Plant Archives Volume 21, No 1, 2021 pp. 1554-1560 *e-ISSN:2581-6063 (online), ISSN:0972-5210*

Plant Archives

Journal home page: www.plantarchives.org

DOI Url: https://doi.org/10.51470/PLANTARCHIVES.2021.v21.no1.212

GENETIC VARIATION OF FRUIT TRAITS AMONG NATURAL POPULATIONS OF *TERMINALIA PANICULATA* ROTHIN SOUTHERN WESTERN GHATS, PENINSULAR INDIA

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(Date of Receiving-17-01-2021; Date of Acceptance-11-04-2021)

ABSTRACT

A reconnaissance survey was conducted in Southern Western Ghats, India to identify the wild populations of *Terminalia paniculata*. From the explorative survey, 16 natural populations from different localities of the study area were identified. Collected 36 fruits from each tree and fruit trait quantification of total 3456 fruits (36 x 16 x 6) from 16 populations were used for the study. Hierarchical clustering of selected populations and correlations among fruit traits and between tree traits and fruit traits visualised using a dendrogram. The results indicated significant differences in fruit traits like fruit fresh mass, fruit large wing length and fruit large wing width. Clustering of fruit characters for all the accessions revealed the genetic relatedness between accessions. It reveals that selected populations of *T. paniculata* belong to two major clusters and confirms that 16 populations are either adjacent or distant in-terms of fruit traits are independent of the geographical station. The relationship between fruit traits indicates a significant positive correlation between fruit traits ranging from 0.352 to 0.739. Even though fruit traits show significant correlation within, a non-significant and very week correlation was obtained with tree stand-up traits except tree girth with fruit large wing length (21.4 %).

Keywords: Hierarchical clustering, Correlation, Tree breeding, Winged fruits, Kerala

INTRODUCTION

Participatory tree selection is one of the key steps in a community-based tree domestication program. It is an approach whereby a rural community selects, propagates and manages trees according to their own needs in partnership with scientists and other stakeholders. Traditional breeding programs have always assessed intra-specific genetic and genomic variation within and among populations and families involving thousands of individuals in attempts to increase selection differential and, hence, maximize genetic and genomic gains. An advantage of such a strategy is the control of environmental effects on the phenotype, to increase accuracy in computing breeding values and narrow-sense heritability estimates, provided the genotype x environment interaction and the number of genotypes that are evaluated is known. Assessing phenotypic variation in naturally-occurring trees that are distributed in a restricted ecological area with little or no variation in edapho-climatic conditions would certainly contribute to yielding accurate estimates of heritability for the study sites if the surveyed trees are not sampled within families. *Terminalia paniculata* Roth (Combretaceae) is one of the multipurpose tree species endemic to Peninsular India and commonly distributed to Southern Western Ghats (SWG) of India (Chakrabarty and Kumar, 2017). The tree grows up to 30 m height and more than 250 cm diameter at breast height and distribution ranged from 800 MSL-1200 MSL (Pillai, 2017). Wood is commonly used for construction, agricultural implements, boat building, plywood, blackboards, packing cases and non-wood products are used for drug preparation, tannins, gums, oils, fodder and certain organic compounds (Nazma *et al.,* 1981; Jain and Dangwal, 1985). Botanical Garden Conservation International and several other agencies listed *T. paniculata* as one of the commercially important tree species in India (Nazma *et al.,* 1981; Mark *et al.,* 2014). But tree breeding and domestication of *T. paniculata* is still in its infancy.

