

**ASSESSMENT OF GENETIC VARIABILITY FOR
PRODUCTIVITY AND QUALITY TRAITS IN
TAMARIND (*Tamarindus indica* L.) GENOTYPES**

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**ASSESSMENT OF GENETIC VARIABILITY FOR
PRODUCTIVITY AND QUALITY TRAITS IN
TAMARIND (*Tamarindus indica* L.) GENOTYPES**

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CERTIFICATE

This is to certify that the thesis entitled “ASSESSMENT OF GENETIC VARIABILITY FOR PRODUCTIVITY AND QUALITY TRAITS IN TAMARIND (*Tamarindus indica* L.) GENOTYPES” submitted by Miss. PRIYANKA G P, ID No. UHS18PGM1003 for the degree of MASTER OF SCIENCE (HORTICULTURE) in FRUIT SCIENCE to the University of Horticultural Sciences, Bagalkot, is a record of research work carried out by her during the period of her study at University of Horticultural Sciences, Bagalkot under my guidance, supervision and the thesis has not previously been formed the basis for the award of any other degree, diploma, associateship, fellowship or other similar titles.

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Affectionately Dedicated to

***My beloved parents and All
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LIST OF ABBREVIATIONS

Sl. No.	Abbreviations	
1.	cm	Centimetre
2.	m	Meter
3.	%	Per cent
4.	g	Gram
5.	kg	Kilo gram
6.	⁰ B	Degree Brix
7.	S. Em	Standard Error of Mean
8.	mg/l	milligram per litre
9.	g/l	gram per litre
10.	@	At
11.	<i>et al</i>	Et alii (and his coworkers)
12.	<i>i.e</i>	That is
13.	<i>viz</i>	As fallows
14.	SD	Standard Deviation
15.	PCV	Phenotypic Coefficient of Variation
16.	GCV	Genotypic Coefficient of Variation
17.	h^2	Heritability
18.	GA	Genetic Advance
19.	GAM	Genetic Advance over Mean
20.	CD	Critical Difference
21.	N-S	North-South
22.	E-W	East-West
23.	SRAP	Sequence Related Amplified Polymorphism
24.	ISSR	Inter Simple Sequence Repeats
25.	DNA	Deoxyribose Nucleic Acid

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1. INTRODUCTION

Tamarind (*Tamarindus indica* L.) is a hardwood evergreen monotypic genus, multipurpose tree species belongs to dicotyledonous family Leguminosae and sub-family Ceasalpiniae. It is a diploid species with somatic chromosome number of $2n=24$ (Kumar *et al.*, 2015). The species is natural to tropical Africa, it has a broad geographical distribution throughout the world in tropical, subtropical and semi-arid zones with a prime concentration in India, apart from western dry regions and Himalayas. The term tamarind is derived from the Arabic word “Tamar-E-Hind” meaning “Date of India” (Pooja *et al.*, 2018).

It has been acclimatized to many places of the world and extensively cultivated in Bangladesh, India, Malaysia, Myanmar, Thailand, several African, European and central American countries (Rao and Mathew, 2012). It is predominantly found in the Indian states of Andhra Pradesh, Maharashtra, Karnataka, Madhya Pradesh, Tamil Nadu, West Bengal, Bihar and Chhattisgarh. Pulp was the most exported product of tamarind, India is the main producer of tamarind in the world with the yearly production of 3 lakh tons, of which 1.15 lakh tons of pulp per annum exported to various countries viz. USA, Australia, Sri Lanka, Malaysia, Pakistan beside some European countries *etc.* (Sinha *et al.*, 2015).

Tamarind conventionally grown mainly for its pulp since ages, which is a chief culinary ingredient. Virtually whole tree has some specific use, but the utmost useful part is the pod (fruit). Fruit encompasses a sweetish, acidic pulp, which is commonly used for souring curries, sauces, chutneys and certain beverages. It is an ironic source of vitamins, minerals and similarly contains more of calcium than any other fruit. Hence, it has a potential and commercial future in the post-harvest products like pickles, candy, juices, soft drinks, jams and confectioneries. The pulp comprises a small amount of carotene, thiamine, nicotinic acid which is used to cure dysentery and it also have some other medicinal values (Pooja *et al.*, 2018). In traditional medicine, it is used in wound

healing, abdominal pain, dysentery, diarrhea, parasitic infestation, malaria, fever and respiratory problems because of its fungicidal and bactericidal properties. It is typically used in tropical countries because of its laxative, carminative, refrigerant and aphrodisiac properties (Kuru, 2014).

Tamarind kernel powder is extensively used for starching of cotton yarns, jute fabrics and woolen. Seed powder also finds place in preparation of jelly, fortified bread, biscuits and in the confectionery industry for manufacturing of chocolates. It is also used as coating material, adsorbent, gelatinizing agent, thickener, emulsifying agent, binder and in cosmetic preparations, greaseless ointments, penicillin production, concentration of rubber latex. Seed gum is used as emulsifier, palatability improver, odour improver, antimicrobial agent, insulator, stickiness preventer, glazing agent, and bodying agent. It translates organic waste into biofertilizer and allows production of gram-negative bacteria. Seed polysaccharide/ oligosaccharides used as low-calorie food, crystallization inhibition, preservative, mineral disperser, paste material and stabilizer. Seed coat is used as antioxidative element, anti-acne medicine, tanning material, antidiabetic activity (Hemshekhhar *et al.*, 2011). Hard wood is used for manufacturing wheels mallets, rich funders and very good for tannery. Leaves comprise 12 to 15 per cent of crude protein and used as a fodder throughout dry period.

Tamarind has thick foliage and huge tree canopy so, it is grown up as avenue tree in various regions and it is said to be an ideal crop for social forestry, agro-forestry programs as good wind break. Tamarind is a strong plant, it can bear very poor, saline, alkaline soils and it can be fully-fledged in degraded unused lands, even in mine spoil waste. It can be effectively grown up in sodic soils and succeeds well on deep alluvial soils. The tree usually desires a warm climate and can resist drought but it is more sensitive to frost. Tamarind is a slow growing tree with annual growth rate of seedlings is about 60 cm and the tree can reach a maximum height of up to 20-30 m. Tamarind tree has a long-life span of about 200 years (Yahia and Salih 2011).

Tamarind bears flowers terminally with raceme inflorescence which are pale green or yellowish orange in color and bisexual in nature. Pods are usually oblong and reddish brown in color (Azad, 2018). Fruit harvesting is done during the month of February-March. The tamarind fruit mainly comprises of pulp and seed. The ripe fruits contain 30-50 per cent of pulp, the shell and Vein account for 11-30 per cent and the seed comprises for about 25-40 per cent. The fruit, both ripe and dry, contains mainly tartaric acid, reducing sugars, pectin, tannin, fiber, and cellulose (Rao *et al.*, 1999). The pulp is also rich source of vitamin B and C (Yahia and Salih, 2011).

Tamarind is highly cross-pollinated crop, heterozygous and it is grown as backyard, roadside tree even in waste and barren lands with seedling origin trees. Seedlings exhibit a wide range of variation which aids in the selection of the superior desirable genotypes. The plants show high degree of variations found in natural population as the trees are generally cross pollinated, hence they show wide range of heterozygosity. The variation primarily is observed for characteristics such as growth, pod weight, pod shape, pulp colour and fruit yield. So, it is very essential to study the existence of variability among several genotypes based on morphological difference and also by using markers to select the genotypes with superior characteristics for better yield and quality fruits.

Identification of genotypes and studying about genetic diversity using phenotypic markers have some restrictions in perennial crops (Purushotham *et al.*, 2008). DNA and protein-based markers are used to known diversity at molecular level, it is authentic and not affected by environmental factors (Dhanraj *et al.*, 2002). Among DNA-based markers ISSR proved as a tool to estimate genetic diversity and relationship among

genotypes. To identify elite genotype and to know the amount of diversity exist in tamarind crop, the present study was undertaken with a following objectives.

1. To assess the extent of genetic variability for yield and quality traits in tamarind genotypes.
2. To study the correlation and path analysis for yield contributing traits in tamarind.
3. Identification and molecular characterization of superior tamarind genotypes.

2. REVIEW OF LITERATURE

Tamarind is one of the slow growing, long-lived important multipurpose fruit trees, whose commercial food and by-products are used widely around the world. Tamarind leaves contain high ascorbic acid which play a major role in absorption of metabolites. Almost all parts of the tamarind tree have benefits, the major one is pulp which contain tartaric acid and ascorbic acid. Hence, it is used as a preservative in many processed food products. Although tamarind is an ancient domesticated tree, little attempt has been directed to its genetic improvement. Therefore, identifying superior elite trees and plantations were established aiding genetically improved superior clones will help in maximizing production per unit area and ultimately leads to better economic and social benefits.

Tamarind exhibit maximum diversity for most of the characteristics, therefore identifying elite genotypes is gaining more scope and importance. Tamarind fruits which are commonly available are not generally consumed as table fruit due to their sour and astringent taste. Though it can be eaten fresh (ripe or unripe), but it is mostly consumed after processing into different products. The excellent nutritive and therapeutic values of this fruit offer a great potential for processing of tamarind fruits into quality products. This has necessity for identifying superior elite trees like genotypes for monoculture plantations, without causing genetic erosion. Thus, tree improvement through the application of genetic principles is basically directed towards modifying the heredity of tree populations to meet the needs of the farmers. Therefore, a brief review of work done in regard to crop improvement and molecular characterization in tamarind is made under the following heads.

- 2.1 Selection of desirable tamarind trees
- 2.2 Morphological traits of the tamarind tree
- 2.3 Tree yield and yield attributing traits in tamarind
- 2.4 Quality parameters of the tamarind pulp
- 2.5 Variability, heritability and genetic advance

2.6 Correlation studies, Path analysis and genetic divergence

2.7 Molecular characterization

2.1 Selection of desirable tamarind trees

Shivanandam *et al.* (1984) stated that there was a wide variation with regard to fruit, seed and flower characters among the genotypes and thus, there is a great scope for the selection of superior types of tamarind.

Kokate (1988) surveyed at Mahatma Phule Krishi Vidyapeeth (MPKV), Rahuri and reported that there were no standard varieties of tamarind. However, six promising trees were identified based on their fruit quality and productive aspects.

Shivanandam and Thimmaraju (1988), reported that a large number of existing seedling tamarind trees can be evaluated preliminarily on the basis of fruit size. According to Keskar *et al.*, (1989) high variability for quantitative and qualitative parameters was the sign for effectual improvement by selection among current tamarind types.

According to Deshmukh *et al.* (1993) two promising trees were identified from existing 350 old trees in Fruit Research Station, Aurangabad, Marathwada Agriculture University, Parbhani. The two-promising selection were Pratisthan and Selection 263.

Shinde and Ingle, (1995) conducted a detailed screening work of 350 tamarind trees and survey is conducted in different villages by department of horticulture, Marathwada Agriculture University, Parbhani to recognize superior types revealed enormous variability in different traits of pods.

It was more necessary to point out high yielding, regular bearing trees from the existing population, which were scattered and the population present in India is of seedling origin. Hence, it gave more opportunity to the researchers to survey the population for required traits (Shinde and Kulwal, 1995).

Shinde *et al.* (1997), resulted in identifying some elite strains like OBD-5, OBD-7, BHR-3, OBD-9, LAT-6 and LAT-7 in the survey work of tamarind in Marathwada.

which shows superior characters in regard of weight, acidity, color and total soluble solids.

According to Naidu *et al.* (1997) high yielding tamarind plus trees were subjected to screening and selection process based on the parameters like fruiting habit, high fruit yield, big crown size, quality of tamarind rind and sourness in Chittoor district of Andhra Pradesh during fruiting season of November-March.

Bennet *et al.* (1997) reported that huge heterozygosity and more variation with respect to fruit morphology can be seen in tamarind, which brings wide scope for selection of relevant high earning genotypes of tamarind.

Azhakiamanavalam and Vadivel (1997) studied on the agronomic, biochemical and genetic traits in Horticulture college and Research Institute, Periyakulam, Tamil Nadu thereby released PKM-1 variety of tamarind in 1992.

Karale *et al.* 1999 suggested that during evaluation of tamarind seedling trees, it was essential to consider fruit characters, that would serve as credible measure for selection of noble genotype.

Divakara (2008) conducted a survey work on tamarind in Forest college and Research Institute, Mettupalayam (Tamil Nadu), identified few elite types (35 genotypes) with good tree height, girth, crown size, age of the tree and pod parameters such as length, width and weight of the pod and pulp characters such as weight of the pulp, shell, vein and seed.

Survey work is conducted by Sunil *et al.* (2008) in East Godavari and other parts of Andhra Pradesh such as Vishakapatnam to locate trees showing adequate and good variability with respect to yielding, bearing habit, fruit size, content and taste of the pulp for collection and preservation of representative diversity.

According to Nyadoi *et al.* (2010) mean height of tamarind (<5 – 14 m), trunk diameter (61 – 189 cm) and size of the crown (28 – 229 m³) were enhanced from island to mainland, which were emulative by elevations, phytocoria and dwelling place respectively.

Nandini *et al.* (2011) conducted a study on magnitude of morphometric characters of 100 genotypes of tamarind present at legendary tamarind grove at Nallur, Devanahalli taluk, Karnataka. She noticed that more variability was observed with respect to the shape of the crown which is ranged from cone, dome, semicircle, circle, oval and irregular shapes. More number of trees recorded irregular shaped crown and only one tree showed circle shaped crown. Most of the trees were having single trunk, however double and multiple trunk was also observed in some trees.

According to Komkhuntod *et al.* (2012) 19 accessions were selected as tested in the method of tropical fruit descriptors (IBPGR, Rome). Among the selected accessions, five accessions fit to sweet type of tamarind and 14 accessions were fit to sour type of tamarind group.

2.2 Morphological traits of the tamarind tree

Challapilli (1992) noticed height and spread (East-West and North-South) of various tamarind trees which ranged from 9.40 to 13.0 m and 14.00 to 12.19 m respectively in tamarind.

According to Gangaprasad (1993), more diversity was quoted in growth traits of tamarind trees where trunk length and trunk radius of the tree ranges from 90 to 314 cm and 6.13 to 23.27 cm respectively, trunk volume of the tree ranges from 24461.32 to 405227.81 cm³.

According to Geetha (1995), Urigam is one of the most popularly cultivated tamarind variety of Tamil Nadu which is of dwarf stature and having umbrella like branching nature.

Two varieties of plant growth pattern were observed in tamarind like orthotropic and plagiotropic. 24 genotypes showed orthotropic pattern of growth among the 40 genotypes and remaining genotypes shows plagiotropic pattern of growth (Hanamashetti, 1996).

Hanamashetti (1996) reported that a considerable range of diversity was noticed in vegetative growth characters viz., height of the tree (1.47m to 2.99 m), trunk diameter (6.94 cm to 11.58 cm), spreading of the plant in East-West direction (1.34 to 3.10 m)

and in North-South direction (1.28 to 2.98 m) and size of the crown (1.38 m to 3.04 m) in six years old tamarind genotypes.

According to Mastan *et al.* (1997), the highest tree height (23.00 m) and girth of the tree (6.00 m) were observed in tamarind genotypes which are located near Begarapalli village of Anantapur district, Andhra Pradesh.

According to Biradar (2001) two types of plant growth pattern was observed in 17 tamarind genotypes at forest research center, Gungargatti (Dharwad). Where, 11 genotypes showed orthotropic growth pattern and rest genotypes showed plagiotropic kind of growth pattern. The tree height and trunk diameter varied from 3.65 m to 6.32 m and 12.53 cm to 22.87 cm respectively, spread of the tree in east-west direction varied from 3.50 m (NTI-70) to 6.08 m (NTI-14) and in north-south direction it ranges from 3.42 m (NTI-70) to 5.79 m (NTI-14). Crown area varied from 3.46 m (NTI-70) to 5.93 (NTI-14).

Biradar (2001), studied on 16 seed propagated progenies of tamarind at Kittur Rani Channamma College of Horticulture, Arabhavi. Where, 10 seedling progenies (NTI-2, 5, 7, 15, 62, 71, 77, 79, 83 and S-4) showed orthotropic pattern of growth and remaining 6 progenies (NTI-14, 19, 32, 57, 70 and 75) showed plagiotropic growth pattern. Growth parameters like height of the tree was varied from 0.68 m (NTI-2) to 2.49 m (NTI-19), diameter of the tree ranged from 4.50 cm (NTI-2) to 9.50cm (NTI-70), spreading of the tree in east-west and north-south direction was found minimum in NTI-2 (0.60 m and 0.80 m) and maximum in NTI-14 (2.47 m and 2.55 m, respectively), highest crown size was observed in NTI-14 (2.51 m) and lowest in NTI-2 (0.70 m) at the age of fourth year of plantation.

Patil (2004) studied on 38 clonally propagated progenies of tamarind at forest research station, Gungaragatti (Dharwad), orthotropic growth pattern was recorded in 31 clonal progenies and remaining 7 progenies exhibited plagiotropic pattern of growth. Maximum tree height was noticed in NTI-6 (6.54 m) and minimum in NTI-58 (3.09 m), crown area was ranged from 2.43 m (NTI-58) to 5.25 m (SMG-13), tree spread in east-west direction ranged from 2.36 m (NTI-58) to 5.19 m (SGM-13) and plant spread in north-south direction ranged from 2.49 m (NTI-58) to 5.33 m (NTI-56).

Further, he studied on 14 clonal propagated genotypes of tamarind at main agriculture research station (MARS), Dharwad (Kumbhapur Farm), 9 clonal progenies (NTI-79, 80, PKM-1, NTI-32, 82, 84, 62 and SGM-4) possessed orthotropic pattern of growth and remaining 5 progenies (NTI-19, 14, 32, 57, 70 and 75) possessed plagiotropic pattern of growth. Growth parameters were observed individually, maximum height of the plant was noticed in NTI-79 (4.94 m) and minimum in NTI-80 (2.27 m), crown area was ranged from 1.47 m (NTI-80) to 3.05 m (NTI-79), tree spread in east-west and north-south directions was noticed lowest in NTI-80 (1.49 and 1.46 m respectively), highest in NTI-79 (3.15 m and 2.95 m, respectively).

According to Ganachary (2005), 2 different types of plant growth pattern was studied in 21 genotypes of tamarind at Chitradurga and Kudligi (Bellary). 12 genotypes possessed orthotropic pattern of growth and 9 genotypes showed plagiotropic pattern of growth. Plant height ranged from minimum of 10.24 m (MNH-2) to maximum 27.00 m (SKR-3), tree spread in east-west direction was ranged from 7.87 m (HMR-3) to 20.60 m (SKP-3) and in north-south direction the range was between 9.39 m (KMG-2) to 22.12 m (KMG-4), size of the crown ranged between 9.23 m (HMR-3) to 21.06 m (KMG-4).

Further, at Kudligi (Bellary) and Jagalur (Davangere) area a study was done on growth habit of 17 tamarind genotypes. Where, 6 genotypes possessed orthotropic type of growth habit and 11 genotypes showed plagiotropic pattern of growth habit. Growth parameters also recorded, maximum plant height was observed in VBL-2 (36.10 m) and minimum in ALR-1 (14.00 m). stem diameter was noticed highest in KMH-1 (1.53 m) and lowest in ALR-1 (0.43 m), spread of the tree in north south direction ranged from 8.30 m (ALR-2) to 28.00 m (YBL-2) and in east-west direction varied from 10.10 m (ALR-1) to 29.40 m (YBL-2), maximum crown size recorded in YBL-2 (28.70 m) and minimum in ALR-1 (9.20 m).

According to Rao and Subramanyam (2010), 15 tamarind germplasm which are grown under less rainfall zone for 3 years at Anantapur were evaluated for vegetative growth parameters. The maximum height of the plant was noticed in V-59 (5.3 m) germplasm during 2005. The maximum stem girth was noticed in PKM-1 (62.1 cm) which is followed by V-29 (59.4 cm) during 2005 whereas, in 2006 maximum stem

girth was recorded in PKM-1 (63.2 cm). Maximum number of branches per tree were recorded in B-163 (6.1 and 6.3 in 2005 and 2006 years respectively) succeeded by V-59 (5.6). maximum seasonal growth was recorded in H-77 (43.8 cm) succeeded by ATPS-2 (33.6 cm).

Saraladevi *et al.* (2010) recorded vegetative growth parameters in 78 seed propagated progenies of sweet tamarind type which were planted at horticulture college and research institute, Periyakulam. Maximum plant height was recorded in genotype TIS-40 (5.88 m) and minimum in TIS-22 (2.00 m), maximum tree girth was recorded in TIS-23 (53 cm) and minimum in TIS-53 (20 cm), canopy spread of the tree was ranged from 5.2 m² to 17.64 m² (TIS-48)

The research on clonal diversity and deviation among 35 high yielding tamarind genotypes for genetic improvement was done by Divakara and Rathakrishnan (2011) and reported that appreciable diversity was noticed for all the growth parameters under open field condition. The highest plant height (60.33 cm), number of primary and secondary shoots (19.78) and trunk diameter at the collar region (1.49 cm) was observed in CPT-22, CPT-5 and CPT-7 respectively.

Bhatnagar *et al.* (2013) compared 15 genotypes of tamarind for growth parameters which are originated from various geographical locations of Rajasthan state, the maximum tree height recorded was 28.54 m, leaf length and leaf breadth recorded was 9.62 cm and 3.82 cm, respectively.

