.13	0.21	0.24	0.09	0.03	-0.03	0.65	-0.73	1		
Ascorbic acid	0.1	0.05	-0.13	0.28	0.07	-0.08	0.26	0.05	-0.04	-0.05	-0.3	0.19	0.19	-0.08	1	
Total Sugar	-0.11	-0.07	-0.32	0.17	-0.07	0.04	0.05	0.28	-0.01	-0.16	0.07	0.18	-0.18	0.06	0.14	1

Fig. 5. Correlation coefficients among morpho-biochemical characters of tamarind genotypes. (TSS-Total soluble solids, TA-Titratable acidity, TAC-Total antioxidant capacity)

association with fibre percentage (−0.26), suggesting that an increase in fibre content may reduce pulp content (Divakara *et al*., 2012). Fiber percentage, on the other hand, exhibited a moderate positive correlation with pod weight (0.47) and TSS (0.49). According to the findings of Mayavel *et al.* (2024), significant positive correlations were observed between yield and several key fruit quality traits, including fruit weight, pulp weight, seed weight per pod, ascorbic acid content, and total sugar content. These results suggest that selective breeding or agronomic interventions targeting these traits could potentially enhance overall crop productivity. The strong associations underscore the importance of these parameters as potential selection criteria in yield improvement programs. Most floral traits, such as panicle length, exhibited weak correlations with pod and seed traits, suggesting that their direct impact on pod yield and quality is minimal. However, these traits may indirectly influence productivity by improving pollination efficiency. Corolla spread showed a moderate positive correlation with fibre percentage (0.386) and TSS (0.404), suggesting that floral traits may have an indirect influence on pod quality. Pistil length did not exhibit significant correlations with major pod traits but showed a weak negative association with ascorbic acid content (−0.297).

Total soluble solids (TSS) showed a strong positive correlation with total antioxidant capacity (TAC) (0.653), suggesting that tamarind accessions with higher sugar content also possess higher antioxidant properties. However, TSS exhibited a negative correlation with titratable acidity (TA) (−0.359), implying an inverse relationship between sweetness and acidity (Raut *et al*., 2022). Titratable acidity (TA) was significantly and negatively correlated with TAC (−0.735), indicating that highly acidic accessions tend to have lower antioxidant capacity.

The hierarchical cluster analysis was performed using the 15 characters like pod weight, pod length, pulp percentage, fibre percentage, seed weight per pod, number of seeds per pod, panicle length, spread of corolla, length of petal, length of sepal, TSS, titratable acidity, total anti-oxidant capacity, ascorbic acid content and total sugar content which showed significant critical differences among the genotypes. The dendrogram (**Fig. 6**) grouped the 30 genotypes into four clusters (**Table 2**). The membership profile recognized cluster III as the largest one with fourteen accessions followed by cluster IV (9), while the cluster I and II are the smallest with three and four accessions respectively. Cluster I emerged as the most superior group having higher values for all yield-contributing traits like pod weight (34.97–42.17 g), pod length (17.66–24.08 cm), and seed weight per pod (9.68–13.82 g), indicating superior pod size and seed yield. These accessions also exhibited moderate pulp percentage (41.02–50.92%) and fibre percentage (2.89–5.91%). Notably, they displayed the highest number of seeds per pod (7.16–10.13) and the longest panicles (14.77–22.47 cm). Biochemically, this cluster included genotypes having total soluble solids ranged from 51.96–75.28°Brix, total antioxidant capacity from 26.5 to 45.94 mg AAE/g), and ascorbic acid content between 10–18.14 mg/g. These accessions are potentially suitable for commercial cultivation due to their large pod size and high seed yield. Cluster II included the accessions with highest TSS (73.37–85.97 Brix) and total sugar content (25.38–41.0%), suggesting sweetness and potential for use in food processing. However, they exhibited the lowest pod weight (6.33–15.43 g) and pod length (10.04–12.41 cm), along with reduced seed weight per pod (2.15–5.33 g) and fewer seeds per pod (3.2–6.76). Despite these limitations, they showed high total antioxidant capacity (43.75–58.36 mg AAE/g) and ascorbic acid content (10.47–20.93 mg/g), making them valuable for nutraceutical applications. Rao and Mathew (2012) demonstrated that tamarind accessions with high antioxidant activity are promising for nutraceutical applications, particularly in combating oxidative stress-related diseases. The largest cluster (cluster III), representing nearly half of the accessions, displayed intermediate values for most of the traits, including pod weight (13.84–27.87 g), pod length (10.93–17.16 cm), and seed weight per pod (3.22–7.99 g). The pulp percentage (35.91–55.8%) and fibre percentage (1.95–5.81%) were also moderate. This finding is consistent with the work of Diallo *et al*. (2008), who reported that intermediate-value clusters often serve as a rich genetic reservoir for breeding programs. Biochemically, these accessions showed a wide range of total soluble solids (57.39–85.15 Brix) and total antioxidant capacity (35.18–55.78 mg AAE/g), with variable ascorbic acid content (5.12–20.93 mg/g). The diversity within this cluster suggests its potential for selective breeding to improve specific traits. Chaturvedi *et al.* (2024) also emphasized the importance of such diverse clusters in developing improved tamarind varieties with tailored characteristics for different end uses. Accessions in the cluster IV exhibited the lowest pod weight (6.34–25.01 g) and pod length (6.93–14.67 cm), along with reduced seed weight per pod (1.76–7.35 g) and fewer seeds per pod (2.4–6.17). However, they displayed moderate pulp percentage (36.28–46.14%) and the lowest fibre percentage (1.09–5.51%), indicating relatively higher pulp yield. Biochemically, they showed the lowest total soluble solids (46.35–72.7 Brix) but a wide range of total antioxidant capacity (27.21–50.31 mg AAE/g) and ascorbic acid content (6.98–18.61 mg/g). These accessions may be suitable for pulp extraction and antioxidant-rich product development.