As stated above, the assessment of a tree species phenotypic variation is a key starting point in any domestication program (Eriksson *et al*., 2006; Neale and Kremer, 2011). Traits relating to fruit weight and size of wings are most commonly focused on in the case of winged fruits along with tree stand-up characteristics. Several studies related to population variation in terms of different fruit sizes and weights have already been conducted, but no such studies have yet been carried out on *T. paniculata* (Abasse *et al.,* 2011; Mousumi *et al*., 2013; Onyekwelu *et al.,* 2014; Tsobeng *et al.,* 2015). Former studies confirmed that *T. paniculata* is one of the tropical trees with high seed emptiness and poor germinability. Even though the tree shows high seed emptiness which results in poor germinability, tree maintains its natural population by producing a large number of fruits annually. It is important to study the variation in fruit traits of targeted species to observe superior fruit traits. Quantitative characters such as yield and its determinants exhibit a substantial degree of interaction with the environment, thus it is imperative to analyze the variability present in the germplasm and partition it into genotypic, phenotypic nature. Release of high yielding cultivars is impossible without ascertaining the magnitude of variation present in the available germplasm, interdependence of growth pattern with yield. Selection for improved biomass is best estimated by growth attributes and should be made during the first 2 years especially in trees and shrubs of perennial nature. Subsequently, environmental effects will have caused too much variation to distinguish effectively between genotypes (Dierig *et al.,* 2001). In practice, if a tree planter would like to develop a business plan based on tree planting, in addition to tree traits (e.g. total height, girth at breast height, crown diameter and crown length), the fruit traits must also be known. This study aims to gather the information that could aid the improvement of *T. paniculata* through a domestication program for this high-value species.

MATERIALS AND METHODS

Study sites

The present study was carried out in 16 natural populations of *T. paniculata*, located in the Kerala part of SWG, Peninsular India. The location and geographical coordinates for each population are presented in Table 1. These localities harbour pure forest patches including wet evergreen, semi-evergreen and dry deciduous forests with approximate annual rainfall between 1400 mm-2300 mm and average temperature range of 15˚C-37˚C (Pascal *et al*., 2004). The locations were identified as the part of regional plus tree selection program that aims at tree improvement of common timber species for plantation development. Six phenotypically superior trees were selected from each population by recording the tree stand-up characteristics such as total height (TH), tree girth at breast height (TG), crown length (CL), and crown diameter (CD) using Haga Altimeter, TruPulse 200 Rangefinder and measuring tapes during fruit collection from each individual.

Sampling and Fruit morphology

The fruiting period in *T. paniculata* begins at end of September and extends up to the first of February. Hence, the sampling was carried out during the peak fruiting season (December 2018 to January 2019). Thirty-six fruits were collected per candidate plus tree. Tree characteristics were recorded during the plus tree selection program (Clark and Wilson, 2005). Credential data for all trees were recorded as part of plus tree selection program including fruit collection period, location (administrative and GPS coordinates), phenotypic characteristics, name of the collector, collection date and accession number of each population and deposited in the KFRI. The accession number of each population recorded as follows: Tp1, Tp2…Tp6 and Tp denote *T. paniculata*. Fruits were collected from NEWS (north, east, west and south) directions to ensure that the variations within the trees were captured. Collected fruits were labelled as per the accession number of the candidate plus tree and placed in collection bag before transporting to the forest genetics and tree breeding laboratory of KFRI for fruit trait quantification. 36 fruits per candidate plus tree and a sum of 3456 (36 x 6 x 16) fruits from 16 locations were measured for fruit fresh mass (FFM), fruit dry mass (FDM), fruit large wing length (FLL), fruit large wing width (FLW) and fruit small wings length (FSL). Fruits were dried to constant weight at 130°C to record the dry biomass recommended by ISTA (ISTA, 2018).

Data analysis

One-way analysis of variance was carried out for all the fruit traits and the means were separated by least significant differences (LSD) Dendrogram constructed on the by Hierarchical cluster analysis of fruit traits was conducted in Paleontological Statistics (PAST) software package. Euclidean as distances measure and dendrogram was obtained. Pearson bivariate correlation analysis was carried out using IBM SPSS 22 Statistics Software's to relate fruit traits to tree traits.