According to Bhogave *et al.* (2018) reported the diversity in 26 genotypes of tamarind at 'AICRP for Dryland Agriculture and Department of Horticulture, Dr. Panjab Rao Deshmukh Krishi Vidyapeeth', Akola. Significant range of diversity was observed for all the characters of different tamarind genotypes. 5 various canopy shapes were observed viz., dome, cone, oval, semicircle and irregular. Three various bark colors were recorded and differentiated as light brown, brown and thick brown among 26 genotypes. Whereas, 15 genotypes showed spreading growth pattern and 11 genotypes showed upright growth pattern. Among 26 tamarind genotypes only four genotypes were showing annual nature of growth and remaining twenty-two genotypes were showing biennial in growth habit.

2.3 Tree yield and yield attributing traits in tamarind

According to Challapilli (1992) wide variation was recorded during evaluation of seedling originated 24 tamarind progenies. The significant diversity in regard of weight of the pulp per fruit was ranged from 2.7 to 9.18 g, per cent pulp per fruit was ranged from 25.71 to 62.02 per cent, maximum fruit weight and seed weight recorded was 25.22 g and 8.18 g respectively and minimum fruit weight and seed weight recorded was 7.78 g and 1.6 g respectively. These diversity and heterozygosity observed in tamarind was a result of natural cross-pollination and observed three kinds of pod shapes viz., curved type, semi-curved type and straight type in tamarind genotypes.

Gangaprasad (1993) conducted a survey and recorded the diversity in tamarind among 282 genotypes from 6 districts of Southern Karnataka. The wide diversity was noticed for the parameters like fruit weight, seeds number per fruit, yield of the pulp, seed to pod ratio and tartaric acid content, *etc.* he also recorded pod yield which is varied from 30 to 210 kg per tree from Chitradurga I to Kolar-II areas respectively from 40-45 years old trees.

According to Hanamashetti (1996) pod produce per tree and number of pods per tree was reported from various tamarind genotypes at the age of 6 years which was in the range of 0.00 kg to 0.73 kg and 0.80 to 65.27 respectively. He also reported pod parameters in 40 promising genotypes of tamarind at Forest Research Center Gungararatti (Dharwad), the maximum pod height was observed in NTI-2 (11.48 cm), maximum width and weight of the pod was observed in NTI-19 (2.60 cm and 14.32 g respectively).

Evaluation of 52 tamarind genotypes in areas of Chittoor and Anantapur districts of Andhra Pradesh, reported that wide diversity was observed with respect to pod parameters. Fruit weight that is ranged from 16.40 g to 63.56 g, weight of the shell is varied from 3.0 to 13.40 g, ratio of rind to shell was ranged from 0.83:1 to 3.80:1 and weight of the vein varied from 0.37 g to 4.30 g (Mastan *et al.*, 1997).

Azhakiamanavalan and Vadivel (1997) compared the morphological traits of pod between two varieties *i.e.* PKM-1 and locally grown variety at Horticultural College and Research Institute, Tamil Nadu. It was observed that pod length (16.70 cm), pulp

recovery per cent (39 %) and seeds number (9.70) was found maximum in PKM-1 compare to local variety (16.5 cm, 28 % and 9.10, respectively). Local type variety showed maximum shell weight (302 g/kg of fruit) and fiber content (38 g / kg of fruit) compare to PKM-1 (260 g /kg of fruit and 30 g /kg of fruit).

Singh *et al.* (1997) reported that Urigam genotype is extremely distinct from the other trees by bearing much bigger fruits. The size of the pod was ranged from 18.0 x 3.0 cm to 36.5 x 5.0 cm which was nearly three times larger the size of the pods collected at Coimbatore.

According to Hanamashetti and Sulikeri (1997), there is existence of wide variability for pod parameters that are observed in 40 tamarind genotypes which are 6-7 years old genotypes in Karnataka. Maximum pod length was observed in NTI-32 (11.83 cm), maximum pod width was observed in NTI-19 (2.60 cm), pods of NTI-57 was found to be thicker (1.70 cm) compare to other pods, pod weight varied from 5.73 g (S-4) to 16.84 g (NTI-32), maximum number of seeds per pod was found in NTI-62 (7.30) with highest seed weight observed in NTI-75 (5.33 g). the maximum pulp weight per pod (5.68 g) and per cent pulp (43.05 %) were observed in NTI-62. The maximum shell weight per pod and shell weight per cent was observed in NTI-19 (5.04 g) and S-4 (42.04 %), respectively whereas yield was reported to be less than 5 kg per tree.

Kennedy *et al.* (1998) observed wide diversity with respect to pod and pulp characters in 84 tamarind genotypes at Tamil Nadu Agricultural University, Coimbatore. The fruit length was varied from 7.32 to 20.68 cm, the average weight of the fruit was ranged from 7 to 46.8 g. within the tamarind genotypes, sweet pulp type reported median values for different physical parameters. The colour of the pulp was ranged from reddish brown to various shades of blackish colour.

According to Rao *et al.* (1999), the aged trees having large plant stature with huge canopy yields approximately more yield than the trees of younger plantations having small plant stature with less canopy size. Near Urigam village in Tamil Nadu, a tree of 200 years old was recorded to yield 2 tonnes of pods per year. The average yield observations normally recorded was to be around 200 kg per tree per year. In Andhra Pradesh, the average yield per tree per year was significantly varied from 300-1500 kg per tree depends on various age levels of the plants.

Sivakumar (2000) reported that the average quantity of pods obtained by tamarind genotypes of 3-12 years aged trees was significantly ranged from 5-25 kg per tree and pulp content occupies 55 per cent of the tamarind pod.

According to Biradar (2001), wide variation was observed with respect to pod parameters within the 17 tamarind genotypes at forest research centre, Gungaragatti (Dharwad), the maximum length of the pod, pod width and maximum pod weight was observed in NTI-19 (12.16 cm, 2.93 cm and 16.20 g respectively), maximum pod girth was noticed in NTI-57 (1.64 cm) the weight of the pulp per pod ranges from minimum 2.78 g (S-4) to maximum 5.81 g (NTI-19), shell weight and vein weight per pod was varied from 2.30 g (NTI-70) to maximum 5.40 g (NTI-19) and 0.23 g (NTI-70) to 0.88 g (NTI-19) respectively. The pulp per cent per pod varied from 27.71 (S-4) to 39.59 (NTI-32), seeds number per pod was varied from 4.20 (NTI-15) to 7.70 (7.70) and maximum seed weight per fruit was observed in NTI-75 (5.10 g).

Biradar (2001) studied the pod parameters with in the 21 genotypes at Agricultural Research Station, Arabhavi, found the highest pod tallness and pod weight was observed in ATI-4 (15.75 cm and 16.44 g respectively), maximum pod width was found in ATI-16 (3.02 cm) and maximum pod girth was noticed in ATI-13 (1.73 cm).The maximum weight of the pulp per pod was observed in ATI-7 (6.27 g), highest shell weight per pod, vein weight per pod and per cent pulp per pod was observed in ATI-5 (4.92 g), ATI-19 (1.10 g) and ATI-10 (41.27 %) respectively. Seed weight per pod and number of seeds per pod was found maximum in ATI-5 (5.10 g and 8.50 respectively).

According to Biradar *et al.* (2002) the highest pod length, pod width and pod weight was noticed in HTI-3 (13.75 cm, 2.75 cm and 14.22 g respectively), maximum pod girth was observed in HTI-12 (1.69 cm), genotype HTI-3 showed highest pulp weight (5.23 g) and shell weight per pod (4.22 g), vein weight per pod was found maximum in HTI-15 (0.60 g), seed weight was found maximum in HTI-32 (4.74 g) and more number of seeds per pod was observed in HTI-27 (7.00) among 30 tamarind trees at Forest nursery near Halki (Soundatti forest range).

According to Kotecha and Kadam (2002), there is presence of wide variability with regard to physical characters of pods of three varieties viz., Prathisthan, No. 265

and Local variety. Fruit length was varied from 9.94-11.35 cm, maximum fruit weight observed was 18.52 g and minimum was 15.97 g, the highest fruit width and fruit thickness was 3.72 cm and 7.44 cm respectively. Pulp contributes 44.76 to 57.28 per cent to the pod weight.

Patil (2004) examined 38 various tamarind genotypes for the analysis of variation with respect to pod characters and yield related parameters at Forest Research Station, Gungaragatti (Dharwad). Among various genotypes, NTI-19 recorded maximum pod length (14.24 cm), pod width (3.15 cm), pod girth (1.78 cm), minimum pod length, pod width and pod girth was observed in NTI-74 (9.11 cm, 1.77 cm and 1.15 cm, respectively), the highest weight of the pulp was found in genotype NTI-19 (10.25 g), shell weight was observed high in NTI-6 (6.98 g), NTI-19 showed maximum vein weight per pod (1.149 g), NTI-85 showed highest seed weight per pod (5.67 g) and NTI-85 recorded maximum number of seeds per pod (8.07).

Similarly, Patil (2004) studied variability in 14 clonally propagated progenies in regard to pod parameters at Main Agriculture Research Station, Dharwad (Kumbapur farm). Progeny NTI-19 reported maximum pod length (16.02 cm) and minimum pod length was reported by PKM-1 (9.37 cm), width of the pod was varied from 1.89 cm (NTI-5) to 3.19 cm (NTI-80), maximum pod girth was noticed in NTI-80 (1.93 cm) and minimum in SMG-13 (1.44 cm), pulp weight was found maximum in NTI-19 (9.96 g), shell weight and vein weight per pod was found maximum in NTI-80 (7.59 g and 1.82 g, respectively), the highest seed weight was noticed in NTI-15 (5.49 g) and lowest in NTI-84 (2.69 g).

Patil (2004) reported diversity study in 20 clonal genotypes of tamarind at Kittur Rani Channamma College of Horticulture, Arabhavi. Genotype SMG-4 reported highest pod length (15.11 cm) and lowest in NTI-2 (9.28 cm), the highest pod width and pod girth was observed in NTI-19 (3.49 cm and 2.03 cm) and the lowest in NTI-7 (1.99 cm) and NTI-5 (1.40 cm) respectively, NTI-15 reported the highest pulp weight per pod (4.35 g) and the lowest in NTI-70 (2.10 g), the highest shell weight per pod was found in NTI-5 (5.30 g) and the lowest in NTI-57 (2.58 g), the highest vein weight per pod was observed in NTI-14 (0.70 g) and the lowest in NTI-5 (0.18 g), NTI-75 recorded the

highest seed weight per pod (5.76 g) and PKM-1 showed the lowest seed weight per pod (1.99 g).

Prabhushankar *et al.* (2004) evaluated 15 clones of tamarind for pod parameters at Bangalore. Among them, maximum pod length, pod width and pod girth was observed in Urigam (18.57 cm, 3.73 cm and 2.46 cm). Whereas, the highest pulp per cent was observed in Urigam (64.25 %) and the lowest in P-10 (23.98%), the highest shell per cent was observed in P-10 (36.76%) and lowest in Urigam (18.77), it was reported that, the highest seed weight per cent was noticed in P-13 (35.13) and lowest in Urigam (11.42), highest fiber per cent per pod was observed in P-14 (7.59) and lowest in S-18 (3.13%).

Ganachary (2005) conducted a analysis with respect to pod characters on 21 tamarind genotypes at Chitradurga and Kudligi (Bellary) districts of Karnataka. The maximum length of the fruit reported was 15.37 cm and pod weight was 16.29 g in genotype SKR-3. Weight of the pulp was varied from 2.73 (HMR-1) to 6.08 g (HMR-4), the maximum pulp per cent was found in HMR-3 (46.63 %) and minimum in SKR-4 (31.67 %), SKR-3 genotype reported maximum shell weight per pod (4.96 g), HMR-3 reported maximum number of seeds per pod (8.60) and minimum seed weight per pod (2.44 g), HMR-1 recorded minimum shell weight (1.00g) and minimum number of seeds per pod (2.13). Whereas, maximum seed weight per pod was noticed in genotype MNH-3 (5.60 g).

Ganachary (2005) conducted a research on 10 tamarind trees which are analyzed for pod parameters at Bellary and Davanagere area, results reported that, the maximum fruit length and pod weight was reported in the genotype YBL-1 (17.03 cm and 18.71 g, respectively), highest pod width was observed in ALR-1 (2.38 cm), and highest pod girth was reported in AGH-1 (1.33 cm), genotype YBL-1 reported maximum pulp weight per pod (7.82 g), shell weight per pod (5.47 g) and pulp per cent (41.80%). DBH-2 showed minimum pulp weight (3.26 g), AGH-2 reported minimum shell weight (2.34 g) and per cent pulp (33.92 %), JTP-2 reported lowest fiber weight per pod (0.35 g).

Abraham *et al.* (2006) conducted a study related to physical parameters of 56 Malabar tamarind genotypes at National Bureau of Plant Genetic Resources Regional

Station, Thrissur. Among them, maximum length of the pod and weight of the pulp reported was 82 mm and 56 g, minimum 43 mm and 7.5 g, respectively. Maximum number of seeds reported was 8 per pod and minimum 2 per pod, maximum seed weight reported was 3.0 g and minimum 0.6 g.

Divakara (2008) conducted a study with regard to pod parameters on 35 tamarind trees at Forest College and Research Institute, Mettupalayam (Tamil Nadu). The maximum pod length was observed in TI-22 genotype (26.60 cm), genotype TI-9 showed the highest pod width and pod girth (5.48 cm and 2.43 cm respectively). TI-9 reported the highest pulp weight (51.33 g), shell weight (17.90 g), vein weight (4.15 g), pulp per cent (61.42 %), pod weight (83.06 g) and seed weight (5.89 g). Whereas, minimum pod length was 8.31 cm, vein weight was 0.20 g, shell weight was 2.11 g, pod weight was 8.46 g, pulp weight was 4.23 g, seed weight was 1.91 g recorded in the genotype TI-26.

According to Rao and Subramanyam (2010), the highest weight of the pod was recorded in the genotype V-2 (32.8 g) followed by V-1 (31.3 g), genotype V-1 showed maximum pod length (18.4 cm), shell weight was 4.5 g, number of seeds per pod was 8.8 and seed weight per pod was 4.5 g. the minimum seed weight and shell weight observed was 1.8 g and 1.8 g respectively in genotype S-102 among 15 germplasm tamarind trees evaluated at Anantapur district of Andhra Pradesh, under less rainfall area for three years.

Fandohan *et al.* (2011) conducted a survey to study quantitative physical parameters of pods and seeds obtained from 10 locally selected tamarind genotypes that are grown under three various ecological zones. The average pod length was in the range from 11.76 cm to 28.24 cm, pod width was in the range from 1.53 to 3.88 cm and pod thickness was in the range of 1.4 cm to 2.3 cm. the mean number of seeds per pod was in the range of 5.32 to 10.9.

According to Nandini *et al.* (2011), a study was conducted on morphometric parameters of 100 tamarind trees that are located at legendary tamarind grove at Nallur village. Tree no. 167 reported maximum pod length (20.04 cm) and tree no. 110 reported minimum pod length (6.65 cm). The highest pod width was observed in tree no. 47 (4.84 cm) and the lowest in tree no. 69 (2.30 cm). Pulp weight was in the range of

0.93 g (tree no. 217) to 6.99 g (tree no. 131) and maximum pulp to seed ratio recorded was 11.2:1 in the genotype tree no. 201. Seed weight per pod was varied significantly in the range of 0.41 g to 5.31 g.

According to Lokesh *et al.* (2014), a study was conducted to analyze the morphometric diversity in pod and seed parameters of tamarind genotypes obtained from various agro-climatic zones of Tamil Nadu. Range of pod length observed was 8.59 cm to 13.67 cm, pod width was ranged from 2.21 cm to 3.37 cm and pod girth was in the range of 1.03 cm to 1.69 cm. weight of the pulp per pod, fresh fruit mass and fruit dry mass varied significantly in the range of 3.30 g to 9.42 g, 9.74 g to 16.41 g and 8.13 g to 14.83 g, respectively. Number of seeds per pod was ranged from 2.14 to 8.10.

A study was undertaken by Tadas *et al.* (2015) to analyze 25 tamarind trees at PDKV, Akola. Among them, genotype DAAT-W-7 recorded maximum pod length (19.46 cm) and 9.58 cm was the minimum pod length recorded by genotype DAAT-E-8. Pod width was in the range of 1.77 cm (DAAT-W-3) to 2.83 cm (DAAT-WF-4), genotype DAAT-W-4 recorded maximum weight of the pulp (5.82 g) and minimum was 3.57 g by genotype DAAT-E-4. Shell weight per pod and vein weight per pod was in the range of 2.36 g (DAAT-E-5) to 3.91 g (DAAT-WF-6) and 0.28 g (DAAT-W-8) to 0.69 g (DAAT-WF-7) respectively. Number of seeds and seed weight per pod was in the range of 4.00 to 8.80 and 2.81 g to 4.54 g, respectively.

According to Sharma *et al.* (2015), 12 tamarind genotypes were used for variability and physical parameters of pods and seed like pod weight which was in the range of 8.64 g to 27.70 g, pod length was in the range of 8.64 cm to 17.76 cm, pod width was in the range of 2.48 cm to 3.16 cm, number of seeds per pod was ranged from 3.38 to 9.77, seed weight ranged from 2.02 to 8.33 g, pulp weight, pulp per cent and pod yield was in the range from 4.10 g to 15.77 g, 47 – 55% and 47.44 kg/tree to 248.8 kg/tree.

Sinha (2015) conducted a study on physical parameters like pod length, pod width, pod girth, pod volume and pod density of the tamarind pod samples. The mean pod length observed was 9.04 cm, average pod breadth observed was 4.03 cm and pod thickness were 0.12 cm. the mean of pod weight, volume and density of pulp were observed to be 6.87 g, 4.21 cm³ and 1.48 g per cm³, respectively.

2.3.1 Other fruit crops

Saran *et al.* (2006) evaluated 35 genotypes of ber and reported that highest yield, number of flowers, fruit weight and flesh thickness was observed in variety Umran. Maximum tree height was observed in Desi Alwar genotype and Chhuhara reported maximum stem girth.

According to Lal *et al.* (2018), maximum TSS was observed in IC-0615610 genotype, highest ascorbic acid and total sugars was reported in IC0615613 and Coll.35.

Evaluation of five different banana cultivars for morphological traits was conducted by Jena *et al.* (2020) and reported that, NRCB Selection-10 showed 40.68% increase in yield compare to Budubale. Manjeri Nendran was observed to be superior in quality traits compare to other genotypes.

According to Bhalekar and Chalak (2016), cultivar PKM-1 reported maximum plant spread, number of fruits per tree (523.5), tree yield (46.2 kg) but highest fruit weight was noticed in PKM-2 (99.3 g).

Evaluation of 11 guava genotypes for morphological and quality traits was conducted by Patel *et al.* (2011) and reported that genotype RCGH-1 reported highest plant tallness, stem girth and fruit yield (14.18 kg/tree).

2.4 Quality parameters of the tamarind pulp

Lewis *et al.* (1954) reported that tamarind is the highly acidic fruit among all the natural foods and the main acid present in tamarind is tartaric acid which is in the range of 14 per cent to 18 per cent.

According to Shivanandam (1980) the maximum percentage of tartaric acid was observed in curved and bulged varieties (3.16%) of tamarind fruits succeeded by straight and bulged varieties (2.99 %).

According to Ishola *et al.* (1990) tamarind fruit consists a minute amount of vitamins like carotene, amino acids like thiamine and nicotinic acid. It has been reported that ascorbic acid was found in less amount in the range of 2 to 20 mg/100 g. percentage of tarataric acid present in the tamarind pulp ranged from 8 to 18 per cent, proteins and

crude fiber per cent in tamarind pulp ranged from 2.00 to 8.79 per cent and 2.20 to 18.30 per cent respectively. Total amount of sugar present in tamarind pulp was 41.20 per cent.

Keskar *et al.* (1989) conducted a survey on 14 tamarind types in Satara and Aurangabad districts of Maharashtra and reported that the per cent acidity in tamarind pulp varied from 5.25 per cent to 12.60 per cent.

A vast diversity was observed by Challapilli (1992) with respect to the amount of tartaric acid present in tamarind pulp, which was in the range of 8.94 to 14.98 per cent.

A study was under taken to evaluate the tamarind genotypes by Hanamanshetti and Sulikeri (1997) and observed that amount of tartaric acid was in the range of 5.43 per cent (NTI-62) to 16.70 per cent (NTI-32).

Two tamarind varieties like PKM-1 and locally grown cultivar were used from the analysis of chemical characters by Azhakiamanavalan and Vadivel (1997) at Horticulture College and Research Institute, Tamil Nadu. They observed that, variety PKM-1 reported maximum TSS (9.10°Brix), total sugars (28.50 %) and ascorbic acid (3.95 mg/100g). minimum TSS (8.80°Brix), total sugars (27.90 %) and ascorbic acid (1.98 mg/100g) was noticed in locally grown cultivar.

Mastan *et al.* (1997) analyzed 52 high yielding tamarind genotypes for chemical parameters like tartaric acid and total sugar content. Among them, Devaganipalli-1 tree reported maximum tartaric acid content (14.20 %) and minimum was observed in Palaram-1 tree (9.10 %). Devaganipalli-1 and Kothapalli-1 reported maximum total sugar content (24.8%), Dodda Swaragiri-1 reported minimum total sugar content (21.40%).

A study was conducted by Shankaracharya (1998) and reported the quantity of tannin (600 mg per 100g), reducing sugar (25-45%) and tartaric acid (8-18%) present in tamarind pulp.

According to Grollier *et al.* (1998), the tamarind pulp contains more quantity of reducing sugar and desirable quantity of organic acids, among them 98 per cent was contributed by tartaric acid.