This clustering pattern can aid in selecting parental crosses and identifying cross combinations that are likely to produce the greatest variability for different traits. Similar findings were reported by Khadivi *et al.* (2024) and Mayavel *et al*. (2024) and demonstrated that hierarchical clustering based on morphological and biochemical traits is an effective tool for identifying diverse parental combinations in tamarind, emphasizing the importance

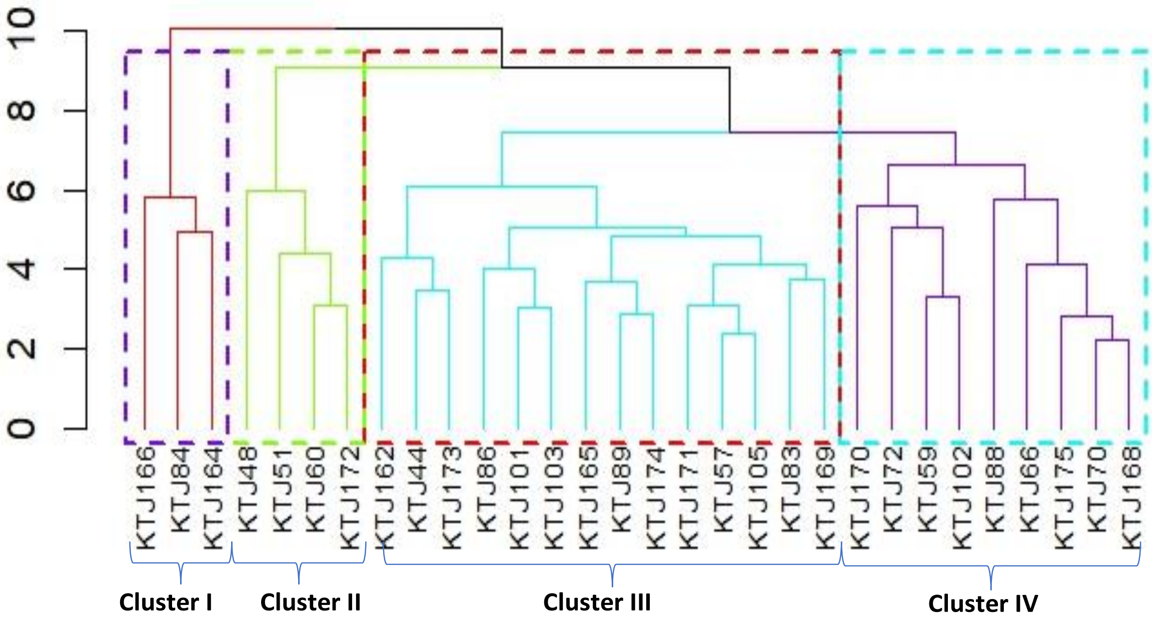


Fig. 6. Dendrogram representing hierarchical clustering of tamarind accessions based on morpho-biochemical characters

Table 2. Cluster-wise summary of the selected tamarind accessions

Characters	Cluster 1	Cluster 2	Cluster 3	Cluster 4
No. of accessions	3	4	14	9
Pod weight (g)	34.97-42.17	6.33-15.43	13.84-27.87	6.34-25.01
Pod length (cm)	17.66-24.08	10.04-12.41	10.93-17.16	6.93-14.67
Pulp percentage (%)	41.02-50.92	26.23-37.98	35.91-55.8	36.28-46.14
Fibre percentage (%)	2.89-5.91	3.16-5.27	1.95-5.81	1.09-5.51
Seed weight per pod (g)	9.68-13.82	2.15-5.33	3.22-7.99	1.76-7.35
Number of Seeds	7.16-10.13	3.2-6.76	2.93-8.53	2.4-6.17
Length of panicle (cm)	14.77-22.47	14.13-19.4	12.7-22.83	11.43-21.77
Spread of corolla (cm)	2.9-3.13	2.78-3.4	2.28-3.03	2.45-2.87
Length of petal (cm)	1.37-1.48	1.45-1.54	1.37-1.58	1.26-1.58
Length of sepal (cm)	1.14-1.44	1.17-1.5	1.21-1.47	1.17-1.51
Total soluble solids (Brix)	51.96-75.28	73.37-85.97	57.39-85.15	46.35-72.7
Titratable acidity (%)	10.34-13.07	7.59-10.49	9.18-11.1	8.2-13.27
Total antioxidant capacity (mg AAE/g)	26.5-45.94	43.75-58.36	35.18-55.78	27.21-50.31
Ascorbic acid content (mg/g)	10-18.14	10.47-20.93	5.12-20.93	6.98-18.61
Total sugar content (%)	23.34-26.53	25.38-41.0	13.96-31.45	14.53-40.52