RESULTS AND DISCUSSION

Fruit trait variations among the populations

Analysis of variance revealed significant differences in the fruit morphological parameters viz. FFM (p=0.01), FDM (p=0.05) and FLL (p=0.05), FLW (p=0.05) and no significant variation was obtained in FSL (Tab.2). The FFM was the highest in Tp2 (0.1921± 0.0708 g) followed by Tp3 (0.1894±0.0195 g) and the lowest values were recorded in Tp1 (0.0714± 0.0472 g). FDM was the highest in Tp9 population (0.0485 ± 0.0068 g) followed by Tp1 (0.0461 ± 0.0158 g) and least FDM recorded in Tp12 (0.0311 ± 0.0083 g). Maximum fruit moisture content recorded in population Tp2 (80.53%), Tp3 (79.99%) and minimum fruit moisture content was recorded in population Tp12 (56.44%). Highest FLL and FLW displayed in Tp3 (21.44 ± 1.16 mm) and Tp9 (13.51 ± 0.83 mm) followed by Tp5 (20.3 ± 0.89 mm) and Tp16 (13.27 ± 0.23 mm) respectively. Least FLL and FLW were displayed in population Tp15 (15.69 ± 1.35 mm) and Tp14 (10.13 ± 0.75 mm), respectively. The FSL was the highest in population Tp2 (14.7 ± 3.63 mm) followed by Tp3 (14.66 ± 2.34 mm) and the least FSL was recorded in population Tp12 (11.41 ± 2.06 mm). Analysis of Variance of all the fruits traits from 16 populations of *T. paniculata* in SWG shows that there is highly significant (p = 0.0) variation between the populations in terms of fruit fresh mass, fruit large wing length and fruit large wing width (Tab.2).

Correlation between tree and fruit traits

Table 1: Selected tree populations of *Terminalia paniculata* in Southern Western Ghats with GPS coordinates.

Population	Forest Division	Forest Range	Forest Section	GPS Location E	GPS Location N	Altitude (MSL)
Tp01	Thenmala	Aryankavu	Aryankavu	8.97283	77.15061	240
Tp02	Kottayam	Erumely	Kombukuthy	9.48811	76.95854	414
Tp03	Nilambur South	Karulai	Nedumkayam	11.30777	76.37333	068
Tp04	Nilambur South	Karulai	Mundankadav	11.30805	76.37500	073
Tp05	Nilambur South	Karulai	Mundankadav	11.29000	76.35305	073
Tp06	Nilambur South	Karulai	Chakkikuzhi	11.26833	76.34888	068
Tp07	Nilambur South	Karulai	Pattakarimba	11.27500	76.38638	084
Tp08	Nilambur South	Karulai	Pattakarimba	11.27500	76.35472	084
Tp09	Parambikulam	Parambikulam	Vengoli	10.41213	76.80645	660
Tp10	Parambikulam	Parambikulam	Vengoli	10.41869	76.80121	693
Tp11	Parambikulam	Parambikulam	Kallippara	10.40935	76.81005	692
Tp12	Peechi	Peechi	Jandamukk	10.51666	76.37391	096
Tp13	Peechi	Peechi	Olakara	10.51444	76.43944	143
Tp14	Parambikulam	Sungam	Anappadi	10.41764	76.79482	530
Tp15	Parambikulam	Sungam	Thellikkal	10.45083	76.74444	570
Tp16	Palakkad	Walayar	Puthussery	10.86087	76.79849	236

Table 2: Mean fruit traits values of all selected populations of *Terminalia paniculata* in Southern Western Ghats, India

Populations	Fruit traits				
	FFM (g)	FDM (g)	FLL (mm)	FLW (mm)	FSL (mm)
Tp1	0.1626 ± 0.0472	0.0461 ± 0.0158	19.29 ± 2.08	12.74 ± 1.89	14.17 ± 3.91
Tp2	0.1921 ± 0.0708	0.0374 ± 0.0115	19.91 ± 2.26	12.11 ± 1.85	14.70 ± 3.63
Tp3	0.1849 ± 0.0195	0.0370 ± 0.0047	21.44 ± 1.16	12.93 ± 0.79	14.66 ± 2.34
Tp4	0.1560 ± 0.0498	0.0314 ± 0.0095	18.81 ± 2.90	12.07 ± 1.59	13.48 ± 3.35
Tp5	0.1682 ± 0.0182	0.0339 ± 0.0028	20.30 ± 0.89	12.18 ± 1.34	14.19 ± 2.05
Tp6	0.1580 ± 0.0207	0.0317 ± 0.0045	19.15 ± 1.91	11.75 ± 1.35	13.92 ± 3.39
Tp7	0.1658 ± 0.0309	0.0341 ± 0.0085	20.07 ± 0.54	11.88 ± 1.24	14.39 ± 1.86
Tp8	0.1451 ± 0.0376	0.0379 ± 0.0114	18.48 ± 1.84	12.58 ± 2.00	13.46 ± 2.61
Tp9	0.1649 ± 0.0131	0.0485 ± 0.0068	19.53 ± 1.30	13.51 ± 0.83	12.98 ± 1.16
Tp10	0.1518 ± 0.0275	0.0382 ± 0.0128	18.84 ± 1.70	12.73 ± 1.76	12.60 ± 2.02
Tp11	0.1106 ± 0.0392	0.0327 ± 0.0074	18.02 ± 1.10	11.63 ± 2.37	12.57 ± 1.94
Tp12	0.0714 ± 0.0245	0.0311 ± 0.0083	15.90 ± 1.10	10.50 ± 1.37	11.41 ± 2.06
Tp13	0.0861 ± 0.0444	0.0348 ± 0.0113	16.58 ± 1.43	12.41 ± 1.21	11.96 ± 1.85
Tp14	0.1422 ± 0.0080	0.0321 ± 0.0053	16.04 ± 0.50	10.13 ± 0.75	12.05 ± 1.61
Tp15	0.1376 ± 0.0078	0.0354 ± 0.0090	15.69 ± 1.35	10.71 ± 1.24	12.08 ± 1.77
Tp16	0.1025 ± 0.0048	0.0345 ± 0.0019	17.81 ± 0.51	13.27 ± 0.23	12.92 ± 1.07
Mean ± S.D.	0.1437 ± 0.0457	0.0360 ± 0.0096	18.49 ± 2.19	12.07 ± 1.64	13.22 ± 2.46
p value	0.000	0.045	0.000	0.003	0.357