According to Kennedy *et al.* (1998), the tartaric acid content present in tamarind pulp was in the range of 14.91 to 17.40 per cent among 84 tamarind genotypes which were grown at Tamil Nadu Agriculture University, Coimbatore. Sweet type varieties reported minimum tartaric acid content and small pods of tamarind reported maximum tartaric acid value.

The average quantity of total soluble solids reported was 9.35°Brix and mean titrable acidity recorded was 13.73 per cent by Benjamin and Seegobin (1999).

According to Biradar (2001), maximum tartaric acid content was observed in genotype NTI-32 (17.04%) and minimum in NTI-62 (9.92%) among 17 tamarind trees which were evaluated at Forest Research Station, Gungargatti, Dharwad. Meanwhile, another study was conducted at Agriculture Research Station, Arabhavi by selecting 21 tamarind genotypes, among them, ATI-7 genotype recorded maximum tartaric acid content (16.17%) and minimum was observed in ATI-14 (12.27%).

A study was undertaken by Kotecha and Kadam (2002) to analyze the chemical parameters in three varieties such as Prathisthan, No.265 and Local variety. They reported that, range of moisture content present in pulp was 12.60 to 13.60 per cent, titrable acidity was varied from 6.98 to 11.93 per cent, ascorbic acid content was in the range of 6.27 to 8.20 mg/100g and total sugar content was varied from 34.80 to 36.27%.

According to Hanamashetti *et al.* (2003) the maximum tartaric acid content was observed in ATI-7 (15.95%) and minimum in ATI-14 (12.27%) among 21 tamarind trees grown at Agricultural Research Station, Arabhavi.

Analysis was conducted by Prabhushankar *et al.* (2004) in regard of chemical composition by selecting 15 tamarind clonal genotypes and reported that, the quantity of titrable acidity present in tamarind pulp was in the range of 7.66 per cent (P-13) to 18.01 per cent (PKM-1) and S-18 reported maximum total soluble solids (19.77°Brix) and minimum in genotype P-10 (12.10°Brix).

Patil (2004) reported that tartaric acid content observed in tamarind pulp was ranged from 3.24 per cent (NTI-60) to 24.38 per cent (NTI-55) among the 38 tamarind trees grown at Gungaragatti. Another study was conducted on chemical parameters by selecting 20 tamarind genotypes at Arabhavi, genotype NTI-19 reported maximum tartaric acid content (17.44 %) and NTI-7 reported the lowest tartaric acid content (9.43%).

2.5 Genetic variability, heritability and genetic advance

According to Mastan *et al.* (1997), broad range of genetic variability was observed in tamarind genotypes for pod and yield traits. Fruit length, average weight of the fruit, pod girth, seeds per pod and pulp content reported high genotypic coefficient of variation and phenotypic coefficient of variation.

Biradar (2001) reported that genotypic coefficient of variation was observed to be lower than phenotypic coefficient of variation for plant height, number of leaves and plant girth. Tree height reported maximum heritability (68.16%) whereas, tree girth reported moderate heritability (48.70%).

According to Patil (2004), pod and yield attributes showed maximum phenotypic coefficient of variation compare to genotypic variation. Pod yield per tree and tree height reported maximum heritability (60.80% and 63.70% respectively). Crown size, number of pods per tree, shell weight and vein weight per pod showed modest heritability.

Mayavel *et al.* (2018) carried out an experiment to evaluate genetic variability studies for yield and quality traits and observed high genotypic variation was recorded for number of flowers/inflorescence, length of inflorescence, fruit length, fruit weight, fruit breath, pulp weight, seed weight and fruit yield/tree. All the attributes recorded high phenotypic coefficient of variation than the genotypic coefficient of variation.

Agasimani *et al.* (2019) reported that high degree of variation was observed for all characters in all cases, phenotypic variances were higher than the genotypic variance and the difference between phenotypic coefficient of variation and genotypic coefficient of variation were found to be narrow for most of the characters except crown size, plant

spread in east to west and north to south, trunk diameter, pod thickness, shell per cent, seed per cent and pulp per cent.

2.6 Correlation, path analysis and genetic divergence studies

Shivanandam and Thimmaraju (1988) conducted a correlation study in tamarind and reported that pod length was associated positively and significantly correlated with pod weight, number of seeds per pod, and pulp weight. Thickness of the pod was correlated negatively with seed weight, fiber weight and number of seeds.

A study was conducted by evaluating 300 tamarind genotypes for correlation study and reported that parameters like pod length, primary branches, trunk volume, and yield of the pulp found positively associated and highly significant correlation with pod yield (Samiullah and Sheriff, 1993).

Samiullah (1993) studied the genetic divergence for 20 yield and yield attributing traits among 300 tamarind genotypes through principal component analysis. The starting twelve components accounted for 99.63 per cent of variation among them, first two principal components accounted for 42.37 per cent of variation. Number of primary branches, trunk length, and pod yield per tree were the most important traits accounted towards divergence. Clustering was done based on the principal component scores and all 300 genotypes studied were grouped into sixteen clusters.

According to Hanamashetti (1996) height of the plant was associated positively and substantially correlated with diameter, spread and crown size of the tree. Tree diameter and spread of the tree in east to west direction were associated positively and substantially correlated with crown size and tree spread in north to south direction. Length of the tamarind pod was associated positively and correlated with pod weight, pod width, pulp weight, vein weight, shell weight, seed weight and number of seeds per pod significantly. There was a positive and non-significant correlation between pod length and pod thickness.

An experiment was conducted on correlation studies related to several pod characters and reported that high pulp weight was significantly and positively correlated with high shell weight, pod weight and low seed weight. (Karale *et al.*, 1999)

The plant height was associated with plant girth, crown size, spread of the tree in east to west and north to south and yield per plant positively and significantly correlation was observed among 21 tamarind plants Ganachary (2005).

According to Prasad *et al.* (2009) there was a significant and positive correlation between number of seeds and seed weight, significant and wide genetic diversity was observed for other pod characters.

According to Divakara (2009) an experiment was conducted on variability and correlation study for different pulp bio-chemical characters. The results showed that, there was a negative association between most of the traits and total tartaric acid content. Anthocyanin pigment was found to be negatively and significant associated with moisture content at genotype level.

According to Fandohan *et al.* (2011), the canonical discriminant analysis performed on the 10 morphophytes showed that the first two axes explained 82 per cent of the observed variation these axes were thus used to describe the relationships between the investigated descriptors and traditional morphophytes.

According to Divakara *et al.* (2011) 35 tamarind genotypes were selected for clustering analysis which resulted into two broad clusters. Genotypes comes under cluster-2 had combination of desirable traits and can be directly selected for further improvement by breeding.

According to Bileke *et al.* (2014) morphological traits of the tamarind pod (pod length, pulp weight, seed weight, real pulp value, seeds number and seed weight) were positively and significantly correlated with one another.

Pooja *et al.* (2018) conducted an experiment to evaluate and study the character association on yield and quality parameters of tamarind by considering 16 genotypes. The results of correlation co-efficient analysis revealed that pod length (cm), pod width (cm), pod weight (g), pulp weight (g), titrable acidity (%), total sugar (%), total soluble solids (⁰Brix) and pH attributes could be effectively used in tamarind improvement programme for selecting genotypes as they show positive association for higher yield.

Mayavel *et al.* (2018) conducted an experiment on correlation and path coefficient analysis to identify suitable selection indices in 21 red tamarind genotypes for 15 characters and reported that, in path coefficient analysis, the length of inflorescence, fruit length, anthocyanin content and total sugar contributing directly to the yield and hence it might be inferred that these traits could be considered as most important yield contributing traits in red tamarind.

2.7 Molecular characterization of tamarind genotypes

2.7.1 Molecular markers

Algabal *et al.* (2011) evaluated genetic relatedness among 36 tamarind trees using AFLP markers. 12 primer pairs were used for screening purpose and produced 702 bands, out of which 627 (89.3%) were polymorphic. The dissimilarity coefficient was in the range of 4.4 to 14.

Gangaprasad *et al.* (2013) studied genetic relatedness and molecular diversity among 13 Indian collections of tamarind and reported that twenty eight selected arbitrary primers were used for characterization using RAPD primers that generated 131 fragments, of which 116 (88.54%) were polymorphic. Two genotypes, NTI62 and NTI84 were distinguished by unique band specific to them. This could be attributed to highly cross-pollinating nature, small distribution area and that most tamarind genotypes grown in India are from seed source.

Kumar *et al.* (2015) used ten random amplified polymorphic DNA primers to evaluate the genetic variation in four flowering genotypes and five non- flowering of tamarind plants and reported that, the similarity level among these accessions grouped into six cluster groups at 0.76% and RAPD profiles of all the tamarind were compared. Total of 58 scorable bands were formed with seven primers that are ranges from one for OPG-13 to twelve for OPA-R15. Morphological closely linked genotypes were found to be dissimilar at the molecular level.

According to Nandini *et al.* (2011), RAPD primers were used to analyse the tamarind genotypes, total 61 scorable bands were obtained by using six primers which was in the range of 8 (OPA-R15) to 13 (OPA-Y01).

Sarmiento *et al.* (2017) investigated genetic variation study among 32 tamarind plus trees by using ISSR markers. 12 markers were used to evaluate eighty four loci and reported that, 8 loci (9.52 %) showed monomorphic and 76 (90.48 %) showed polymorphic banding pattern.

2.7.3 Other crops

Muzher *et al.* (2016) evaluated apple genotypes by using 8 pairs of SSR primers that produces 22 alleles, out of which 21 were polymorphic (95.45%).

The study was conducted to evaluate different pineapple genotypes and to estimate genetic diversity among the genotypes by using 18 microsatellite markers (SSR). Among them 10 markers were polymorphic that produces 22 reproducible bands with 2.2 bands per primer pair and bands was in the range of 1 to 3 with average 1.5 per primer pair Makaranga *et al.* (2018).

Caliskan *et al.* (2017) reported that, six SSR primers were used to evaluate 78 pomegranate genotypes from turkey and the data revealed that high level of polymorphism was observed in pomegranate germplasm.

Shinde *et al.* (2016) selected six grape genotypes for molecular characterization by using 8 RAPD primers and 5 ISSR primers. The study revealed that RAPD primers polymorphism was in the range of 33 to 100 per cent whereas, ISSR primers polymorphism was in the range of 42 to 100 per cent.

3. MATERIALS AND METHODS

The present investigation on “Assessment of genetic variability for productivity and quality traits in Tamarind (*Tamarindus indica* L.)” was carried out during 2019 and 2020 at Horticulture research experiment station, Hidkal Dam, Belagavi district and molecular study was conducted in the laboratory of the department of biotechnology, Kittur Rani Channamma College of Horticulture (University of Horticultural Sciences, Bagalkot), Arabhavi, Gokak taluk, Belagavi district of Karnataka state. The details of the experimental techniques, materials and criteria adopted during the course of investigation are presented in this chapter.

3.1 Geographical location and climatic conditions

The experiment was conducted at Hidkal Dam which is situated at 16.16⁰ latitude and 74.57⁰ longitude. Bio-chemical analysis was carried out at fruit science laboratory and molecular work was done in department of biotechnology, KRCCH, Arabhavi. Belagavi district, situated in agro-climatic zone-3 and region-2 of Karnataka state. Arabhavi lies at 15.84⁰North latitude and 74.51⁰East longitude, at a altitude of 612.05m above mean sea level. The average rainfall at Arabhavi is about 550mm and it is distributed over a period of seven months from May to November. The mean maximum temperature goes to 38.5⁰C (May) and the mean minimum temperature drops down to 18.5⁰C (February). The mean relative humidity ranges from 42.65 per cent (April) and 81 per cent (December).

3.2 Experiment No. 1: Assessment of genetic variability for yield and quality traits in tamarind genotypes

3.2.1 Materials

The materials for the present study consists of 61 tamarind genotypes, which are of 20 years old plants (Plate 1). The details of tamarind genotypes used in the study were presented in the below table.

3.2.2 List of genotypes used in experimental work

Sl.No.	Genotypes	Sl.No.	Genotypes	Sl.No.	Genotypes
1	G-1	22	G-24	43	G-46
2	G-2	23	G-25	44	G-47
3	G-3	24	G-26	45	G-48
4	G-4	25	G-27	46	G-50
5	G-5	26	G-28	47	G-51
6	G-6	27	G-29	48	G-52
7	G-7	28	G-30	49	G-53
8	G-8	29	G-31	50	G-54
9	G-9	30	G-32	51	G-55
10	G-10	31	G-33	52	G-56
11	G-11	32	G-34	53	G-57
12	G-12	33	G-35	54	G-58
13	G-13	34	G-36	55	G-59
14	G-14	35	G-37	56	G-60
15	G-15	36	G-38	57	G-61
16	G-16	37	G-39	58	G-62
17	G-17	38	G-40	59	G-63
18	G-18	39	G-41	60	G-64
19	G-19	40	G-42	61	G-65
20	G-20	41	G-44		
21	G-22	42	G-45		



Plate 1. General view of tamarind genotypes in the experimental plot

3.3 Observations recorded

The following vegetative and pod yield parameters were recorded in each of the selected tree.

3.3.1 Vegetative growth parameters

3.3.1.1 Plant height (m)

The tree height was measured from the bottom most level of the ground to the tip of the leading shoot using 'clinometer' and it is expressed in meters. The height of the tree is calculated using the formula.

$$\text{Height of the tree} = C \times D/100 + H_0$$

Where,

C – Clinometer reading

D – Distance at which the observer stands to shoot the clinometer

H₀ - Height of observer at his eye level

3.3.1.2 Trunk diameter (m)

The circumference of the trunk was measured at 1.3 meter height from the bottom most level of the ground. It was measured using measuring tape and the value was expressed in meters.

3.3.1.3 Spread of the tree (m)

The tree spread was obtained with the aid of measuring tape from east to west as well as north to south direction and the value is expressed in meters.

3.3.1.4 Crown size (m)

The size of the crown was obtained by adding tree spread from east to west, north to south direction and the average value was taken which was expressed in meters.

3.3.1.5 Days to flowering

The total number of days taken by the tree from the present season harvesting to the next season flowering was recorded.

3.3.1.6 Days to harvest

The total number of days taken by the tree from the previous season flowering to present season harvesting was recorded.

3.3.2 Pod parameters

Pods were harvested at full maturity stage and five pods in each tree is collected randomly and average was calculated. The per cent contribution of pulp, seed, shell and vein to the pod was worked out.

3.3.2.1 Pod length (cm)

The pod length was computed from bottom of the pod to the point where pod is attached to stalk with the help of measuring tape and the value is expressed in centimeters.

3.3.2.2 Pod width (cm)

The width of the pod was measured with the aid of verniercalliper and the value was expressed in centimeters.

3.3.2.3 Pod girth (cm)

The girth of the pod was measured with the aid of verniercalliper and it was expressed in centimeters.

3.3.2.5 Pulp weight per pod (g)

The pulp separated from each pod was weighed and average value was calculated and expressed as pulp weight per pod in grams.

3.3.2.6 Shell weight per pod (g)

The shell separated from each pod was weighed with the help of weighing balance and the average weight was calculated and expressed as shell weight per pod in grams.

3.3.2.7 Seed weight per pod (g)

The seeds were separated from the pods and the average weight of seeds was calculated with the help of weighing balance and expressed in gram.

3.3.2.8 Vein weight per pod (g)

The veins were separated from the pods and the average weight of vein was calculated with the help of weighing balance and expressed as vein weight per pod in gram.

3.3.2.9 Number of seeds per pod

The seeds were separated from the pods and the average number of seeds in each pod was calculated and expressed as number of seeds per pod.

3.3.2.10 Pulp per cent (%)

The pulp obtained from the known quantity of pods and it is expressed in percentage.

3.3.2.11 Shell per cent (%)

The shell obtained from the known quantity of pods and it is expressed in percentage.

3.3.2.12 Seed per cent (%)

The seed obtained from the known quantity of pods and it is expressed in percentage.

3.3.2.13 Vein per cent (%)

The vein obtained from the known quantity of pods and it is expressed in percentage.

3.3.2.14 Pulp: Shell ratio

The pulp and shell separated from each pod was weighed and the average ratio was calculated.

3.3.2.15 Pod weight (g)

The weight of the pod was recorded with the help of electrical weighing balance and the average value was calculated which was expressed in centimeters.

3.3.2.16 Pod yield per tree (kg/tree)

The pods were harvested at full maturity stage from individual tree and weighed with the aid of weighing balance and recorded as kilogram per tree.

3.3.2.11 Pod shape and pulp color

Pod shape was recorded in different genotypes and was expressed as straight, semi-curved and curved. Pod colour was recorded based on appearance of the pulp which was varied from brown to dark brown and to blackish brown.

3.3.3 Quality traits

3.3.3.1 TSS (°Brix)

Total soluble solids from each pod was recorded by using refractometer and the average value was obtained.

3.3.3.2 Per cent tartaric acid / Total acidity (%)

The mature pods were harvested during February and subjected for estimation of tartaric acid content in different genotypes of tamarind.

The tartaric acid of pulp was determined by the procedure given by Anon. (1975). The acid content was estimated by titrating 1 g of pulp extract was taken made up to 30 ml with the use of distilled water, 5ml of sample was taken from that and titrated against standard solution of 0.1N NaOH using few drops of one per cent

phenolphthalein as an indicator. The appearance of pink colour was marked as the end point.

$$\text{Tartaric acid (\%)} = \frac{T \times E \times N \times V_1}{V_2 \times W \times 1000} \times 100$$

Where,

T – Titre value

E – Equivalent weight of the acid (g) based on which organic acid is expressed (77.5 g)

N – Normality of alkali NaOH (0.1N)

V₁ – total volume made up with distilled water

V₂ – volume of the sample taken for estimation

W – weight of the sample taken

3.3.3.3 Ascorbic acid (mg/100g)

The estimation of ascorbic acid through titration method was adopted from Ranganna (1979). 1 gram of pulp was crushed in 4 per cent oxalic acid and homogenized extract of tamarind pulp was filtered carefully through a layers of muslin cloth. taken for estimation. The total volume was made up to 30 ml with the use of 4 per cent oxalic acid, 5 ml aliquot was taken in a 50 ml beaker and 5 ml of 4 per cent oxalic acid was added and stirred. It was titrated against 2, 6-dichlorophenol indophenol dye solution until pink end point was found which retained for few minutes.

$$\text{Ascorbic acid (mg/100g)} = \frac{\text{Ascorbic acid in standard} \times \text{TV}_2 \times \text{Vol. made up} \times 100}{\text{Aliquot taken} \times \text{TV}_1 \times \text{weight of sample}}$$

Where,

TV₂ - Volume of dye consumed for each sample was noted.

TV₁ – Volume of dye consumed for standard sample.

3.3.3.4 Total sugars (%)

The total sugar content present in tamarind pulp was estimated using dilute Hydrochloric acid by adopting Dinitro-salicylic acid (DNSA) method. One ml of evaporated extract was taken and kept in water bath till alcohol completely evaporated and allowed it to cool. Then phenolphthalein indicator was added followed by 1N sodium hydroxide till the solution turned to pink and 0.1 N hydrochloric acid was added to discolor the solution. Then Dinitro-salicylic acid was added to discolour the solution, 40 per cent Rochelle salt was added and the spectrometer readings were taken at O.D 540 nm. The results obtained were expressed in terms of percentage.

3.3.4 Analysis of Variance (ANOVA)

The data was analyzed by the methods outlined by Gomez and Gomez (1983) for Randomized Complete Block Design using the mean values of 12 characters to find out the significance of genotypes. The model of analysis of variance table adopted is given below.

Source	D.F	SS	MSS	Cal. F
Replication	(r-1)	RS	RSS/ (r-1)	
Treatments	(t-1)	TrSS	TSS/ (t-1)	TrMSS/EMSS
Error	(r-1) (t-1)	ESS	ESS/ (r-1) (t-1)	
Total	(rt-1)	TSS		

Where,

t = number of treatments

r = number of replications

SS = sum of square

MSS= Mean sum of square

DF = Degrees of freedom

TrMSS= Treatment mean sum of square

EMSS = Error mean sum of square

The standard error was calculated as, $SEm = \sqrt{\frac{EMSS}{r}}$

The significance of treatments mean sum of square and replication mean squares were tested by comparing with error mean squares referring to 'F' table values at 5 and 1 per cent level of probabilities.

In the present study, each genotype was considered as a treatment. 10 fruits from one tree were collected and 5 fruits are grouped as one replication hence, 2 replications are made (61 treatments and 2 replications).

3.3.5 Genetic variability

3.3.5.1 Assessment of variance components

Phenotypic and genotypic components of variances were estimated from ANOVA with the help of the formula suggested by Singh and Choudhary (1979).

$$\text{Genotypic variance (GV)} = \frac{\text{MSS (treatment)} - \text{MSS (error)}}{\text{Number of replications}}$$

$$\text{Phenotypic variance (PV)} = \text{GV} + \text{Environmental variation}$$

3.3.5.2 Coefficient of variation

Genotypic and phenotypic coefficients of variability were designed by the method given by Burton and Dewane (1953) based on estimate of genotypic and phenotypic variance.

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{GV}}{\bar{X}} \times 100$$

$$\text{Phenotypic coefficient of variance (PCV)} = \frac{\sqrt{PV}}{\bar{X}} \times 100$$

Where,

GV = Genotypic variance

PV = Phenotypic variance

$\bar{X}$ = General mean

GCV and PCV estimates were classified as per Shivasubramanian and Menon (1973).