of integrating phenotypic and biochemical data to develop improved tamarind varieties with enhanced yield, quality, and nutraceutical properties. The numerical characteristics that defined the best values for each cluster are presented as **Table 2**.

Plus trees were identified based on the yield and quality traits like pod weight, pod length, pulp percentage, total sugar, titratable acidity, antioxidant-capacity and ascorbic acid content.

Accession KTJ 166 emerged as the most promising candidate, excelling across multiple traits. It recorded the highest pod weight (42.17 g), seed weight per pod (13.82g), number of seeds per pod (10.13) and pod length (24.08 cm), along with an impressive pulp percentage of 41.02%, total antioxidant capacity of 45.94 mg AAE/g, and total sugar content of 26.53%. This combination of high yield and superior biochemical quality makes KTJ166 an excellent choice for both fresh consumption and processing.

KTJ164 exhibited outstanding performance in pod weight (41.78 g), pod length (22.47 cm), and seed weight per pod (10.21 g) and highest pulp percentage (50.92%). It also recorded high values for TSS (62.64 °Brix), and anti-oxidant capacity (26.50 mg/g). Additionally, it showed a balanced titratable acidity (13.07%) and a high total sugar content (24.77%), making it a promising candidate for applications that require both high productivity and antioxidant-rich profiles. The accession KTJ 174 exhibited significant potential, with pod weight of 26.90 g, pod length of 17.16 cm, seed weight per pod of 7.34 g and pulp percentage of 48.32%. Its high antioxidant value (47.16 mg/g) and TSS (77.27 °Brix) and total sugar content of 24.93% makes it an ideal candidate for producing value-added products with enhanced antioxidant properties. KTJ162 emerged as a promising accession based on its performance across multiple traits. It exhibited a high pod weight of 17.44 g and a pod length of 10.93 cm, indicating good yield potential as well as highest panicle length of 22.83cm. It showed the highest pulp percentage of 55.80% and antioxidant capacity of 55.78 mg/g as well as a high TSS value of 85.15°Brix suggesting excellent fruit quality and superiority in sweetness and flavor for processing or fresh consumption. KTJ 165 rounded out the top-performing genotypes with a pod weight of 27.87 g, a pulp percentage of 43.06%, and a total antioxidant capacity of 27.90 mg AAE/g. Additionally, it recorded high TSS value (72.38 °Brix), anti-oxidant capacity (46.79 mg/g), and total sugar content (15.16%), positioning it as a strong contender for premium-quality tamarind-based products.

Four genotypes exhibiting notable total sugar content were identified: KTJ 48 (41%), KTJ 60 (36.3%), KTJ 72 (40.52%), and KTJ 172 (36.37%). These genotypes also demonstrated low to moderate titratable acidity, with values of 7.59% (KTJ 48), 7.76% (KTJ 60), 9.18% (KTJ 72), and 9.80% (KTJ 172), as per PPVFRA (2017). The combination of high sugar content and low to moderate acidity underscores their potential suitability for applications where sweetness is a key quality attribute.

Based on comprehensive evaluation of yield and quality traits, five genotypes—KTJ 162, KTJ 164, KTJ 165, KTJ 166, and KTJ 174—were identified as the plus trees These promising trees hold significant potential for clonal propagation, commercial cultivation, or as valuable genetic resources for future hybridization programs aimed at tamarind improvement. (Mayavel *et al*., 2024). The plus trees identified will be observed for both yield and quality parameters for few more years and will be clonally raised and tested before using in breeding programmes.

The tamarind populations in the southern Kerala region exhibited remarkable diversity in morpho-biochemical and floral traits, providing a valuable resource for genetic improvement. This diversity presents a unique opportunity to enhance tamarind through the selection of superior genotypes, particularly for traits such as higher yield, improved pulp recovery, and elevated sugar content and for developing tamarind genotypes suited for different land-use systems, such as agroforestry, orchards, and high-density plantations. (Mayavel *et al*., 2024). The identification of plus trees such as KTJ 166, KTJ 164, KTJ 162, KTJ 174, and KTJ 165 underscores this potential. The selected genotypes from this study represent valuable genetic resources for both commercial cultivation and future hybridization programs, offering significant scope for addressing the growing demand for high-quality tamarind in both fresh and processed markets.

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