Note: (FFM: fruit fresh mass; FDM: fruit dry mass; FLL: fruit large wing length; FLW: fruit large wing width; FSL: fruit small wings length; SD: standard deviation).

Tree traits such as TH, TG, CD and CL shows an average of 2.86 ± 0.29 m (p= 0.05), 29.14 ± 2.58 m (p= 0.01), 18.1 ± 3.15 m (p= 0.01) and 13.51 ± 1.79 m (p= 0.01) respectively in selected populations of *T. paniculata* in SWG (Tab.5). Pearson bivariate correlation analysis done to understand the relationship between tree and fruit traits. Correlation analysis between fruit traits shows significant correlation, where FFM showed strong positive correlation with FLL and FDM showed strong positive correlation with FLW. The correlation matrix indicates that that only tree girth shows significant correlation with FLL at 0.05 level (Tab.4).Tree stand-up traits shows a range of 0.214 to 0.001 correlation with fruit traits such as TH (0.027-0.109), TG (0.020-0.214), CD (0.001-0.097) and CL (0.009-0.135). TH shows negative correlation with FDM (-0.031), FLL (-0.027), FLW (-0.109), FSL (-0.058), and positive correlation with FFM (0.087). TG shows negative correlation only with FDM (-0.028) and positive correlation with FFM (0.151), FLL (0.214), FLW (0.020) and FSL (0.146). CD shows positive correlation with FFM (0.012), FLL (0.005) and negative correlation with FDM (-0.097), FLW (-0.001) and FSL (-0.004). CL shows positive correlation with FDM (0.012), FLL (5.8%) and negative correlation with FFM (-0.009), FLW (-0.135) and FSL (-0.110).

Hierarchical cluster analysis of on fruit traits

Hierarchical cluster analysis of fruit traits of different population resulted in two homogenous major clusters. The cluster α includes five populations (Tp11 to Tp15) and all other 11 populations (Tp1-Tp10 and Tp16) included in cluster β (Fig.1). Populations included in cluster α are geographically adjacent, but not in cluster β. Populations (Tp9, Tp10, Tp11, and Tp14, and Tp15) recorded from the Parambikulam forest division placed in both clusters. Also, populations (Tp3 to Tp8) belongs to Karulai forest range, Nilambur South shows more closeness with geographically far populations (Tp1 and Tp2). For instance, the Southern population, Tp1 (Aryankavu and Thenmala) shows closeness with Tp4, Tp6 and Tp8 and, Tp2 shows closeness with Tp7. Analysis of cluster α and β results that Tp3 is the population retain maximum distance from other population in cluster β and no population in cluster α shows the same behaviour. Among the 16 populations of *T. paniculata* in SWG, Tp2 and Tp7 populations shows minimum Euclidean distance (> 0.5) followed by Tp5 (>1) with Tp2 and Tp7. Populations such as Tp4 and Tp8 placed within 1 Euclidean distance followed by Tp14 and Tp15 with Tp12 (>1). In cluster α, the minimum Euclidean distance between two populations is >1 (Tp14 and Tp15) and maximum Euclidean distance is > 2.5 (Tp11 and Tp13 with others). Among cluster β, the minimum Euclidean distance is > 0.5 (Tp2 and Tp7) and maximum Euclidean distance > 3 (Tp3 with others). All the selected populations of *T. paniculata* in SWG placed in Euclidean distance > 4 in hierarchical clustering.