0 – 10%	= Low
10 – 20%	= Moderate
20% and above	= High

3.3.5.3 Heritability (h^2)

Heritability for all the traits was calculated as the ratio of genetic variance to the phenotypic variance and expressed in percentage (Falconer, 1981).

$$h^2 = \frac{GV}{PV} \times 100$$

Where,

GV = Genotypic variance

PV = phenotypic variance

Scales for broad sense heritability was given by Searle (1965)

Below 40%	: Low
40 – 60%	: Moderate
60 – 80%	: High
Above 80%	: Very High

3.3.5.4 Genetic advance (GA)

Genetic advance for each parameter was worked out by adopting the formula given by Johnson *et al.* (1955).

$$GA = h^2 \times \sigma_p \times k$$

Where,

h^2 = Heritability

k = Selection differential which is equal to 2.06 at 5 per cent intensity of selection (Lush, 1949)

σ_p = Phenotypic standard deviation

3.4 Correlation, path analysis and genetic divergence

3.4.1 Simple correlation

The correlation coefficients were computed to determine the degree of association with yield and its components. It is estimated among all possible combinations at phenotypic and genotypic level using the formula given by Aljibourie *et al.* (1958).

$$r_p = \frac{\text{Cov. P (x,y)}}{\sqrt{\sigma^2_{px} \sigma^2_{py}}}$$

$$r_g = \frac{\text{Cov. g (x,y)}}{\sqrt{\sigma^2_{gx} \sigma^2_{gy}}}$$

Where,

- r_g and r_p are genotypic and phenotypic correlation coefficients, respectively.
- Cov. g (x,y) and Cov. P (x,y) are the genotypic and phenotypic covariance between the character X and Y, respectively.
- σ^2_{px} and σ^2_{py} are the phenotypic variance of the character of X and Y
- σ^2_{gx} and σ^2_{gy} are the genotypic variance of the character of X and Y

Test of significance of correlation was tested by comparing the 'r' value with obtained value.

3.4.2 Path coefficient analysis

The path coefficient analysis was performed as given by Wright (1921) and illustrated by Dewy and Lu (1959). The following set of simultaneous equations were formed and used for estimating direct and indirect effects of the important component traits on yield per plant.

$$r_{1y} = a + r_{12}b + r_{13}c + \dots + r_{1i}i$$

$$r_{2y} = r_{21}a + b + r_{23}c + \dots + r_{2i}i$$

$$r_{3y} = r_{31}a + r_{32}b + c + \dots + r_{3i}i$$

$$r_{ny} = r_{n1}a + r_{n2}b + r_{n3}c + \dots + r_{ni}i$$

Where,

- r_{1y} to r_{ny} = correlation coefficients between causal factors 1 to n dependent character Y
- $r_{12}, r_{21}, r_{13}, r_{31}, \dots, r_{ni}$ = correlation coefficient among the causal factor 1 to n
- $a, b, c, \dots, i$ = Direct effects of characters a to I on dependent character Y
- Residual effect (R) = $1 - (a^2 + b^2 + c^2 + \dots + i^2 + 2abr_{12} + 2acr_{13} + \dots)$

3.4.3 Genetic divergence

3.4.3.1 Mahalanobis D^2 analysis

Mahalanobis (1936) D^2 statistics was used for assessing the genetic divergence between populations. The original correlated unstandardized character mean values were transformed into standardized uncorrelated values to simplify the computational procedure. The D^2 values were obtained as the sum of squares of the differences between the pairs of corresponding uncorrelated values of any two genotypes (Rao, 1952). A total of D^2 values were calculated.

Where n = number of genotypes.

3.4.3.2 Clustering of genotypes

Using all $\frac{n(n-1)}{2}$ D^2 values, the genotypes were grouped into clusters using Tocher's method as described by Rao (1952).

3.4.3.3 Intra- and Inter-cluster distances

The intra- and inter-cluster distances were calculated by the formula given by Singh and Chaudhary (1977).

$$\text{Intra-cluster distance} = \sqrt{\frac{D_i^2}{n}}$$

Where D_i^2 is the sum of D^2 values between all possible combinations of the genotypes included in cluster 'i'.

$$\text{Inter-cluster distance} = \sqrt{\frac{D_{ji}^2}{n_i n_j}}$$

Where D_{ji}^2 is the sum of distances between all possible combinations ($n_i n_j$) of the genotypes included in the clusters 'i' and 'j'.

n_i = number of genotypes in cluster 'i'

n_j = number of genotypes in cluster 'j'

3.5 Experiment No. 2 : Molecular characterization of superior tamarind genotypes

In this experiment, 12 superior tamarind genotypes were screened for different SRAP primer combinations and ISSR primers for molecular characterization. The genotypes selected were G-16, G-17, G-22, G-24, G-25, G-26, G-27, G-30, G-32, G-33, and G-34.

3.5.1 Sample preparation

The leaf samples for DNA extraction were collected from all the 12 superior genotypes of tamarind individually which are fresh, matured and free from pest and disease symptoms. The leaves were washed firstly with distilled water and used immediately for DNA extraction.

3.5.2 Genomic DNA isolation

Following protocol was used for extracting DNA from all the samples.

1. Fresh young leaves were used for genomic DNA extraction using a modified CTAB method (Saiki *et al.*, 1998).
2. About 200mg of young leaves free from pest and diseases were selected and grinded using extraction buffer (consisting of 100mM Tris HCl of 8 pH, 2M NaCl, 25 mM EDTA, 2% C-TAB, 2% PVP and 0.2% β -Mercaptoethanol) with the help of pestle and mortar.
3. Homogenate was transferred to 2 ml Eppendorf tubes and kept in water bath at 60°C with occasional shaking for 1hr. After incubation, the tubes are allowed to cool to the room temperature.
4. one ml of chloroform: Iso-amyl alcohol (24:1) was added to the tubes and gently mixed by inverting the tubes for atleast 20 times. Then, the tubes were centrifuged at 8000 rpm for 15 minutes.
5. The upper supernatant (aqueous solution) was taken through pippete without touching the lower solid portion and transferred it to other tubes and was repeated once again.
6. The supernatant was transferred to 1.5 ml tubes. Then, 3/4th volume of isopropanol was added and gently shake. Kept in deep freezer over night to precipitate the DNA strands.
7. The sample was gently shaken by inverting the tubes and centrifuged at 8000 rpm for 20 minutes.
8. The pellet formed was washed and centrifuged with 70% (v/v) alcohol at 8000 rpm for 10 minutes. Then, the alcohol was drained out and alcohol was evaporated.
9. Later, storage buffer (T₁₀E₁) 100 μ l was added to the tubes after the tubes get rid of alcohol smell and make the DNA get dissolved in storage buffer by gentle tapping and the sample was stored in deep freezer for future usage.

10. RNase treatment: 3 μ l of RNase was added to the DNA sample and incubated in water bath at 37°C for 1hr and heat deactivation of RNAase was done by placing it at 50°C for 5 minutes. The stock of genomic DNA was stored at -20°C for quantification and further PCR analysis.

3.5.2 Quality check of DNA by gel electrophoresis

The quality of extracted genomic DNA was assessed by agarose gel electrophoresis.

3.5.2.1 Equipment and reagents used

- a. Electrophoresis unit, power pack, gel casting tray and comb
- b. Gel documentation unit
- c. Agarose – 0.8 per cent (for genomic DNA)
- d. 50X TAE buffer (pH 8.0)
 - a. Tris buffer
 - b. 0.5mM EDTA
- e. Loading/Tracking dye (6X)
- f. Ethidium bromide (6 μ l/100ml)

3.5.2.2 Procedure

1. Working area, swabbed gel tray and comb was cleaned with 70 per cent alcohol
2. Prepare gel tray by sealing the ends with tape. Comb was placed in the gel tray.
3. 0.8 per cent agarose gel was prepared by dissolving 0.8g agarose in 100 ml 1X TAE buffer and boiled in a microwave oven until the agarose melted completely and the solution become clear.
4. Agarose solution was allowed to cool for about 42-45°C and ethidium bromide was added to the solution at a concentration of 6 μ l/100ml and mixed well thoroughly.
5. The warm agarose gel solution was poured into the tray after placing combs and allowed to solidify for about 30 to 45 minutes at room temperature.

6. The comb and tape (used for sealing the tray) were removed carefully without disturbing the gel and the gel was placed in the electrophoresis tank containing 1X TAE buffer.
7. The tray was kept in such a way that the well side directed towards the cathode.
8. The samples were prepared by adding 7 μ l of DNA sample with 2 μ l of tracking dye, mixed well and was loaded into wells using a micro pipette.
9. Electrophoresed at 50-80 volts until dye has migrated to two third length of the gel.
10. The agarose gel was photographed under UV light by using Canon MF3010 camera and BioBEE gel doc system and saved in computer for further analysis.

3.5.3 Quality and Quantity check of the genomic DNA

1 μ l DNA aliquot was used as a sample and Tris-EDTA buffer was considered as blank and the DNA was quantified with the help of NanoDrop™ 2000/2000c Spectrophotometers. Meanwhile, spectrophotometer gives the readings of quantity of DNA present in stock with unit of ng/ μ l. Then working stock of DNA was made to 20 ng/ μ l for all individual samples of all genotypes.

3.5.4 Primer selection

The PCR product was loaded on 2.0 per cent agarose gel in 1X TAE buffer stained with ethidium bromide and bromophenol blue as a loading dye. Amplicons were separated in an electrophoresis unit at 80 V for two hours using 1X TAE buffer.

3.5.4.1 Sequence-related amplified polymorphism (SRAP)

The goal of the sequence related amplified polymorphism (SRAP) marker system is the amplification of open reading frames (ORFs) in the genome (Li and Quiros 2001). This molecular technique is based on two-primer amplification (forward and reverse primers). These primers are generally 17 or 18 nucleotides long. The SRAP marker system is a simple and efficient technique. They have a high ratio of codominance, give multiple bands and allow easy isolation for sequencing. The Primer sequence used in the present study is detailed below.

3.5.4.2 PCR amplification

Reagents used in PCR reaction mixture are as follows

Sl. No	Reagents	Reaction volume
1	Master mix	7.5 μ l
2	Forward primer (3 μ M)	1.5 μ l
3	Backward primer (3 μ M)	1.5 μ l
4	Sterile water	3.5 μ l
5	Template DNA (10 ng/ μ l)	1 μ l
Total		15 μl

Original DNA was diluted to 20 ng/ μ l in sterile distilled water.

3.5.4.3 Sequence of SRAP forward and reverse primers and their combination used for fingerprinting and diversity analysis

Forward primer		Reverse primer		Primer combination	
Name	Sequence	Name	Sequence	Forward	Reverse
Me11	TGAGTCCAA ACCGGACA	Em11	GACTGCGTA CGAATTTTCG	Me11	Em14
Me12	TGAGTCCAA ACCGGGAT	Em12	GACTGCGTA CGAATTGTC	Me12	Em13/Em14/ Em15
Me13	TGAGTCCAA ACCGGTAA	Em13	GACTGCGTA CGAATTGGT	Me13	Em13/Em15
Me14	TGAGTCCAA ACCGGGCT	Em14	GACTGCGTA CGAATTCAG	Me14	Em15
Me15	TGAGTCCAA ACCGGTGC	Em15	GACTGCGTA CGAATTCTG	Me15	Em11/Em12/ Em14

3.5.4.4 PCR temperature profile for SRAP markers

The thermal cycling was done on the guidance of Mishra *et al.*, 2011.

Sl. No.	Step	Temperature (°C)	Time (minutes)	Number of cycles
1	Initial denaturation	95	5	1
2	Denaturation	94	1	5
3	Annealing	38	1.15	
4	Extension	72	2	
5	Denaturation	94	1	30
6	Annealing	50	1.15	
7	Extension	72	2	
8	Final extension	72	10	1
9	Hold	10	1	-

After completion of 35 cycles, the samples were stored at 4⁰C in thermocycler and all the contents were loaded on to the gel for electrophoresis. Separation of PCR amplified products by agarose gel electrophoresis.

3.5.4.5 Inter Simple Sequence Repeats (ISSR) marker analysis

The quantified DNA of superior tamarind genotypes were diluted to a working solution with concentration of 20ng/ µl from the stock of known concentration and subjected to analysis using Inter Simple Sequence Repeats (ISSR) primers.

ISSR markers are DNA fragments having 100-3000 bp, they produce reproducible bands and need not go for sequencing of the data for primer construction.

3.5.4.6 Sequence of ISSR primers used for fingerprinting and diversity analysis

SL NO.	Primers name	Primers sequence
1	UBC 811	GAGAGAGAGAGAGAGAC
2	UBC 826	ACACACACACACACACC
3	UBC 810	GAGAGAGAGAGAGAGAT
4	UBC 855	ACACACACACACACACYT
5	P 817	CACACACACACACACAA
6	UBC 840	GAGAGAGAGAGAGAGAYT

3.5.4.7 PCR temperature profile for ISSR primers

Sl. No.	Steps	Temperature (°C)	Time (minutes)	Number of cycles
1	Initial denaturation	95	5	-
2	Denaturation	94	1	35
3	Annealing	50	1	
4	Extension	72	2	
6	Final Extension	72	10	-
7	Holding	10	∞ (Infinite time)	

3.5.5 Procedure for Gel electrophoresis.

1. Two per cent agarose gel was prepared by adding 2.0 g of agarose in 100 ml 1X TAE buffer and the solution was heated in microwave oven until the contents get completely dissolved and clear solution was obtained.
2. The solution was allowed to cool to 50°C with occasional swirling of the flask to cool uniformly and ethidium bromide was added at a concentration of 6µl /100 ml of solution and mixed well.
3. Gel casting tray was cleaned and end frame were placed on it and sealed well with a tape so as to hold the agarose gel in it. The tray was placed on a flat platform to maintain the uniform spread of the gel. The comb was properly placed on the frame *i.e.*, about 2mm, above the bottom of tray.
4. The molten agarose solution was slowly poured into the casting tray. The formation of air bubbles was avoided and allowed it to set completely till it becomes solid.
5. The combs were pulled out carefully from the solidified gel, removed the frames at the open ends and the gel was placed in the electrophoresis chamber.
6. The electrophoresis chamber was filled with 1X TAE Buffer sufficiently so that the gel got immersed about 2-3 mm below the surface of the buffer.
7. 15 µl PCR product of DNA sample was pipetted and loaded into separate individual wells in the gel.
8. Electrode were connected to the power supply, making sure the positive (red) and negative (black), are correctly connected to the electrophoresis unit

9. Power supply was about 47 volts for 15 minutes and later raised to 80 volts for 1.5hr. After the electrophoresis run, power was turned off and the gel was taken out of the buffer carefully using the gloves for DNA visualization.
10. The gel containing DNA was visualized under U.V. light using UV trans-illuminator and the photographs were captured and recorded.

3.5.6 Gel scoring

The base pairs ranging from 100 bp to 1.5 kb were scored manually. Only prominent clear bands were scored whereas, the faint bands were not considered. For a primer at a specific base pair if the band was present it was scored as '1' and if absent it was scored as '0'. This data was used for further analysis.

3.5.7 Cluster analysis

The genetic association were evaluated by calculating the Jaccard similarity coefficient for pair-wise comparisons based on the proportion of shared bands produced by the primers. The similarity matrix was subjected to the cluster analysis and dendrogram were generated by using NTSYS-PC Ver. 2.2 software (Rohlf, 2000). Jaccard co-efficient (S_{Jaccard}) computed as:

$$S_{\text{Jaccard}} = n_{AB}/n_A + n_B = n_{AB}$$

n_{AB} = number of bands common for samples A and B

n_A = Total number of bands in sample A

n_B = Total number of bands in sample B

3.5.8 Per cent polymorphism computed as,

$$\text{Per cent polymorphism} = \frac{\text{Total number of polymorphic bands}}{\text{Total number of bands}}$$

3.5.9 P.I.C. (Polymorphism Information Content) value

$$\text{P.I.C} = 1 - (T/n)^2$$

Where,

T – Total bands

n – number of genotypes

4. EXPERIMENTAL RESULTS

Evaluation of 61 tamarind genotypes with respect to several morphological and quality attributes were conducted at Horticultural research experimental station, Hidkal Dam. The results obtained in the present experiment are discussed under the following sub headings.

4.1 Variation for yield and quality traits in tamarind genotypes

4.1.1 Vegetative parameters

The observations regarding growth characteristics of the 61 tamarind genotypes are presented in Table 1.

4.1.1.1 Plant height (m)

The plant height showed wide variation among 61 genotypes which was ranged from 3.01 m to 7.63 m with a mean height of 5.22 m. Maximum plant height was observed in G-64 (7.63 m) followed by G-26 (7.52 m) and minimum plant height was reported in G-7 (3.01 m) followed by G-58 (3.02 m).

4.1.1.2 Plant spread (m)

The data reported in Table 1 stated that, G-22 showed maximum plant spread of 7.02 m in East-West direction and minimum was found in G-40 (3.02 m) genotype whereas, G-25 (7.98 m) showed maximum plant spread in North-South direction and minimum was observed in genotype G-7 (3.30 m).

4.1.1.3 Crown size (m)

Wide variation was found with respect to crown size among all the genotypes, where the mean crown size reported was 5.14 m. Maximum crown size was observed in genotype G-25 (7.48 m) followed by G-22 (7.26 m) and G-40 genotype reported minimum crown size of 3.26 m followed by G-1 (3.40 m).

4.1.1.4 Trunk diameter (m)

The data depicted in Table 1 showed the mean trunk diameter of 0.86 m and Maximum was reported by genotype G-16 (1.50 m) followed by G-25 (1.40 m)

Table 1. Estimates of growth parameters of seedling progenies of different tamarind genotypes

Sl. No.	Genotypes	Plant height (m)	Plant spread		Crown size (m)	Trunk diameter (m)	DTF (days)	DTH (days)
			E – W (m)	N -S (m)				
1	G -1	4.02	3.26	3.53	3.40	0.75	70	272
2	G - 2	3.05	3.76	3.50	3.63	0.75	80	276
3	G - 3	5.03	4.05	4.52	4.29	0.76	80	274
4	G - 4	3.81	3.31	3.51	3.41	0.62	78	274
5	G - 5	4.22	4.02	3.85	3.94	0.62	65	274
6	G - 6	4.19	3.38	3.54	3.46	0.92	79	274
7	G - 7	3.01	3.52	3.30	3.41	0.55	76	274
8	G - 8	4.81	3.89	4.23	4.06	0.87	72	268
9	G - 9	4.85	4.09	4.15	4.12	0.88	78	274
10	G - 10	3.63	3.51	3.75	3.63	0.55	79	274
11	G - 11	4.20	3.57	3.86	3.72	0.86	76	274
12	G - 12	6.08	6.01	6.49	6.25	1.10	76	274
13	G - 13	5.50	5.08	4.89	4.99	0.68	74	272
14	G - 14	5.23	4.52	5.51	5.02	0.81	80	272
15	G - 15	6.12	4.49	5.48	4.99	0.70	66	268
16	G - 16	6.78	6.47	7.45	6.96	1.50	65	262
17	G - 17	5.89	5.51	6.29	5.90	0.83	65	262
18	G - 18	4.25	3.79	4.15	3.97	0.54	78	272
19	G - 19	5.08	3.96	3.81	3.89	0.90	75	272
20	G - 20	6.27	5.01	5.12	5.07	0.81	80	272
21	G - 22	7.01	7.02	7.49	7.26	1.10	70	268
22	G - 24	5.79	5.98	7.45	6.72	1.00	70	262
23	G - 25	7.03	6.97	7.98	7.48	1.40	65	268
24	G - 26	7.52	5.48	5.97	5.73	1.30	66	270
25	G - 27	6.43	6.63	6.52	6.58	0.90	76	270
26	G - 28	4.52	5.99	6.53	6.26	0.86	80	272
27	G - 29	5.04	6.48	7.49	6.99	0.95	71	272
28	G - 30	6.54	5.51	6.32	5.92	0.84	80	274
29	G - 31	5.99	6.52	6.43	6.48	1.10	78	274
30	G - 32	5.55	6.03	6.56	6.30	0.95	70	272
31	G - 33	5.98	6.51	6.12	6.32	1.00	71	271

Contd.....

Sl. No.	Genotypes	Plant height (m)	Plant spread		Crown size (m)	Trunk diameter (m)	DTF (days)	DTH (days)
			E – W (m)	N -S (m)				
32	G - 34	6.03	6.49	6.23	6.36	0.99	72	270
33	G - 35	4.51	5.50	6.51	6.01	0.72	72	268
34	G - 36	5.72	5.18	5.03	5.11	0.97	70	262
35	G - 37	4.23	4.02	4.08	4.05	0.65	76	268
36	G - 38	4.99	4.99	4.49	4.74	0.85	68	274
37	G - 39	6.09	5.51	6.21	5.86	0.90	77	278
38	G - 40	5.01	3.02	3.50	3.26	0.75	76	278
39	G - 41	5.11	5.99	6.04	6.02	0.82	68	274
40	G - 42	5.98	5.49	5.05	5.27	0.93	76	278
41	G - 44	5.19	5.19	4.51	4.85	0.83	80	278
42	G - 45	4.17	4.98	5.01	5.00	0.77	76	276
43	G - 46	5.43	5.52	4.52	5.02	0.80	70	276
44	G - 47	4.82	3.49	3.81	3.65	0.73	78	278
45	G - 48	6.03	4.82	5.05	4.94	1.11	79	278
46	G - 50	5.47	5.98	4.98	5.48	0.73	68	274
47	G - 51	4.96	4.48	4.88	4.68	0.86	80	274
48	G - 52	5.62	5.01	4.52	4.77	0.83	76	276
49	G - 53	5.79	4.29	5.49	4.89	0.85	67	274
50	G - 54	4.29	4.31	4.21	4.26	0.70	80	274
51	G – 55	4.18	4.25	4.10	4.18	0.78	72	274
52	G – 56	4.31	4.87	4.47	4.67	0.80	76	272
53	G – 57	5.02	6.51	6.53	6.52	0.92	78	272
54	G – 58	3.02	4.48	5.08	4.78	0.38	80	268
55	G – 59	4.91	4.52	5.40	4.96	0.80	79	270
56	G – 60	5.98	5.51	5.51	5.51	0.86	76	276
57	G – 61	4.86	6.32	6.04	6.18	0.78	71	276
58	G – 62	4.52	5.08	4.98	5.03	0.80	70	276
59	G – 63	4.61	4.11	4.32	4.22	0.70	68	268
60	G – 64	7.63	7.01	6.52	6.77	1.27	69	278
61	G – 65	6.82	5.99	6.54	6.27	1.40	72	278
	Mean	5.22	5.04	5.24	5.14	0.86	73.92	272.51
	Min.	3.01	3.02	3.30	3.26	0.38	65	268
	Max.	7.63	7.02	7.98	7.48	1.50	80	278

whereas, minimum trunk diameter was reported by genotype G-58 (0.38 m) followed by G-4 and G-5 genotypes with a trunk diameter of 0.62 m.