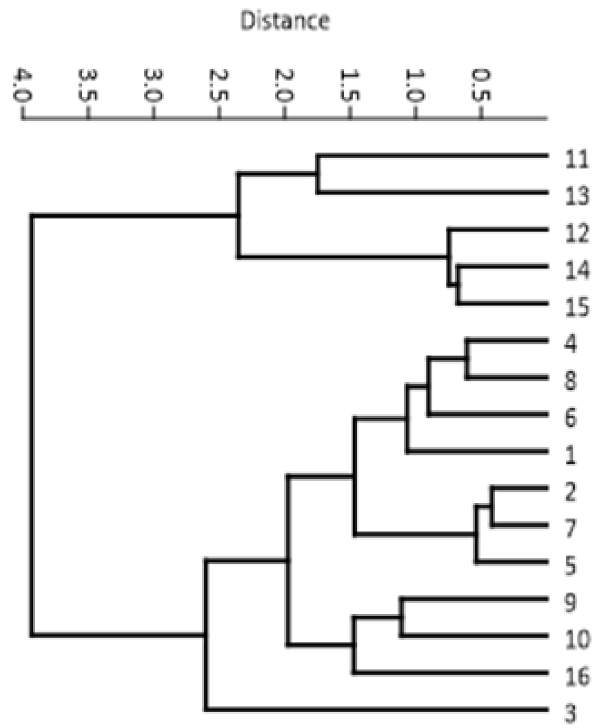

Figure.1. Dendrogram constructed based on the Euclidean distances by hierarchical clustering of fruit traits of selected *Terminalia paniculata* populations of Southern Western Ghats (1=Tp1, 2= Tp2…16= Tp16).

Discussion

T. paniculata naturally propagated through the small three-winged seeds dispersed by winds and water. Even though seed germinability is very less (< 1%), single tree producing a huge number of seeds annually. It's proven that the size of the seed or fruit is positively correlated with seed germinability (Giles, 1990; Khan *et al.,* 1999; Moles and Westoby, 2006; Zimmerman and Weis, 2011). The present study investigated whether the size of fruits of *T. paniculata* significantly varies in its native range which could be a viable strategy for the development of superior planting materials of species at the farmer level in the SWG. If any population shows significant large-sized fruits among the natural population strands, it could be a suitable population for further tree breeding programs.

Tree breeding is an extensive program that begins with plus tree selection which includes three phases such as base population identification, candidate tree selection and finally superior tree selection. Selection provides superior quality phenotypes for further breeding programs through the production of quality planting materials. Even though the target species is endemic and distributed throughout SWG, the species is still underutilized because there is no popularization and tree breeding program initiated, however. Conventional tree selection methods are comparatively easily practicable in the tropics to get superior individuals and germplasm using phenotypic characteristics. Selection is proven efficient for the development of superior individuals from the whole population targets quality products for industrial and tertiary sectors in the second generation. Many studies conducted all over the world focused on fruit morphological variation. In tropical forests, fruit production highly varies among the trees of the same species may be due to environmental factors. The study conducted in Costa Rica compared the fruit production with tree size and neighbourhood crowding results that there is direct influence between fruit production with tree size and neighbouring tree crowding, rather than soil nutrients (Minor and Kobe, 2018). Fruit characteristics, seed germination and seedling traits of *Adansoniadigitata* were evaluated in Benin at climatic zone level using 1,200 fruits. The evaluation concluded that significant differences in fruit characteristics not only between climatic zones but also between individuals from the same zone and within-trees (Assongbadjo *et al.,* 2011).