4.1.1.5 Days to flowering

The data regarding days to flowering was depicted in Table 1. The number of days taken for flowering in all tamarind genotypes ranged from 65 days to 80 days from harvesting.

4.1.1.6 Days to harvesting

The data regarding days to harvesting was depicted in Table 1. The number of days taken for harvesting of pods in all tamarind genotypes ranged from 262 days to 278 days from flowering.

4.1.2 Yield related parameters

Data regarding yield characteristics were presented in Table 2. for all the tamarind genotypes (Plate-2).

4.1.2.1 Pod length (cm)

The average pod length of 11.90 cm was reported among 61 genotypes. The highest pod length was 15.49 cm found in G-26 genotype followed by G-25 with pod length of 15.08 cm. Whereas, minimum pod length was reported in G-54 (7.42 cm) followed by G-4 (8.13 cm) genotype.

4.1.2.2 Pod width (cm)

The data depicted in table 2 showed the mean pod width of 2.27 cm and pod width was varied from 1.84 cm to 3.33 cm among all genotypes. Maximum pod width was reported by genotype G-51 (3.33 cm) followed by G-26 (2.79 cm). Whereas, minimum pod width was reported by genotype G-4 (1.84 cm) followed by G-3 (1.85 cm) and G-7 (1.85 cm) genotypes.

4.1.2.3 Pod girth (cm)

The pod girth was significantly varied among different genotypes which was presented in table 2. where the mean pod girth reported was 1.46 cm. Maximum pod

Table 2. Estimates of pod length, pod width, pod girth, pulp weight per pod, shell weight per pod and seed weight per pod of the tamarind genotypes

Sl. No.	Genotypes	Pod length (cm)	Pod width (cm)	Pod girth (cm)	Pulp weight per pod (g)	Shell weight per pod (g)	Seed weight per pod (g)
1	G -1	11.70	2.35	1.26	3.06	3.59	3.79
2	G – 2	10.80	1.91	1.32	3.23	3.38	3.62
3	G – 3	9.57	1.85	1.25	3.55	2.78	3.13
4	G – 4	8.13	1.88	1.32	3.32	2.64	2.60
5	G – 5	12.63	1.91	1.50	6.12	4.75	5.90
6	G – 6	10.05	1.84	1.33	3.90	3.32	3.16
7	G – 7	9.21	1.85	1.22	3.91	2.81	2.75
8	G – 8	10.11	2.03	1.33	5.85	2.81	4.38
9	G – 9	13.28	2.41	1.48	8.46	4.30	7.30
10	G – 10	11.12	2.16	1.41	4.92	3.16	4.64
11	G – 11	9.50	2.37	1.54	6.49	2.92	4.29
12	G – 12	11.75	2.59	1.68	6.52	3.90	6.48
13	G – 13	9.28	2.36	1.45	5.03	3.49	4.27
14	G – 14	9.21	2.42	1.29	5.70	2.88	4.43
15	G – 15	12.60	2.24	1.40	6.61	4.09	5.08
16	G – 16	13.38	2.28	1.43	5.91	4.70	7.25
17	G – 17	11.68	2.12	1.44	5.68	3.56	5.38
18	G – 18	9.59	2.20	1.54	6.49	3.54	4.14
19	G – 19	10.30	1.99	1.40	4.80	2.60	5.26
20	G – 20	9.85	1.87	1.35	4.00	3.50	3.25
21	G – 22	13.89	2.42	1.51	7.18	5.13	6.59
22	G – 24	14.36	2.64	1.43	8.51	3.93	5.84
23	G – 25	15.08	2.35	1.48	7.83	3.95	6.02
24	G – 26	15.49	2.79	1.30	9.85	4.47	7.51
25	G – 27	13.92	2.45	1.55	8.95	4.27	7.33
26	G – 28	13.67	2.27	1.54	7.10	3.83	5.69
27	G – 29	13.43	2.17	1.48	7.03	3.02	5.76
28	G – 30	12.50	2.01	1.56	6.10	3.10	4.68
29	G – 31	12.19	2.00	1.46	5.32	4.98	4.21
30	G – 32	11.28	2.21	1.39	6.49	3.00	4.91
31	G – 33	13.75	2.30	1.64	7.46	4.13	5.67
32	G – 34	12.66	2.48	1.72	9.55	4.70	7.25
33	G – 35	11.49	2.18	1.31	6.01	2.82	4.75

Contd.....

Sl. No.	Genotypes	Pod length (cm)	Pod width (cm)	Pod girth (cm)	Pulp weight per pod (g)	Shell weight per pod (g)	Seed weight per pod (g)
34	G – 36	10.93	2.19	1.61	5.73	4.38	5.63
35	G – 37	12.95	2.38	1.33	5.51	3.50	4.26
36	G – 38	14.66	2.29	1.67	7.93	5.24	5.51
37	G – 39	12.33	2.41	1.68	7.15	3.96	5.94
38	G – 40	12.53	2.16	1.53	5.88	4.03	6.81
39	G – 41	12.67	2.39	1.57	7.97	4.00	6.45
40	G – 42	12.08	2.07	1.62	5.19	4.37	5.69
41	G – 44	14.13	2.54	1.69	8.42	5.18	6.62
42	G – 45	13.16	2.55	1.56	8.02	5.43	6.93
43	G – 46	14.13	2.66	1.62	10.63	6.15	9.13
44	G – 47	12.11	2.71	1.44	9.43	4.44	7.74
45	G – 48	12.99	2.28	1.56	6.95	4.95	6.30
46	G – 50	12.99	2.16	1.51	7.06	4.73	5.53
47	G – 51	14.67	3.33	1.65	15.22	5.31	7.71
48	G – 52	10.70	2.11	1.39	4.89	3.23	4.68
49	G – 53	10.88	2.16	1.33	4.04	2.82	4.55
50	G – 54	7.42	2.17	1.31	4.56	3.04	5.07
51	G – 55	11.53	2.20	1.49	5.86	3.39	4.82
52	G – 56	14.58	2.75	1.53	10.54	6.84	7.73
53	G – 57	10.25	2.11	1.15	3.18	3.35	2.66
54	G – 58	11.53	1.93	1.22	3.27	3.54	3.24
55	G – 59	9.89	2.05	1.20	4.14	2.85	4.20
56	G – 60	12.45	2.40	1.52	7.26	3.99	3.55
57	G – 61	12.24	2.35	1.37	5.80	4.29	6.36
58	G – 62	11.18	2.13	1.56	3.86	3.20	3.79
59	G – 63	12.94	2.57	1.55	6.12	5.62	4.36
60	G – 64	8.22	2.21	1.61	5.30	2.65	3.07
61	G – 65	12.48	2.51	1.55	7.25	4.54	4.97
	Mean	11.901	2.273	1.461	6.362	3.919	5.256
	S.Em±	0.795	0.082	0.053	0.615	0.327	0.513
	CD 0.05	2.249	0.232	0.150	1.74	0.926	1.45
	CV (%)	9.450	5.11	5.15	13.67	11.786	13.81

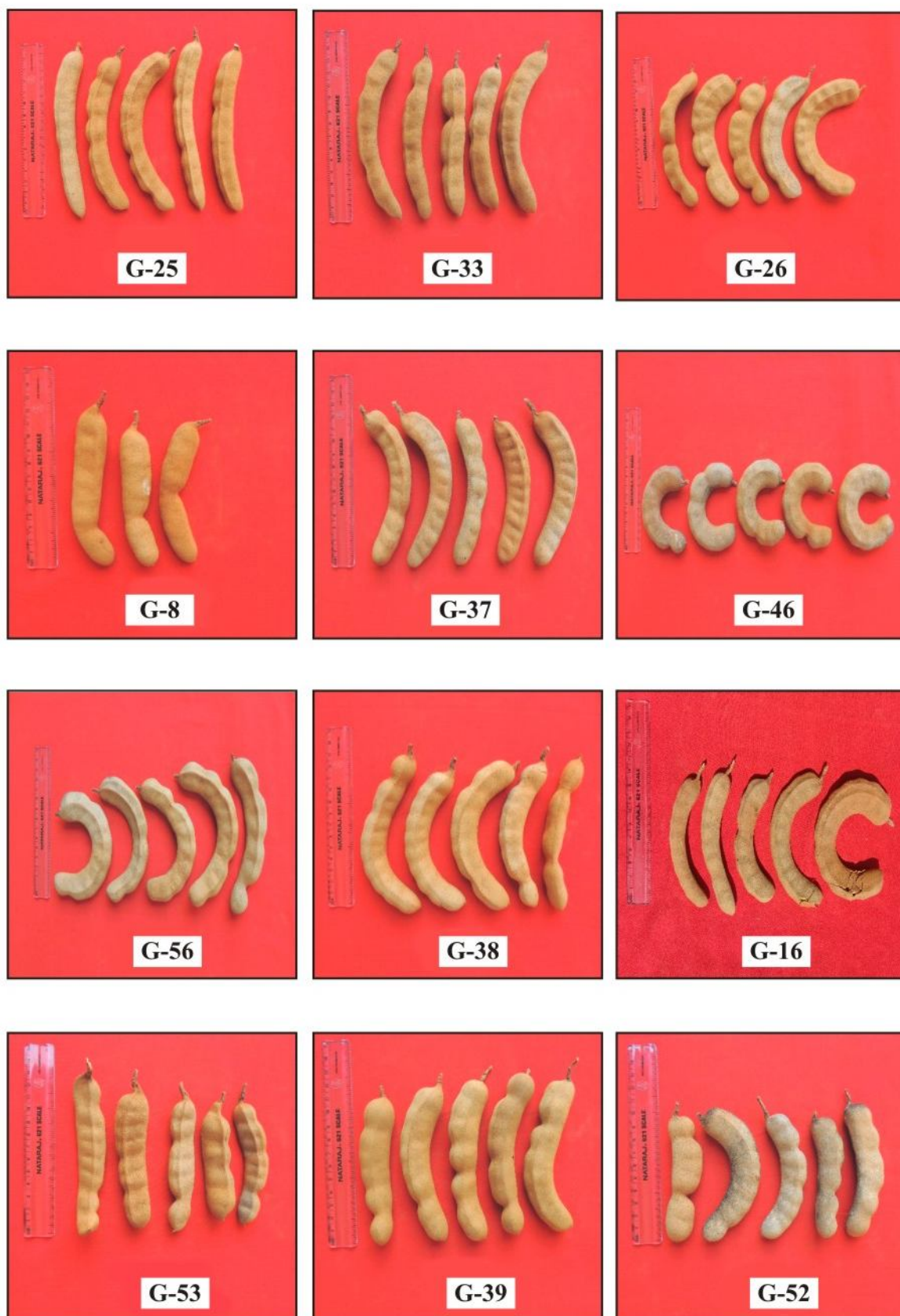


Plate 2a. Variability among pods of different tamarind genotypes

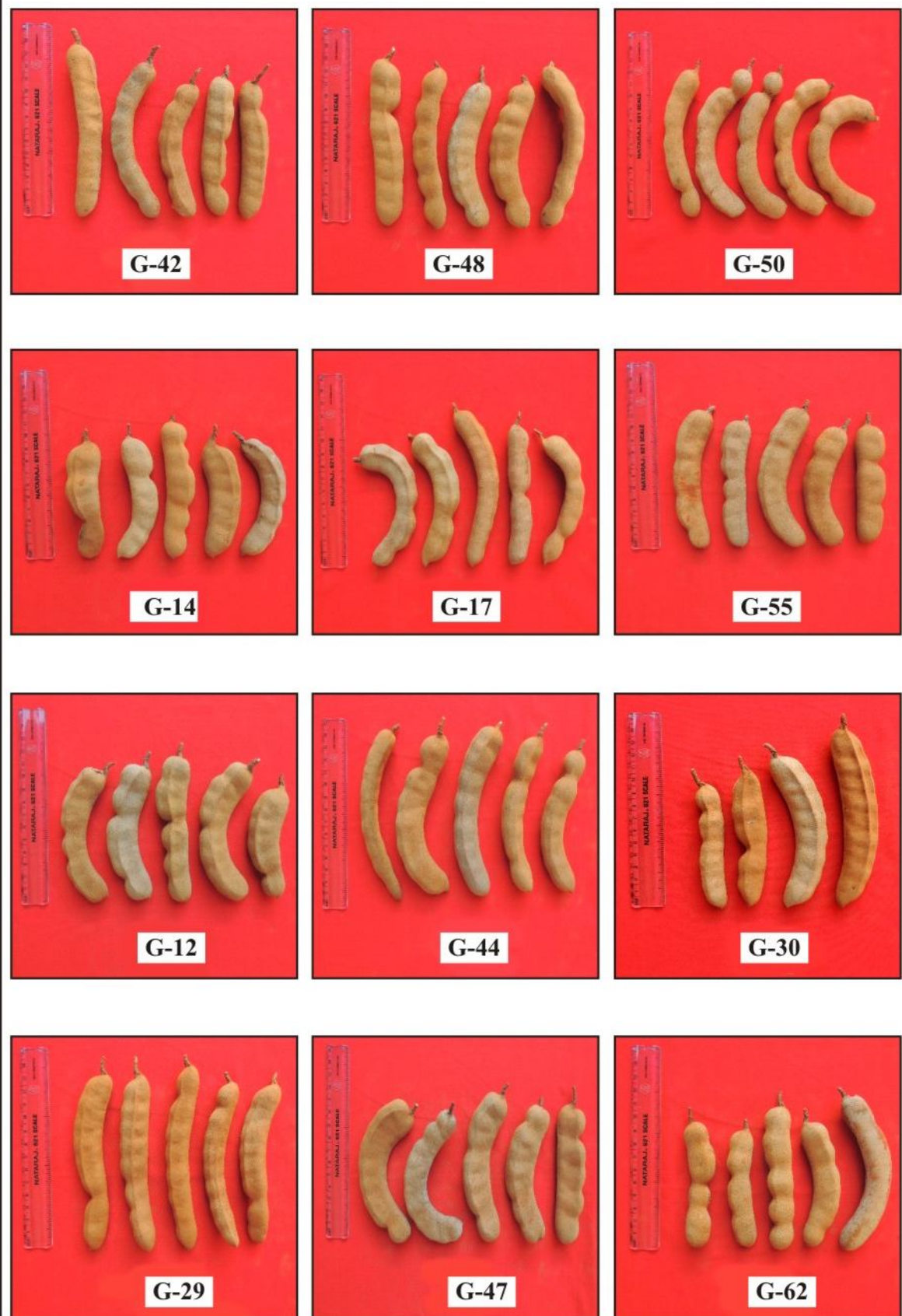


Plate 2b. Variability among pods of different tamarind genotypes



Plate 2c. Variability among pods of different tamarind genotypes

girth was observed in genotype G-33 (1.72 cm) followed by G-44 (1.69cm) and G-57 genotype reported minimum pod girth of 1.15 cm followed by G-59 (1.20 cm).

4.1.2.4 Pulp weight per pod (g)

Significant variation was found with respect to pulp weight among different genotypes (Table 2), where the mean pulp weight reported among tamarind genotypes was 6.36 g. The maximum pulp weight was observed in genotype G-51 (15.22 g) followed by G-46 (10.63 g) and G-56 (10.54 g). Whereas, genotype G-1 reported minimum pulp weight of 3.06 g followed by G-57 with pulp weight of 3.18 g.

4.1.2.5 Shell weight per pod (g)

The data regarding shell weight was depicted in Table 2, which reported significant variation among different genotypes with mean shell weight of 3.92 g. The maximum shell weight was observed in genotype G-56 (6.84 g) followed by G-46 (6.15 g). Whereas, G-19 genotype reported minimum shell weight of 2.60 g followed by G-4 with shell weight of 2.64 g.

4.1.2.6 Seed weight per pod (g)

Significant variation was found with respect to crown size among all the genotypes with the mean seed weight of 5.256 g. The genotype G-46 reported highest seed weight of 9.13 g followed by genotype G-47 (7.74 g) and G-4 genotype reported lowest seed weight of 2.60 g followed by G-57 (2.66 g) and G-7 (2.75 g).

4.1.2.7 Vein weight per pod (g)

Significant variation was found with respect to vein weight among all the genotypes which was depicted in Table 3, where the mean vein weight reported was 0.629 g. Genotype G-44 reported highest vein weight of 1.44 g followed by G-42 (1.27g) and G-34 (1.20 g). Whereas, lowest vein weight was noticed in genotype G-62 (0.22 g) and G-1 (0.22 g) followed by G-2 (0.23 g).

4.1.2.8 Number of seeds per pod

The data regarding number of seeds was depicted in Table 3, which reported significant variation among different genotypes with mean number of seeds of 6.56. The highest number of seeds were found in genotype G-46 (10.25) followed by G-16 (9.67). Whereas, G-2 and G-58 genotypes reported lowest number of seeds of 3.50, followed by genotype G-59 (3.70).

4.1.2.10 Pulp per cent (%)

The data depicted in Table 3, showed significant diversity in regard to pulp per cent with the mean value of 38.828 per cent and pulp per cent was varied from 28.56 to 51.95 per cent. The maximum pulp per cent was reported by genotype G-51 (51.95 %) followed by G-64 (46.91 %). Whereas, minimum pulp per cent was reported by genotype G-1 (28.56 %) followed by G-2 (30.58 %).

4.1.2.11 Shell per cent (%)

Significant variation was found with respect to shell per cent among all the genotypes (Table 3), where the mean shell per cent reported was 24.81 per cent. The maximum shell per cent was observed in genotype G-57 (34.29 %) followed by G-1 (33.75 %) and G-51 genotype reported minimum shell per cent of 18.14 per cent followed by G-29 (18.18 %).

4.1.2.13 Seed per cent (%)

The data depicted in Table 3, showed significant variability in regard to seed per cent with the mean value of 32.49 per cent and seed per cent was varied from 23.09 to 39.87 per cent. The maximum seed per cent was reported by genotype G-19 (39.87 %) followed by G-16 (39.07 %). Whereas, minimum pulp percent was reported by genotype G-60 (23.09 %) followed by G-63 (25.79 %).

4.1.2.12 Vein per cent (%)

The vein per cent showed significant variation among different genotypes with average vein per cent of 3.887 per cent among different genotypes. The highest vein per cent was 7.68 per cent found in G-42 genotype followed by G-44 with vein per cent of

Table 3. Estimates of vein weight per pod, number of seeds per pod, pulp per cent, shell per cent, seed per cent, vein per cent of the tamarind genotypes.

Sl. No.	Genotypes	Vein weight per pod (g)	No. of seeds per pod	Pulp per cent (%)	Shell per cent (%)	Seed per cent (%)	Vein per cent (%)
1	G -1	0.22	4.50	28.56	33.75	35.63	2.07
2	G – 2	0.23	3.50	30.58	32.28	34.92	2.22
3	G – 3	0.32	3.92	36.13	28.42	32.12	3.33
4	G – 4	0.35	4.25	37.42	29.53	29.09	3.96
5	G – 5	0.38	8.33	35.43	27.83	34.53	2.21
6	G – 6	0.35	4.00	36.10	30.96	29.66	3.25
7	G – 7	0.46	4.75	39.63	28.18	27.53	4.67
8	G – 8	0.42	6.42	43.55	20.91	32.39	3.15
9	G – 9	0.56	8.50	41.12	20.85	35.32	2.72
10	G – 10	0.37	7.00	38.02	24.14	35.03	2.81
11	G – 11	0.33	5.50	46.18	20.96	30.52	2.34
12	G – 12	0.82	7.25	36.70	22.07	36.58	4.65
13	G – 13	0.46	4.50	37.89	26.38	32.28	3.45
14	G – 14	0.42	5.50	42.25	21.49	33.17	3.09
15	G – 15	0.64	5.75	40.29	24.89	30.92	3.90
16	G – 16	0.69	9.67	31.89	25.31	39.07	3.73
17	G – 17	0.43	7.67	37.72	23.70	35.72	2.86
18	G – 18	0.62	6.50	43.89	24.21	27.78	4.12
19	G – 19	0.45	7.25	36.76	19.97	39.87	3.41
20	G – 20	0.36	3.61	36.08	31.36	29.35	3.21
21	G – 22	1.12	6.25	36.26	25.83	33.08	5.66
22	G – 24	0.51	7.17	45.27	20.94	31.08	2.71
23	G – 25	1.15	8.50	41.30	20.85	31.79	6.07
24	G – 26	0.70	8.17	43.70	19.84	33.36	3.10
25	G – 27	0.96	8.58	41.70	19.79	34.13	4.58
26	G – 28	0.64	7.42	41.11	22.18	32.96	3.75
27	G – 29	0.78	7.50	42.28	18.18	34.82	4.72
28	G – 30	0.92	7.25	41.19	20.94	31.63	6.25
29	G – 31	0.77	7.67	34.55	33.04	27.32	5.11
30	G – 32	0.53	7.58	43.49	20.11	32.85	3.55
31	G – 33	0.72	6.17	41.51	22.94	31.55	4.00
32	G – 34	1.21	8.00	42.07	20.70	31.91	5.28

Contd.....