Table 4: Pearson Correlation Coefficient (r) between tree and fruit traits of *Terminalia paniculata*populations in Southern Western Ghats

Traits	TH	TG	CD	CL	FFM	FDM	FLL	FLW	FSL
TH	1	0541**	0.512**	-0.154	0.087	-0.031	-0.027	-0.109	-0.058
TG		1	0.307**	0.008	0.151	-0.028	0.214*	0.020	0.146
CD			1	-0.407**	0.012	-0.097	0.005	-0.001	-0.004
CL				1	-0.009	0.012	0.058	-0.135	-0.110
FFM					1	0.467**	0.739**	0.449**	0.580**
FDM						1	0.420**	0.669**	0.352**
FLL							1	0.587**	0.591**
FLW								1	0.530**
FSL									1

(FFM: fruit fresh mass; FDM: fruit dry mass; FLL: fruit large wing length; FLW: fruit large wing width; FSL: fruit small wings length; TH: tree height; TG: girth at breast height; CD: crown diameter; CL: crown length; **Correlation is significant at the level 0.01 level; *Correlation is significant at the 0.05 level).

Table.5: Tree characteristics of selected *Terminalia paniculata*populations in Southern Western Ghats

Population	Tree height (in m)	Girth at breast height (in m)	Diameter of crown (in m)	Length of crown (in m)
Tp1	24.80 ± 4.15	2.54 ± 0.37	12.40 ± 2.19	17.20 ± 2.17
Tp2	30.60 ± 3.78	2.76 ± 0.44	16.80 ± 5.22	15.20 ± 2.28
Tp3	26.00 ± 4.00	3.22 ± 0.29	20.80 ± 2.28	12.60 ± 1.14
Tp4	31.00 ± 1.00	3.24 ± 0.25	19.60 ± 2.19	11.80 ± 0.45
Tp5	32.60 ± 0.89	3.01 ± 0.49	16.40 ± 2.97	12.60 ± 0.89
Tp6	28.80 ± 4.32	3.21 ± 0.56	22.40 ± 2.61	11.20 ± 1.79
Tp7	29.00 ± 3.08	3.10 ± 0.41	21.60 ± 3.85	11.80 ± 2.68
Tp8	30.60 ± 2.88	3.12 ± 0.41	18.80 ± 3.90	14.40 ± 1.67
Tp9	32.20 ± 1.30	2.60 ± 0.44	16.60 ± 0.89	13.40 ± 1.67
Tp10	31.80 ± 1.10	2.69 ± 0.32	17.60 ± 3.85	16.20 ± 2.95
Tp11	28.60 ± 1.34	2.80 ± 0.35	14.60 ± 2.19	15.80 ± 3.35
Tp12	27.60 ± 3.65	2.72 ± 0.41	16.40 ± 2.19	13.80 ± 3.56
Tp13	30.40 ± 2.61	2.98 ± 0.33	23.20 ± 1.10	11.60 ± 2.61
Tp14	28.20 ± 3.70	2.32 ± 052	13.40 ± 1.67	13.40 ± 2.30
Tp15	30.20 ± 1.92	2.94 ± 0.27	20.20 ±4.15	12.80 ± 2.49
Tp16	23.80 ± 1.48	2.45 ± 0.28	18.80 ± 4.82	12.40 ± 1.67
Mean ± S.D	29.14 ± 2.58	2.86 ± 0.29	18.10 ±3.15	13.51 ±1.79
p- value	0.000	0.003	0.000	0.001