Sl. No.	Genotypes	Vein weight per pod (g)	No. of seeds per pod	Pulp per cent (%)	Shell per cent (%)	Seed per cent (%)	Vein per cent (%)
33	G – 35	0.58	6.83	42.43	20.02	33.48	4.07
34	G – 36	0.61	6.67	35.04	26.81	34.39	3.71
35	G – 37	0.67	8.17	39.71	25.43	30.06	5.02
36	G – 38	0.66	6.58	41.17	27.06	28.37	3.40
37	G – 39	0.76	7.33	40.18	22.27	33.28	4.27
38	G – 40	0.88	8.50	33.42	22.93	38.59	5.01
39	G – 41	0.54	8.33	42.02	21.13	33.98	2.87
40	G – 42	1.27	7.67	31.41	26.50	34.41	7.68
41	G – 44	1.44	6.25	38.83	23.92	30.59	6.65
42	G – 45	0.62	8.17	38.19	25.87	32.99	2.96
43	G – 46	0.78	10.25	39.80	23.04	34.25	2.91
44	G – 47	0.65	7.50	42.24	20.10	34.74	2.92
45	G – 48	0.71	7.00	36.77	26.21	33.29	3.72
46	G – 50	0.48	7.42	39.68	26.56	31.04	2.72
47	G – 51	1.07	6.00	51.95	18.14	26.23	3.68
48	G – 52	0.38	6.75	37.20	24.46	35.47	2.88
49	G – 53	0.56	6.17	34.02	23.66	37.69	4.60
50	G – 54	0.83	6.50	33.70	22.57	37.57	6.17
51	G – 55	0.50	6.42	40.02	23.25	33.29	3.43
52	G – 56	0.76	7.75	40.84	26.40	29.85	2.92
53	G – 57	0.62	4.00	32.33	34.29	27.07	6.30
54	G – 58	0.47	3.50	31.02	33.54	30.98	4.46
55	G – 59	0.33	3.70	36.06	24.59	36.48	2.87
56	G – 60	0.74	5.67	46.37	25.75	23.09	4.79
57	G – 61	0.61	7.33	33.99	25.12	37.31	3.58
58	G – 62	0.22	5.42	34.72	28.88	34.38	2.02
59	G – 63	0.77	6.33	36.24	33.38	25.79	4.59
60	G – 64	0.34	3.75	46.91	23.25	26.91	3.14
61	G – 65	0.67	5.50	41.63	26.02	28.52	3.83
	Mean	0.629	6.56	38.828	24.815	32.492	3.887
	S.Em±	0.066	0.71	1.905	1.625	1.660	0.414
	CD 0.05	0.187	2.01	5.403	4.5977	4.697	1.172
	CV (%)	14.84	15.32	6.940	9.262	7.227	15.076

6.65 per cent. Whereas, minimum vein per cent was reported in G-62 (2.02 %) followed by G-1 (2.07 %) genotype.

4.1.2.14 Pulp: Shell ratio

Significant variation was found with respect to pulp: shell ratio among all the genotypes with the average value of 1.632. The maximum pulp: shell ratio was observed in genotype G-51 (2.86) followed by G-29 (2.33) and G-11 (2.24). Whereas, genotype G-1 reported minimum pulp: shell ratio of 0.85 followed by G-58 (0.93) and G-2 (0.95).

4.1.2.9 Pod weight (g)

The pod weight showed significant variation among different genotypes with average pod weight of 16.16 g was reported among 61 genotypes. The highest pod weight was 29.31 g found in G-51 genotype followed by G-46 with pod weight of 26.68 g and minimum pod weight was reported in G-57 (9.81 g) followed by G-3 (9.77 g) genotype.

4.1.2.15 Pod yield per tree (kg/tree)

The pod weight showed significant variation among different genotypes with average pod yield per tree was 33.29kg. The highest pod yield per tree was found in G-25 (115.20 kg/tree) followed by G-26 (83.30 kg/ tree) and minimum pod yield per tree was reported in G-7 (9.8 kg/ tree) followed by G-4 (10.00 kg/tree) genotype.

4.1.2.16 Pod shape

The wide variation was reported in regard to pod shape among various tamarind genotypes (Table 4). The different pod shapes recorded were straight, semi-curved and 'C' shape. Among 61 genotypes twenty four showed straight pods, thirty five genotypes showed semi-curved pods and 'C' shape pods were found in two genotypes.

4.1.2.16 Pulp colour

Genotypes varied significantly with respect to pulp colour (Table 4). The different pulp colour recorded were dark brown, brown and blackish brown. Among 61

Table 4. Estimates of pulp to shell ratio, pod weight, pod yield per tree, pod shape and pod colour of the tamarind genotypes

Sl No.	Genotypes	Pulp : Shell	Pod weight (g)	Pod yield per tree (kg/tree)	Pod shape	Pulp colour
1	G -1	0.85	10.67	13.00	Straight	Dark brown
2	G – 2	0.95	10.46	15.00	Semi-curved	Dark brown
3	G – 3	1.27	9.77	11.00	Semi-curved	Dark brown
4	G – 4	1.28	8.91	10.00	Straight	Brown
5	G – 5	1.29	17.15	20.00	Semi-curved	Dark brown
6	G – 6	1.17	10.72	19.30	Semi-curved	Brown
7	G – 7	1.42	9.93	9.80	Semi-curved	Brown
8	G – 8	2.08	13.46	18.50	Straight	Dark brown
9	G – 9	1.97	20.62	25.60	Semi-curved	Dark brown
10	G – 10	1.58	13.09	15.23	Semi-curved	Dark brown
11	G – 11	2.24	14.03	12.56	Straight	Brown
12	G – 12	1.67	17.72	16.52	Semi-curved	Brown
13	G – 13	1.44	13.24	19.20	Semi-curved	Dark brown
14	G – 14	1.97	13.43	17.00	Semi-curved	Dark brown
15	G – 15	1.62	16.42	37.80	Semi-curved	Dark brown
16	G – 16	1.32	18.56	76.00	Semi-curved	Brown
17	G – 17	1.59	15.05	70.70	Semi-curved	Brown
18	G – 18	1.82	14.79	16.77	Straight	Blackish brown
19	G – 19	1.84	13.11	15.63	Straight	Brown
20	G – 20	1.15	11.10	10.59	Semi-curved	Dark brown
21	G – 22	1.40	19.86	62.10	Semi-curved	Dark brown
22	G – 24	2.16	18.79	65.60	Semi-curved	Dark brown
23	G – 25	1.98	18.96	115.20	Straight	Dark brown
24	G – 26	2.20	22.53	83.30	Semi-curved	Dark brown
25	G – 27	2.11	21.51	64.90	Semi-curved	Dark brown
26	G – 28	1.85	17.26	51.30	Semi-curved	Dark brown
27	G – 29	2.33	16.59	60.40	Straight	Brown
28	G – 30	1.97	14.80	41.30	Straight	Dark brown
29	G – 31	1.06	15.27	56.80	Straight	Dark brown
30	G – 32	2.16	14.94	64.50	Straight	Dark brown
31	G – 33	1.81	17.98	69.30	Semi-curved	Dark brown
32	G – 34	2.03	22.71	48.90	Straight	Brown

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Sl. No.	Genotypes	Pulp : Shell	Pod weight (g)	pod yield per tree (kg/tree)	Pod shape	Pulp colour
33	G – 35	2.12	14.16	43.00	Straight	Dark brown
34	G – 36	1.31	16.35	37.10	Straight	Dark brown
35	G – 37	1.57	13.95	26.80	Semi-curved	Dark brown
36	G – 38	1.52	19.34	36.00	Semi-curved	Dark brown
37	G – 39	1.80	17.81	23.40	Straight	Dark brown
38	G – 40	1.46	17.61	25.30	Semi-curved	Brown
39	G – 41	2.01	18.96	31.00	Straight	Blackish brown
40	G – 42	1.19	16.53	20.23	Straight	Dark brown
41	G – 44	1.62	21.67	31.00	Semi-curved	Dark brown
42	G – 45	1.48	21.01	39.30	Semi-curved	Dark brown
43	G – 46	1.74	26.68	41.30	C shape	Dark brown
44	G – 47	2.11	22.26	26.80	Semi-curved	Dark brown
45	G – 48	1.41	18.91	22.50	Straight	Dark brown
46	G – 50	1.50	17.80	32.30	Semi-curved	Blackish brown
47	G – 51	2.86	29.31	41.50	Semi-curved	Dark brown
48	G – 52	1.53	13.19	25.30	Straight	Brown
49	G – 53	1.43	11.97	36.80	Semi-curved	Brown
50	G – 54	1.54	13.50	15.23	Semi-curved	Brown
51	G – 55	1.72	14.57	13.30	Straight	Brown
52	G – 56	1.56	25.87	25.80	C shape	Dark brown
53	G – 57	1.01	9.81	34.00	Straight	Dark brown
54	G – 58	0.93	10.52	12.56	Semi-curved	Dark brown
55	G – 59	1.47	11.51	14.89	Semi-curved	Dark brown
56	G – 60	1.81	15.54	16.00	Straight	Dark brown
57	G – 61	1.35	17.06	18.56	Semi-curved	Dark brown
58	G – 62	1.20	11.08	13.69	Straight	Dark brown
59	G – 63	1.09	16.87	21.23	Semi-curved	Brown
60	G – 64	2.02	11.35	12.35	Semi-curved	Dark brown
61	G – 65	1.60	17.42	59.80	Straight	Dark brown
	Mean	1.632	16.164	33.29		
	S.Em±	0.14	1.2834	1.34		
	CD 0.05	0.39	3.6305	3.81		
	CV (%)	11.82	11.228	5.72		

genotypes dark brown pulp was observed in forty two genotypes, brown pulp was observed in sixteen genotypes and blackish brown pulp was observed in three genotypes.

4.1.3 Quality parameters

4.1.3.1 TSS (°Brix)

The significant variation was reported among genotypes with respect to total soluble solids (Table 5) showing a mean value of 35.82 °Brix. The maximum TSS was recorded in genotypes G-32 (44.5 °Brix) followed by G-56 (43 °Brix) and minimum TSS was observed in G-33 and G-41 (27.5 °Brix).

4.1.3.3 Tartaric acid (%)

The data depicted in Table 5, showed significant diversity in regard to tartaric acid with the mean value of 14.39 per cent. The maximum tartaric acid content was reported by genotype G-33 (21.14 %) followed by G-63 (20.78 %) and G-41 (20.43). Whereas, minimum per cent of tartaric acid was reported by genotype G-2 (7.14 %) followed by G-35 (8.39 %).

4.1.3.2 Ascorbic acid (mg/100g)

Ascorbic acid showed significant variation among all the tamarind genotypes (Table 5) having average ascorbic acid value of 9.11 (mg/100g). The highest ascorbic acid recorded was 12.69 mg/100g observed in genotypes G-27, G-30 and G-62. Whereas, the minimum ascorbic acid was recorded by genotypes G-31 (4.62 mg/100g), G-13 (5.08 mg/100g).

4.1.3.4 Total sugar (%)

The total sugar showed significant variation among different genotypes with the average value of 33.42 per cent (Table 5). The highest total sugar was found in G-32 (41.67 %) followed by G-56 (41.53 %) and G-48 (40.26 %). Whereas, minimum total sugar was reported in G-33 (25.44 %) followed by G-36 (28.02 %) genotype.

Table 5. Estimates of quality parameters in different tamarind genotypes

Sl. No.	Genotypes	TSS (°Brix)	Tartaric acid (%)	Ascorbic acid (mg/100g)	Total sugars (%)
1	G -1	42.50	15.67	9.75	38.85
2	G – 2	38.50	7.14	6.81	28.91
3	G – 3	35.50	10.90	8.08	31.54
4	G – 4	36.00	8.67	11.19	31.39
5	G – 5	40.50	12.68	12.46	38.85
6	G – 6	36.50	10.24	7.50	32.25
7	G – 7	37.50	9.10	7.38	32.69
8	G – 8	31.00	17.26	9.81	30.66
9	G – 9	33.00	13.97	5.77	31.44
10	G – 10	30.60	18.94	10.38	31.44
11	G – 11	38.50	14.63	9.23	31.12
12	G – 12	40.00	10.69	5.19	36.44
13	G – 13	32.50	16.56	5.08	32.69
14	G – 14	32.00	15.97	7.62	30.38
15	G – 15	31.50	16.79	6.92	32.35
16	G – 16	38.50	10.22	8.08	34.54
17	G – 17	32.50	17.97	7.15	35.08
18	G – 18	28.50	18.67	9.38	36.12
19	G – 19	29.00	15.73	9.18	37.16
20	G – 20	41.50	10.06	7.27	33.14
21	G – 22	31.50	15.85	9.23	31.62
22	G – 24	38.50	12.92	11.54	33.77
23	G – 25	29.00	19.14	8.99	30.37
24	G – 26	40.00	12.85	10.38	39.85
25	G – 27	30.50	17.85	12.69	29.12
26	G – 28	38.00	12.45	7.87	34.29
27	G – 29	38.50	13.62	8.08	35.04
28	G – 30	39.00	12.45	12.69	36.60
29	G – 31	40.00	11.16	4.62	33.88
30	G – 32	44.50	11.74	10.38	41.67
31	G – 33	27.50	21.14	8.08	25.44
32	G – 34	36.50	16.67	6.92	37.38

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Sl. No.	Genotypes	TSS (°Brix)	Tartaric acid (%)	Ascorbic acid (mg/100g)	Total sugars (%)
33	G – 35	40.50	8.39	9.23	33.44
34	G – 36	30.00	15.73	11.54	28.02
35	G – 37	31.00	15.03	9.35	29.03
36	G – 38	29.50	17.26	10.96	28.21
37	G – 39	30.50	16.67	10.38	28.79
38	G – 40	36.00	13.15	9.23	28.87
39	G – 41	27.50	20.43	9.02	29.62
40	G – 42	38.50	12.80	9.11	32.92
41	G – 44	37.50	15.50	8.08	34.04
42	G – 45	37.50	13.62	9.23	30.49
43	G – 46	36.50	13.86	8.08	33.54
44	G – 47	40.50	9.04	12.12	39.00
45	G – 48	42.50	11.73	9.17	40.26
46	G – 50	36.50	17.97	8.08	33.54
47	G – 51	33.50	15.50	10.38	31.30
48	G – 52	31.50	16.67	11.54	29.32
49	G – 53	28.50	20.89	9.23	30.12
50	G – 54	40.50	15.62	9.23	41.40
51	G – 55	42.00	15.73	10.38	39.86
52	G – 56	43.00	11.09	6.92	41.53
53	G – 57	38.00	10.57	8.87	31.37
54	G – 58	32.50	12.23	7.27	31.13
55	G – 59	39.50	10.90	6.81	32.91
56	G – 60	42.50	14.97	10.38	37.69
57	G – 61	39.00	16.20	9.23	35.37
58	G – 62	34.00	17.73	12.69	34.60
59	G – 63	33.50	20.78	11.31	31.35
60	G – 64	41.50	10.25	10.38	34.69
61	G – 65	31.50	17.61	11.54	30.29
	Mean	35.82	14.39	9.11	33.42
	S.Em±	1.45	1.14	1.10	2.69
	CD 0.05	4.12	3.24	3.13	7.61
	CV (%)	5.75	11.25	17.19	11.32

4.2 Genetic variability parameters for yield traits

4.2.1 Pod length (cm)

Genotypic and phenotypic variation for pod length obtained was 2.79 and 4.05, respectively (Table 6) and the estimates of GCV and PCV for pod length was 14.03 and 16.91 respectively, which were moderate. High heritability of 68.80 per cent was obtained along with high genetic advance as per cent of mean (23.97) and genetic advance (2.85) for pod length.

4.2.2 Pod width (cm)

The GV and PV for pod width were depicted in Table 6 which was 0.068 and 0.082, respectively. The moderate estimates of GCV (11.53) and PCV (12.62) was obtained for pod width. Very high heritability (83.58 %) was obtained for pod width along with high genetic advance as per cent of mean (21.73) and genetic advance (0.49).

4.2.3 Pod girth (cm)

The genotypic and phenotypic variation for pod girth were depicted in Table 6. which was found to be 0.02 and 0.022, respectively. The low to moderate estimates of GCV (8.80) and PCV (10.20) was obtained for pod girth. High heritability (74.52) was obtained along with moderate genetic advance as per cent of mean (15.66) and genetic advance (0.23) for pod girth.

4.2.4 Pulp weight per pod (g)

The genotypic and phenotypic variation for pulp weight were depicted in Table 6. which was found to be 4.50 and 5.26, respectively. The high estimates of GCV (33.34) and PCV (36.04) was obtained for pulp weight. Very high heritability (85.61) was obtained along with high genetic advance as per cent of mean (63.56) and genetic advance (4.04) for pulp weight.

4.2.5 Shell weight per pod (g)

The genotypic and phenotypic variation for shell weight were presented in Table 6, which was found to be 0.78 and 0.99, respectively. The high estimates of GCV (22.57) and PCV (25.47) was obtained for shell weight. High heritability (78.52) was

Table 6. Estimates of mean, range and components of variance for yield parameters in tamarind genotypes

Sl. No.	Parameters	Mean	Range	GV	PV	GCV	PCV	h ²	GA	GAM
1	Pod length (cm)	11.90	7.42 - 15.49	2.79	4.05	14.03	16.91	68.80	2.85	23.97
2	Pod width (cm)	2.27	1.83 - 3.33	0.068	0.082	11.53	12.62	83.58	0.49	21.73
3	Pod girth (cm)	1.46	1.155 - 1.715	0.02	0.022	8.80	10.20	74.52	0.23	15.66
4	Pulp weight per pod (g)	6.36	3.06 - 15.22	4.50	5.26	33.34	36.04	85.61	4.04	63.56
5	Shell weight per pod (g)	3.91	2.60 - 6.84	0.78	0.99	22.57	25.47	78.52	1.61	41.20
6	Seed weight per pod (g)	5.26	2.60 - 9.135	1.97	2.50	26.75	30.10	78.98	2.57	48.98
7	Vein weight per pod (g)	0.63	0.22 - 1.44	0.06	0.07	40.58	43.21	88.20	0.49	78.51
8	Pod weight (g)	16.16	8.91 - 29.31	17.87	21.17	26.15	28.46	84.44	8.00	49.50
9	Number of seeds per pod	6.56	3.50 - 10.25	2.08	3.09	22.02	26.82	67.39	2.44	37.24
10	Pulp per cent	38.83	28.55 - 51.95	16.75	24.00	10.54	12.62	69.76	7.04	18.13
11	Shell per cent	24.81	18.14 - 34.29	14.53	19.81	15.36	17.93	73.34	6.72	27.09
12	Seed per cent	32.49	23.09 - 39.87	9.44	14.96	9.46	11.90	63.14	5.03	15.48
13	Vein per cent	3.887	2.02 - 7.68	1.32	1.67	29.64	33.25	79.45	2.11	54.42
14	Pulp : Shell ratio	1.632	0.93 – 2.86	0.14	0.18	23.27	26.10	79.23	0.69	42.74
15	Pod yield per tree (kg)	33.29	9.8 - 115.2	493.99	497.61	66.75	67.00	99.27	45.61	137.02

GV- Genotypic Variation

PV- Phenotypic Variation

GA- Genetic advance

GCV- Genotypic coefficient of variation h² - Heritability

PCV- Phenotypic coefficient of variation

GAM- Genetic advance over mean

obtained along with high genetic advance as per cent of mean (41.20) and genetic advance (1.61) for shell weight.

4.2.6 Seed weight per pod (g)

The genotypic and phenotypic variation for seed weight were 1.97 and 2.50, respectively. The high estimates of GCV (26.75) and PCV (30.10) was obtained for seed weight. High heritability (78.98) was obtained along with high genetic advance as per cent of mean (48.98) and genetic advance (2.57) for seed weight per pod (Table 6).

4.2.7 Vein weight per pod (g)

The genotypic and phenotypic variation for vein weight (Table 6) were 0.06 and 0.07, respectively. The low to moderate estimates of GCV (40.58) and PCV (43.21) was obtained for vein weight. Very high heritability (88.20) was obtained along with high genetic advance as per cent of mean (78.51) and genetic advance (0.49) for vein weight.

4.2.8 Pod weight (g)

The components of variation were depicted in Table 6 which shows that, GV and PV for pod weight was 17.87 and 21.17, respectively. The GCV (26.15) and PCV (28.46) was obtained for pod weight which was found to be high and Very high heritability (84.44) was obtained along with high genetic advance as per cent of mean (49.50) and genetic advance (8.00).

4.2.9 Number of seeds per pod

The genotypic and phenotypic variation for number of seeds (Table 6) were 2.08 and 3.09, respectively. The high estimates of GCV (22.02) and PCV (26.82) was obtained for number of seeds along high heritability (67.39), high genetic advance as per cent of mean (37.24) and genetic advance (2.44).

4.2.10 Pulp per cent (%)

The variation components for pulp per cent was presented in Table 6. With the values of GV (16.75) and PV (24.00) and the moderate estimates of GCV (10.54) and PCV (12.62) was obtained for pulp per cent. Heritability (69.76) was obtained which

was found to be high along with moderate genetic advance as per cent of mean (18.13) and genetic advance (7.04) for pulp per cent.

4.2.11 Shell per cent (%)

The GV and PV obtained for shell per cent was 14.53 and 19.81, respectively (Table 6) and the estimates of GCV (15.36) and PCV (17.93) obtained for shell per cent was found to be moderate. High heritability (73.34) along with high genetic advance as per cent of mean (27.09) and genetic advance (6.72) was obtained for shell per cent.

4.2.12 Seed per cent (%)

The variation components for seed per cent was calculated and presented in Table 6. Genotypic and phenotypic variation for seed per cent obtained was 9.44 and 14.96, respectively. The estimates of GCV (9.46) and PCV (11.90) obtained was found to be low to moderate for seed per cent. Heritability (63.14) obtained was high along with moderate genetic advance as per cent of mean (15.48) and genetic advance (5.03).

4.2.13 Vein per cent (%)

The GV (1.32) and PV (1.67) obtained for vein per cent was presented in Table 6, along with high estimates of GCV (29.64) and PCV (33.25). High heritability (79.45) was obtained along with high genetic advance as per cent of mean (54.42) and genetic advance (2.11) for vein per cent.

4.2.14 Pulp: shell ratio

The genotypic and phenotypic variation for pulp: shell ratio was 0.14 and 0.18, respectively (Table 6). The GCV (23.27) and PCV (26.10) obtained was high for pulp to shell ratio. High heritability (79.23) was obtained along with high genetic advance as per cent of mean (42.74) and genetic advance (0.69) for pulp to shell ratio.

4.2.15 Pod yield per tree (kg/tree)

The genotypic and phenotypic variation for pod yield per tree were 493.99 and 497.61, respectively. The high estimates of GCV (66.75) and PCV (67.00) was obtained

Table 7. Phenotypic correlation coefficients among pod traits in tamarind genotypes

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	1.000	0.535**	0.437**	0.632**	0.629**	0.634**	0.507**	0.518**	0.698**	0.192*	-0.220*	-0.011	0.091	0.577**
2		1.000	0.446**	0.790**	0.558**	0.629**	0.442**	0.352**	0.758**	0.461**	-0.396**	-0.117	-0.032	0.306**
3			1.000	0.550**	0.503**	0.499**	0.502**	0.417**	0.586**	0.300**	-0.291**	-0.093	0.121	0.180*
4				1.000	0.648**	0.790**	0.556**	0.541**	0.944**	0.649**	-0.570**	-0.161	-0.030	0.424**
5					1.000	0.684**	0.488**	0.486**	0.804**	0.002	0.126	-0.149	-0.004	0.268**
6						1.000	0.551**	0.787**	0.920**	0.166	-0.527**	0.395**	-0.028	0.433**
7							1.000	0.433**	0.631**	0.159	-0.327**	-0.074	0.763**	0.429**
8								1.000	0.673**	0.104	-0.470**	0.383**	0.047	0.463**
9									1.000	0.390**	-0.458**	0.020	0.018	0.443**
10										1.000	-0.648**	-0.485**	-0.093	0.221*
11											1.000	-0.304	-0.047	-0.340**
12												1.000	-0.150	0.050
13													1.000	0.196*

* significant at 5 per cent

** significant at 1 per cent

Table 'r' at 5% 0.177 at 1% 0.232

1. Pod length (cm)

5. Shell weight per pod (g)

9. Pod weight (g)

13. Vein per cent (%)

2. Pod width (cm)

6. Seed weight per pod (g)

10. Pulp per cent (%)

14. Pod yield per tree(kg/tree)

3. Pod girth (cm)

7. Vein weight per pod (g)

11. Shell per cent (%)

4. Pulp weight per pod (g)

8. Number of seeds per pod

12. Seed per cent (%)

for pod yield. Very high heritability (99.27) was obtained along with high genetic advance as per cent of mean (137.02) and genetic advance (45.61) for pod yield per tree.

4.3 Correlation, path analysis and genetic divergence for yield contributing traits

The correlation coefficient measures the relationship existing between pairs of characters. But, a dependent character is an interaction product of many mutually associated component characters and change in any one component will disturb whole network of cause and effect system. Phenotypic correlation for fruit yield and other fruit parameters were calculated and depicted in Table 7.

4.3.1 Phenotypic correlation

Pod yield per plant showed highly significant and positive association with pod length (0.577), number of seeds (0.463), pod weight (0.443), seed weight (0.433), vein weight per pod (0.429), pulp weight (0.424), pod width (0.306) and shell weight (0.268). Significant positive association with pulp per cent (0.221), vein per cent (0.196) and pod girth (0.1803). pod yield per plant showed negatively high significant association with shell per cent (-0.3398) and positively non-significant association with seed per cent (0.050) (Table 7).

Pod length showed positive and highly significant association with pod weight (0.698), seed weight (0.634), pulp weight (0.632), shell weight (0.629), pod width (0.535), number of seeds (0.518), vein weight (0.507) and pod girth (0.437). Whereas, significant and positive association with pulp per cent (0.192) and negative association with shell per cent (-0.220). Non-significant positive association with vein per cent (0.091) and negative association with seed per cent (-0.011).

Pod width showed highly significant and positively association with pulp weight (0.790), pod weight (0.758), seed weight (0.629), shell weight (0.558), pulp per cent (0.461), pod girth (0.446), vein weight (0.442), number of seeds (0.352) and negatively associated with shell per cent (-0.396). Whereas, pod width was non-significantly and negatively associated with seed per cent (-0.117) and vein per cent (-0.032).

Pod girth had highly significant and positively correlated with pod weight (0.586), pulp weight (0.550), shell weight (0.503), vein weight (0.502), seed weight (0.499), number of seeds (0.417), pulp per cent (0.300) and negatively associated with shell per cent (-0.291). There was non-significant and positive correlation of vein per cent (0.121) and negative correlation of seed per cent (-0.093) with pod girth.

Pulp weight had highly significant and positively associated with pod weight (0.944), seed weight (0.790), pulp per cent (0.649), shell weight (0.648), number of seeds (0.541), vein weight (0.556) and negatively associated with shell per cent (-0.570). There was non-significant and negative association of seed per cent (-0.161) and vein per cent (-0.030) with pulp weight.

Shell weight had highly significant and positively correlated with pod weight (0.804), seed weight (0.684), vein weight (0.488) and number of seeds (0.486). Whereas, non-significantly and positively correlated with shell per cent (0.126) followed by pulp per cent (0.002) and negatively correlated with seed per cent (-0.149) followed by vein per cent (-0.004).

There was highly significant and positive association of seed weight with pod weight (0.920), number of seeds (0.787), vein weight (0.551), seed per cent (0.395) and negative association with shell per cent (-0.527). Non-significant and positive association between seed weight and pulp per cent (0.166) whereas, negative association with vein per cent (-0.028).

Vein weight showed highly significant and positive correlation with vein per cent (0.763) followed by pod weight (0.631), number of seeds (0.433) and had negative association with shell per cent (-0.327). There was non-significant and positive association with pulp per cent (0.159) and negative association with seed per cent (-0.074).

Number of seeds showed highly significant and positive correlation with pod weight (0.673), seed per cent (0.383) and had negative association with shell per cent (-0.470). There was non-significant and positive association with pulp per cent (0.104) and vein per cent (0.047).

Pod weight showed highly significant and positive correlation with pulp per cent (0.390) and had negative association with shell per cent (-0.458). There was non-significant and positive association with seed per cent (0.020) and vein per cent (0.018).

Pulp per cent showed highly significant and negative association with shell per cent (-0.648) followed by seed per cent (-0.485). There was non-significant and negative association with vein per cent (-0.093).

Shell per cent had highly significant and negative association with seed per cent (-0.304) whereas, non-significant and negative association with vein per cent (-0.047). There was non-significant and negative association between seed per cent and vein per cent (-0.150).

4.3.2 Genotypic correlation

Genotypic correlation for fruit yield and other fruit parameters were calculated and depicted in Table 8.

Pod yield per plant showed highly significant and positive association with pod length (0.710), number of seeds (0.571), seed weight (0.487), pod weight (0.485), vein weight per pod (0.466), pulp weight (0.461), pod width (0.336), shell weight (0.307) and pulp per cent (0.267). Significant positive association with vein per cent (0.228) and pod girth (0.208). pod yield per plant showed negatively high significant association with shell per cent (-0.392) and positively non-significant association with seed per cent (0.051).

Pod length showed positive and highly significant association with pod weight (0.907), shell weight (0.865), seed weight (0.837), pulp weight (0.815), number of seeds (0.776), pod width (0.668), vein weight (0.634), pod girth (0.523) and pulp per cent (0.270). Whereas, negative association with shell per cent (-0.294). Positive and non-significant association of pod length was found with vein per cent (0.096) and negative association with seed per cent (-0.037).

Pod width showed highly significant and positively association with pulp weight (0.917), pod weight (0.877), seed weight (0.758), shell weight (0.649), pulp per cent (0.59), vein weight (0.492), pod girth (0.477), number of seeds (0.447) and negatively

Table 8. Genotypic correlation coefficients f pod traits in tamarind genotypes

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	1.000	0.668**	0.523**	0.815**	0.865**	0.837**	0.634**	0.776**	0.907**	0.270**	-0.294**	-0.037	0.096	0.710**
2		1.000	0.477**	0.917**	0.649**	0.758**	0.492**	0.447**	0.877**	0.590**	-0.501**	-0.139	-0.047	0.336**
3			1.000	0.668**	0.609**	0.605**	0.607**	0.512**	0.699**	0.445**	-0.393**	-0.156	0.171	0.208*
4				1.000	0.689**	0.831**	0.574**	0.599**	0.956**	0.708**	-0.617**	-0.169	0.005	0.461**
5					1.000	0.706**	0.574**	0.494**	0.823**	0.100	0.028	-0.203*	0.124	0.307**
6						1.000	0.595**	0.812**	0.931**	0.318**	-0.604**	0.330**	0.044	0.487**
7							1.000	0.525**	0.666**	0.161	-0.315**	-0.109	0.783**	0.466**
8								1.000	0.704**	0.271**	-0.612**	0.345**	0.182*	0.571**
9									1.000	0.493**	-0.523**	-0.026	0.091	0.485**
10										1.000	-0.709**	-0.392**	-0.179*	0.267**
11											1.000	-0.322**	0.025	-0.392**
12												1.000	-0.170	0.051
13													1.000	0.228*

* significant at 5 per cent

** significant at 1 per cent

1. Pod length (cm)

5. Shell weight per pod (g)

2. Pod width (cm)

6. Seed weight per pod (g)

3. Pod girth (cm)

7. Vein weight per pod (g)

4. Pulp weight per pod (g)

8. Number of seeds per pod

Table 'r' at 5% 0.177 at 1% 0.232

9. Pod weight (g)

13. Vein per cent (%)

10. Pulp per cent (%)

14. Pod yield per tree(kg/tree)

11. Shell per cent (%)

12. Seed per cent (%)

associated with shell per cent (-0.501). Whereas, pod width was non-significantly and negatively associated with seed per cent (-0.139) and vein per cent (-0.047).

Pod girth had highly significant and positively correlated with pod weight (0.699), pulp weight (0.668), shell weight (0.609), vein weight (0.607), seed weight (0.605), number of seeds (0.512), pulp per cent (0.445) and negatively associated with shell per cent (-0.393). There was non-significant and positive correlation of vein per cent (0.170) and negative correlation of seed per cent (-0.156) with pod girth.

Pulp weight had highly significant and positively associated with pod weight (0.956), seed weight (0.831), pulp per cent (0.708), shell weight (0.689), number of seeds (0.599), vein weight (0.574) and negatively associated with shell per cent (-0.617). There was non-significant and positive association of pulp weight with vein per cent (0.005) and negative association with (-0.169).

Shell weight had highly significant and positively correlated with pod weight (0.823), seed weight (0.706), vein weight (0.574) and number of seeds (0.494). Whereas, significant and negative correlation with seed per cent (-0.203). Positive and non-significantly correlated with vein per cent (0.124), pulp per cent (0.100), shell per cent (0.028)

There was highly significant and positive association of seed weight with pod weight (0.931), number of seeds (0.812), vein weight (0.595), seed per cent (0.330) and pulp per cent (0.318). Whereas, negative association with shell per cent (-0.604). non-significant and positive association between seed weight and vein per cent (0.044).

Vein weight showed highly significant and positive correlation with vein per cent (0.783) followed by pod weight (0.666), number of seeds (0.525) and had negative association with shell per cent (-0.315). There was non-significant and positive association with pulp per cent (0.161) and negative association with seed per cent (-0.109).

Number of seeds showed highly significant and positive correlation with pod weight (0.704), seed per cent (0.345), pulp per cent (0.271) and had negative association with shell per cent (-0.612). There was significant and positive association between number of seeds and vein per cent (0.182).

Pod weight showed highly significant and positive correlation with pulp per cent (0.493) and had negative association with shell per cent (-0.523). There was non-significant and positive association with vein per cent (0.091) and negative association with seed per cent (-0.026).

Pulp per cent showed highly significant and negative association with shell per cent (-0.709) followed by seed per cent (-0.392). There was significant and negative association with vein per cent (-0.179).

Shell per cent had highly significant and negative association with seed per cent (-0.322) whereas, non-significant and positive association with vein per cent (0.025). There was non-significant and negative association between seed per cent and vein per cent (-0.170).

4.3.3 Phenotypic path analysis

The path coefficient analysis, a statistical device developed by Wright (1921), which takes into account the cause and effect relation between the variables, is unique in partitioning the association into direct and indirect effects through other independent variables. Path analysis also measures the relative importance of causal factors involved. This is simply a standardized partial regression analysis; wherein total correlation value is subdivided into causal scheme. Phenotypic path coefficient analysis for yield parameters of tamarind genotypes was depicted in Table 9 (figure-1).

4.3.3.1 Direct effect

Pod yield per tree had direct and negative effect by pod weight (-7.466) followed by seed per cent (-1.465), pulp per cent (-1.426), shell per cent (-1.390), vein per cent (-0.792), pod girth (-0.244) and pod width (-0.004). Whereas, direct and positive effect by pulp weight (3.347) followed by seed weight (2.797), shell weight (1.249), vein weight (1.119), pod length (0.523) and number of seeds (0.307).

4.3.3.2 Indirect effect

Pod length had indirect and negative effect on pod weight (-5.214), pulp per cent (-0.274), pod girth (-0.107), vein per cent (-0.072) and pod width (-0.002). whereas, pod length had indirect and positive effect on pulp weight (2.116), seed weight (1.774), shell

Table 9. Phenotypic path analysis for yield traits in tamarind genotypes

	1	2	3	4	5	6	7	8	9	10	11	12	13	rP
1	0.523	-0.002	-0.107	2.116	0.785	1.774	0.568	0.159	-5.214	-0.274	0.305	0.016	-0.072	0.577
2	0.28	-0.004	-0.109	2.645	0.697	1.76	0.495	0.108	-5.657	-0.657	0.551	0.172	0.025	0.306
3	0.228	-0.002	-0.244	1.841	0.628	1.397	0.562	0.128	-4.374	-0.428	0.404	0.136	-0.096	0.180
4	0.331	-0.003	-0.134	3.347	0.809	2.211	0.623	0.166	-7.051	-0.926	0.792	0.235	0.024	0.424
5	0.329	-0.002	-0.123	2.168	1.249	1.914	0.546	0.15	-6.005	-0.003	-0.176	0.218	0.003	0.268
6	0.332	-0.002	-0.122	2.646	0.854	2.797	0.617	0.242	-6.87	-0.237	0.732	-0.578	0.022	0.433
7	0.265	-0.002	-0.123	1.861	0.609	1.542	1.119	0.133	-4.709	-0.227	0.455	0.108	-0.604	0.430
8	0.271	-0.001	-0.102	1.811	0.607	2.201	0.485	0.307	-5.022	-0.148	0.653	-0.561	-0.037	0.463
9	0.365	-0.003	-0.143	3.161	1.004	2.574	0.706	0.207	-7.466	-0.556	0.637	-0.03	-0.014	0.443
10	0.101	-0.002	-0.073	2.173	0.002	0.465	0.178	0.032	-2.912	-1.426	0.9	0.71	0.074	0.221
11	-0.115	0.002	0.071	-1.908	0.158	-1.474	-0.366	-0.144	3.421	0.924	-1.39	0.445	0.037	-0.340
12	-0.006	0.0001	0.023	-0.538	-0.186	1.104	-0.082	0.118	-0.151	0.691	0.422	-1.465	0.119	0.050
13	0.048	0.0001	-0.03	-0.1	-0.005	-0.077	0.854	0.014	-0.133	0.132	0.065	0.219	-0.792	0.196

Residual = 0.7308

* significant at 5 per cent

** significant at 1 per cent

rP- Pod yield per tree (kg/tree)

1. Pod length (cm)

5. Shell weight per pod (g)

9. Pod weight (g)

13. Vein per cent (%)

2. Pod width (cm)

6. Seed weight per pod (g)

10. Pulp per cent (%)

14. Pod yield per tree(kg/tree)

3. Pod girth (cm)

7. Vein weight per pod (g)

11. Shell per cent (%)

4. Pulp weight per pod (g)

8. Number of seeds per pod

12. Seed per cent (%)

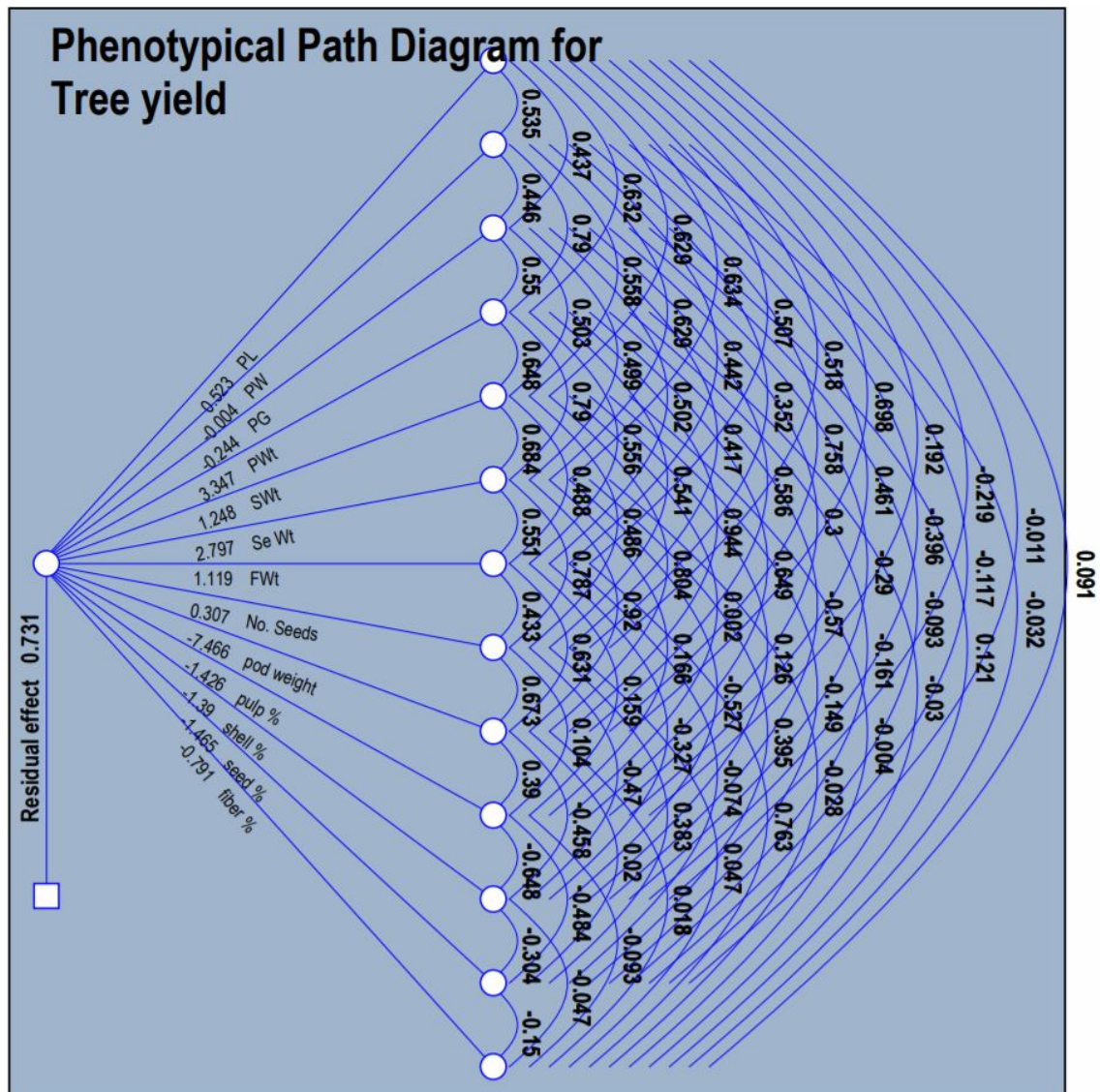


Fig. 1. Phenotypic path analysis diagram for pod yield per tree in tamarind

Weight (0.785), vein weight (0.568), shell per cent (0.305), number of seeds (0.159) and seed per cent (0.016).