The present study observed that there was significant variation between the 16 selected population's in-terms of fruit and tree traits. Similar studies were conducted in all around the world in both annuals and perennials and reported the same kind of variations among the selected population (Atangana *et al.,* 2001; Egbe *et al*., 2013; Mkwezalamba *et al*., 2015; Tsobeng *et al.,* 2015; Tsobeng, 2020). Fresh fruits including three wings of phenotypically superior trees contain 75-80% moisture and the size of the fruit is smaller than any species under the taxa, *Terminalia*. Seed dispersal of *T. paniculata* is anemochorous like *T. tomentosa*, *T. arjuna* and *T. elliptica* due to its winged fruit character. Hierarchical clustering for fruit characters for all the accessions revealed the genetic relatedness between accessions and it reveals that selected populations of *T. paniculata* belong to two major clusters and confirms that 16 populations are either adjacent or distant in-terms of fruit traits, are independent of the geographical station. The first cluster includes populations that are geographically nearer, but the second cluster includes geographically distant populations. Total Euclidean distance (< 4.0) indicated that the taxon is endemic to a restricted region (Ratliff and Mori, 1993). The intra-characteristic relationship among the fruit traits indicates the relationship between each fruit traits on another. We currently noticed that fruit traits such as FFM, FLL and FLW are shows noteworthy variation between the selected populations and FDM and FSL are non-significant. The relationship between the traits may be strong or weak depends on the nature of the traits and analyzed statistically. The statistical analysis resulted that all the fruit traits show either strong or weak positive correlations. Among the fruit traits, fruit fresh mass shows a strong correlation with fruit dry mass, large wing length and large wing width; besides, fruit dry mass shows a strong correlation with large wing length and two small wing length and large wing length with large wing width. Among the traits, small wings length only indicates a strong correlation with fruit dry mass. This kind of correlation of fruit traits was also reported in *Balanitesaegyptica* (Abasse *et al.,* 2011). Week correlation between the central large wing and other small wings in terms of dimension, confirms that none other than fruit parts, there is no relationship between large wing and small wings. Fruit fresh mass shows a strong correlation with large wing width followed by fruit dry mass with small wings length but shows week correlation vice-versa and shows a strong correlation with large wing length. So, we can assume that large wing width is responsible for the fresh mass of fruits and small wings length is responsible for the dry mass of fruits and that confirms that major moisture content in fruits is saved in the large central wing of *T. paniculata* fruits.

In a tree breeding program, it's very important to understand the characteristics of the selected tree species. Here we calculated the average stand-up characters such as total height, girth, crown diameter and crown length of phenotypically superior individuals of *T. paniculata* from 16 selected populations. The tree shows an average length (14.5-16.5 m) of clear bole, which shows its importance as timber in the trade market. So it's very important to comprehend the connection with phenotypically superior trees stand-up characters and its reproductive unit. Exactly how the tree traits correlated with fruit traits? Relationship between tree and fruit traits estimated by Pearson correlation analysis. Correlations between the variables may be either positive or negative and either week or strong. Here we understand that tree stand-up traits show very week positive or negative characteristics with fruit traits. Either positive or negative, the correlation is negligible. Among the tree stand-up traits, tree girth at breast height shows the maximum positive relationship with fruit fresh mass, which is below (21.4%). But stand-up traits like tree girth at breast height with small wings length; tree height with fruit fresh mass, small wing length; crown diameter with fruit fresh mass, dry mass, large wing length, large wing width; and crown diameter with large wing width, small wings length shows exceptionally very weak relationships. Especially in the case of crown diameter and fruit large wing length, they are showing the least or negligible positive correlation frequency. Trait wise analysis resolves that there is no significant impact of tree stand-up traits in fruit traits among the phenotypically superior tree populations of *T. paniculata* in SWG.

CONCLUSION

The present study enlightens the tree breeding program of an underutilized endemic tree, *T. paniculata.* Morphometric results show that fruit traits like fresh mass, large wing length and large wing width and tree stand-up traits like tree height, girth at breast height, crown diameter and crown length show significant variations among the 16 natural populations of *T. paniculata* in its native range. Tree stand-up traits of phenotypically superior individuals of *T. paniculata* shows a significant variation between the selected populations. Even though fruits are the propagating units of this taxa and Pearson correlation analysis concluded that there is a non-significant relationship between tree stand-up and fruit traits. It's very important to study phenotypic variation to understand the genetic character expressed in the present generation. Besides, progeny tests are needed to estimate the genetic character of fruit traits transferred to the next level. The present study suggests further studies to understand the genetic behaviour of an endemic species, *T. paniculata* with poor germinability and secluded distribution in India.

ACKNOWLEDGEMENTS

Financial support for this research was provided by the Kerala Forest Department (KFD) with the support of the Kerala State Council for Science Technology and Environment (KSCSTE) of the Government of Kerala, India. We also thank foresters of KFD for permission to access the remote forest areas and KSCSTE- Kerala Forest Research Institute for providing research facilities. We thank the tribal villagers for fruit collection and transportation in the forest areas. Thanks to Dr. P K Chandrasekhara Pillai for his valuable help during fruit trait quantification.

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