Pod width had indirect and negative effect on pod weight (-5.657), pulp per cent (-0.657) and pod girth (-0.109). Whereas, indirect and positive effect on pulp weight (2.645), seed weight (1.760), shell weight (0.697), shell per cent (0.551), vein weight (0.495), pod length (0.228), seed per cent (0.172), number of seeds (0.108) and vein per cent (0.025).

Pod girth showed indirect and negative effect on pod weight (-4.374), pulp per cent (-0.428), vein per cent (-0.096) and pod width (-0.002). Whereas, indirect and positive effect on pulp weight (1.841), seed weight (1.397), shell weight (0.628), vein weight (0.562), shell per cent (0.404), pod length (0.228), seed per cent (0.136) and number of seeds (0.128)

Pulp weight had indirect and negative effect on pod weight (-7.051), pulp per cent (-0.926), pod girth (-0.134) and pod width (-0.003). Whereas, indirect and positive effect on seed weight (2.211), shell weight (0.809), shell per cent (0.792), vein weight (0.623), pod length (0.331), seed per cent (0.235), number of seeds (0.166) and vein per cent (0.024).

Shell weight had indirect and negative effect on pod weight (-6.005), shell per cent (-0.176), pod girth (-0.123), pulp per cent (-0.003) and pod width (-0.002). Whereas, indirect and positive effect on pulp weight (2.168), seed weight (1.914), vein weight (0.546), pod length (0.329), seed per cent (0.218), number of seeds (0.150) and vein per cent (0.003)

Seed weight had indirect and negative effect on pod weight (-6.870), seed per cent (-0.578), pulp per cent (-0.237), pod girth (-0.122) and pod width (-0.002). Whereas, indirect and positive effect on pulp weight (2.646), shell weight (0.854), shell per cent (0.732), vein weight (0.617), pod length (0.332), number of seeds (0.242) and vein per cent (0.022).

Vein weight had indirect and negative effect on pod weight (-4.709), vein per cent (-0.604), pulp per cent (-0.227), pod girth (-0.123) and pod width (-0.002). Whereas, indirect and positive effect on pulp weight (1.861), seed weight (1.542), shell

weight (0.609), shell per cent (0.455), pod length (0.265), number of seeds (0.133) and seed per cent (0.108).

Number of seeds had indirect and negative effect on pod weight (-5.022), seed per cent (-0.561), pulp per cent (-0.148), pod girth (-0.102), vein per cent (-0.037) and pod width (-0.001). Whereas, indirect and positive effect on seed weight (2.201), pulp weight (1.811), shell per cent (0.653), shell weight (0.607), vein weight (0.485) and pod length (0.271).

Pod weight had indirect and positive effect on pulp weight (3.161), seed weight (2.574), shell weight (1.004), vein weight (0.706), shell per cent (0.637), pod length (0.365) and number of seeds (0.207). Whereas, indirect and negative effect on pulp per cent (-0.556), pod girth (-0.143), seed per cent (-0.030), vein per cent (-0.014) and pod width (-0.003).

Pulp per cent had indirect and negative effect on pod weight (-2.912), pod girth (-0.073) and pod width (-0.003). Whereas, indirect and positive effect on pulp weight (2.173), shell per cent (0.900), seed per cent (0.710), seed weight (0.465), vein weight (0.178), vein per cent (0.074), pod length (0.101), number of seeds (0.032) and shell weight (0.002).

Shell per cent had indirect and positive effect on pod weight (3.421), pulp per cent (0.924), seed per cent (0.445), shell weight (0.158), vein per cent (0.037), pod girth (0.071) and pod width (0.002). Whereas, indirect and negative effect on pulp weight (-1.908), seed weight (-1.474), vein weight (-0.366), number of seeds (-0.144) and pod length (-0.115).

Seed per cent had indirect and positive effect on seed weight (1.104), pulp per cent (0.691), shell per cent (0.422), vein per cent (0.119), number of seeds (0.118), pod girth (0.023) and pod width (0.0001). Whereas, indirect and negative effect on pulp weight (-0.538), shell weight (-0.186), pod weight (-0.151), vein weight (-0.082) and pod length (-0.006).

Vein per cent had indirect and positive effect on vein weight (0.854), seed per cent (0.219), pulp per cent (0.132), shell per cent (0.065), pod length (0.048), number of

Table 10. Genotypic path analysis for yield traits of tamarind genotypes

	1	2	3	4	5	6	7	8	9	10	11	12	13	rG
1	0.471	-0.282	-0.33	-0.055	-0.652	1.146	1.436	0.353	-1.224	-0.251	0.217	0.057	-0.177	0.710
2	0.315	-0.422	-0.301	-0.062	-0.489	1.038	1.113	0.204	-1.183	-0.55	0.369	0.218	0.086	0.336
3	0.246	-0.201	-0.631	-0.045	-0.459	0.828	1.374	0.233	-0.943	-0.415	0.29	0.245	-0.314	0.208
4	0.384	-0.386	-0.421	-0.068	-0.52	1.138	1.300	0.273	-1.29	-0.66	0.455	0.265	-0.008	0.461
5	0.408	-0.273	-0.384	-0.047	-0.754	0.967	1.300	0.225	-1.11	-0.093	-0.021	0.318	-0.228	0.307
6	0.395	-0.32	-0.382	-0.056	-0.532	1.369	1.348	0.37	-1.256	-0.296	0.445	-0.517	-0.081	0.487
7	0.299	-0.207	-0.383	-0.039	-0.433	0.815	2.264	0.239	-0.899	-0.15	0.232	0.17	-1.442	0.466
8	0.366	-0.189	-0.323	-0.041	-0.372	1.112	1.188	0.456	-0.95	-0.252	0.451	-0.541	-0.335	0.571
9	0.428	-0.37	-0.441	-0.065	-0.62	1.275	1.508	0.321	-1.349	-0.459	0.385	0.041	-0.167	0.485
10	0.127	-0.249	-0.281	-0.048	-0.076	0.435	0.365	0.123	-0.665	-0.932	0.522	0.614	0.33	0.267
11	-0.139	0.211	0.248	0.042	-0.021	-0.827	-0.714	-0.279	0.705	0.66	-0.737	0.504	-0.046	-0.392
12	-0.017	0.059	0.099	0.011	0.153	0.451	-0.246	0.157	0.035	0.365	0.237	-1.567	0.314	0.051
13	0.045	0.02	-0.108	0.0003	-0.093	0.06	1.772	0.083	-0.122	0.167	-0.018	0.267	-1.843	0.228

Residual = 0.5779

* significant at 5 per cent

** significant at 1 per cent

rG- Pod yield per tree (kg/tree)

1. Pod length (cm)

5. Shell weight per pod (g)

9. Pod weight (g)

13. Vein per cent (%)

2. Pod width (cm)

6. Seed weight per pod (g)

10. Pulp per cent (%)

14. Pod yield per tree(kg/tree)

3. Pod girth (cm)

7. Vein weight per pod (g)

11. Shell per cent (%)

4. Pulp weight per pod (g)

8. Number of seeds per pod

12. Seed per cent (%)

seeds (0.014) and pod width (0.0001). Whereas, indirect and negative effect on pod weight (-0.133), pulp weight (-0.100), seed weight (-0.077), pod girth (-0.030) and shell weight (-0.005).

4.3.4 Genotypic path analysis

Genotypic path coefficient analysis for yield parameters of tamarind genotypes was depicted in Table-10 (Figure-2).

4.3.4.1 Direct effect

Pod yield per tree had direct and positive effect on vein weight (2.264), seed weight (1.369), pod length (0.471) and number of seeds (0.456). Whereas, direct and negative effect on vein per cent (-1.843), seed per cent (-1.567), pod weight (-1.349), pulp per cent (-0.932), shell weight (-0.754), shell per cent (-0.737), pod girth (-0.631), pod width (-0.422) and pulp weight (-0.068).

4.3.4.2 Indirect effect

Pod length had indirect and positive effect on vein weight (1.436), seed weight (1.146), number of seeds (0.353), shell per cent (0.217) and seed per cent (0.057). Whereas, indirect and negative effect on pod weight (-1.224), shell weight (-0.652), pod girth (-0.330), pod width (-0.282), pulp per cent (-0.251), vein per cent (-0.177) and pulp weight (-0.055).

Pod width had indirect and negative effect on pod weight (-1.183), pulp per cent (-0.550), shell weight (-0.489), pod girth (-0.301) and pulp weight (-0.062). Whereas, indirect and positive effect on vein weight (1.113), seed weight (1.038), shell per cent (0.369), pod length (0.315), seed per cent (0.218), number of seeds (0.204) and vein per cent (0.086).

Pod girth had indirect and positive effect on vein weight (1.374), seed weight (0.828), shell per cent (0.290), pod length (0.246), seed per cent (0.245) and number of seeds (0.233). Whereas, indirect and negative effect on pod weight (-0.943), shell weight (-0.459), pulp per cent (-0.415), vein per cent (-0.314), pod width (-0.201) and pulp weight (-0.045).

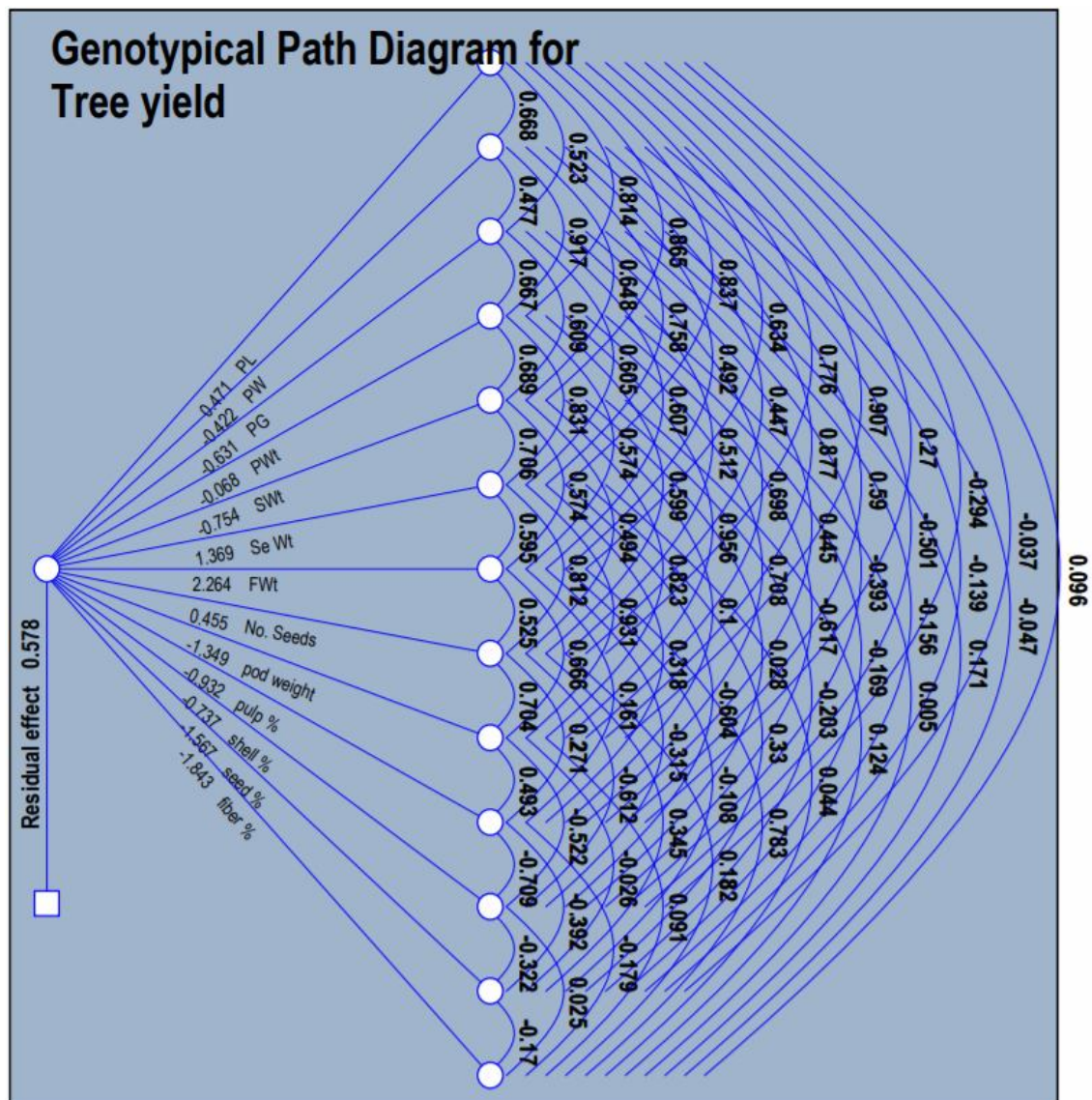


Fig. 2. Genotypic path analysis diagram for pod yield per tree in tamarind

Pulp weight had indirect and positive effect on vein weight (1.300), seed weight (1.138), shell per cent (0.455), pod length (0.384), number of seeds (0.273) and seed per cent (0.265). Whereas indirect and negative effect on pod weight (-1.290), pulp per cent (-0.660), shell weight (-0.520), pod girth (-0.421), pod width (-0.386) and vein per cent (-0.177).

Shell weight had indirect and positive effect on vein weight (1.300), seed weight (0.967), pod length (0.408), seed per cent (0.318) and number of seeds (0.225). Whereas, indirect and negative effect on pod weight (-1.110), pod girth (-0.384), pod width (-0.273), vein per cent (-0.228), pulp per cent (-0.093), pulp weight (-0.047) and shell per cent (-0.021).

Seed weight had indirect and positive effect on vein weight (1.348), shell per cent (0.445), pod length (0.395) and number of seeds (0.370). Whereas, indirect and negative effect on pod weight (-1.256), shell weight (-0.532), seed per cent (-0.517), pod girth (-0.382), pod width (-0.320), pulp per cent (-0.296), vein per cent (-0.081) and pulp weight (-0.056).

Vein weight had indirect and negative effect on vein per cent (-1.442), pod weight (-0.899), shell weight (-0.433), pod girth (-0.383), pod width (-0.207), pulp per cent (-0.150) and pulp weight (-0.039). Whereas, indirect and positive effect on seed weight (0.815), pod length (0.299), number of seeds (0.239), shell per cent (0.232) and seed per cent (0.170).

Number of seeds had indirect and positive effect on vein weight (1.188), seed weight (1.112), shell per cent (0.451) and pod length (0.366). Whereas, indirect and negative effect on pod weight (-0.950), seed weight (-0.541), shell weight (-0.372), vein per cent (-0.335), pod girth (-0.323), pulp per cent (-0.252), pod width (-0.189) and pulp weight (-0.041).

Pod weight had indirect and positive effect on vein weight (1.508), seed weight (1.275), pod length (0.428), shell per cent (0.385), number of seeds (0.321) and seed per cent (0.041). Whereas, indirect and negative effect on shell weight (-0.620), pulp per cent (-0.459), pod girth (-0.441), pod width (-0.370), vein per cent (-0.167) and pulp weight (-0.065).

Pulp per cent had indirect and negative effect on pod weight (-0.665), pod girth (-0.281), pod width (-0.249), shell weight (-0.076) and pulp weight (-0.048). Whereas, indirect and positive effect on seed per cent (0.614), shell per cent (0.522), seed weight (0.435), vein weight (0.365), vein per cent (0.330), pod length (0.127) and number of seeds (0.123).

Shell per cent had indirect and negative effect on seed weight (-0.827), vein weight (-0.714), number of seeds (-0.279), pod length (-0.139), vein per cent (-0.046) and shell weight (-0.021). Whereas, indirect and positive effect on pod weight (0.705), pulp per cent (0.660), seed per cent (0.504), pod girth (0.248), pod width (0.211) and pulp weight (0.042).

Seed per cent had indirect and positive effect on seed weight (0.451), pulp per cent (0.365), vein per cent (0.314), shell per cent (0.237), number of seeds (0.157), shell weight (0.153), pod girth (0.099), pod width (0.059), pod width (0.035) and pulp weight (0.011). Whereas, indirect and negative effect on vein weight (-0.246) and pod length (-0.017).

Vein per cent had indirect and positive effect on vein weight (1.772), seed per cent (0.267), pulp per cent (0.167), number of seeds (0.083), seed weight (0.060), pod length (0.045), pod width (0.020) and pulp weight (0.0003). Whereas, indirect and negative effect on pod weight (-0.122), pod girth (-0.108), shell weight (-0.093) and shell per cent (-0.018).

4.3.5 Genetic Divergence

Mahalanobis standardize distance (D^2) occupies the special place in plant breeding. It's a very sensitive instrument for evaluating the genetic divergence based on the characteristics in selection of parameters for hybridisation.

4.3.5.1 Relative contribution of different characters towards divergence.

The relative contribution of different characters towards the genetic divergence (D^2) is presented in Table 11. Among the traits Pod yield per tree (74.37 %) contributed maximum for genetic diversity followed by, Vein weight (6.28 %), pod width (3.66 %), seed weight (2.4 %), pulp to shell ratio (2.4 %), pulp per cent (2.08 %), pod girth

Table 11. Relative per cent contribution of different traits towards genetic divergence in tamarind genotypes

Parameters	Times ranked first	Contribution %
Pod length	6	0.33
Pod width	67	3.66
Pod girth	30	1.64
Pulp weight	30	1.64
Shell weight	24	1.31
Seed weight	44	2.4
Vein weight	115	6.28
Number of seeds	27	1.48
Pod weight	1	0.05
Pulp per cent	38	2.08
Shell per cent	9	0.49
Seed per cent	28	1.53
Vein per cent	6	0.33
Pulp : Shell ratio	44	2.4
Pod yield per plant	1361	74.37

Table 12. Grouping of tamarind genotypes in to different clusters by Tocher's method

Clusters	Number of genotypes	Genotypes included in the cluster
1	51	G-10, G-55, G-19, G-8, G-14, G-59, G-13, G-61, G-3, G-18, G-20, G-62, G-2, G-6, G-52, G-4, G-7, G-58, G-5, G-1, G-12, G-54, G-11, G-64, G-60, G-48, G-39, G-9, G-40, G-41, G-47, G-63, G-37, G-50, G-53, G-36, G-56, G-42, G-15, G-45, G-38, G-35, G-46, G-57, G-30, G-44, G-28, G-34, G-51, G-65, G-29
2	1	G-32
3	8	G-17, G-33, G-27, G-16, G-22, G-24, G-31, G-26
4	1	G-25

Table 13. Average intra and inter cluster D^2 values for 15 traits formed by 61 selected tamarind genotypes

	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Cluster 1	120.25	352.45	460.22	1811.48
Cluster 2		0.00	49.15	654.69
Cluster 3			62.55	543.99
Cluster 4				0.00

Table 14. Cluster means of pod parameters of tamarind genotypes as per Tocher's method

Sl. No.	Parameters	Cluster 1	Cluster 2	Cluster 3	Cluster 4
1	Pod length	11.59	11.28	13.58	15.09
2	Pod width	2.26	2.21	2.38	2.35
3	Pod girth	1.46	1.39	1.47	1.48
4	Pulp weight	6.18	6.50	7.36	7.84
5	Shell weight	3.86	3.01	4.40	3.95
6	Seed weight	5.10	4.92	6.22	6.03
7	Vein weight	0.60	0.53	0.74	1.16
8	Number of seeds	6.33	7.59	7.67	8.50
9	Pod weight	15.74	14.94	18.69	18.96
10	Pulp per cent	38.65	43.49	39.08	41.30
11	Shell per cent	25.12	20.12	23.92	20.85
12	Seed per cent	32.39	32.85	33.16	31.79
13	Vein per cent	3.84	3.55	3.97	6.07
14	Pulp : Shell ratio	1.60	2.16	1.71	1.98
15	Pod yield per plant	25.54	64.50	68.59	115.20

(1.64 %), pulp weight (1.64 %), seed per cent (1.53 %), number of seeds (1.48 %), shell weight (1.31 %), shell per cent (0.49 %), Vein per cent (0.33 %), pod length (0.33 %) and pod weight (0.05 %).

4.3.5.2 Grouping of tamarind genotypes into different clusters

The clustering details of 61 tamarind genotypes using Tocher's method has been presented in Table 12. All the genotypes were grouped into four clusters. In cluster-I, 51 genotypes (G-10, G-55, G-19, G-8, G-14, G-59, G-13, G-61, G-3, G-18, G-20, G-62, G-2, G-6, G-52, G-4, G-7, G-58, G-5, G-1, G-12, G-54, G-11, G-64, G-60, G-48, G-39, G-9, G-40, G-41, G-47, G-63, G-37, G-50, G-53, G-36, G-56, G-42, G-15, G-45, G-38, G-35, G-46, G-57, G-30, G-44, G-28, G-34, G-51, G-65, G-29) were grouped whereas, in cluster-II one genotype (G-32) was grouped, in cluster-III eight genotypes (G-17, G-33, G-27, G-16, G-22, G-24, G-31, G-26) were grouped and in cluster-IV one genotype (G-25) was grouped.

Average intra and inter cluster divergence values are presented in the Table 13. The diagonal values in the table represent the intra- cluster distances. The intra-cluster distance was found maximum in cluster-I (120.25) followed by cluster-III (62.55) whereas, cluster-II and cluster-IV showed no intra-cluster distance.

The maximum inter cluster distance was observed between cluster-I and cluster-IV (1811.48) followed by cluster-II and cluster-IV (654.69), cluster-III and cluster-IV (543.99), cluster-I and cluster-III (460.22), cluster-I and cluster-II (352.45) whereas, minimum inter cluster distance was found between cluster-II and cluster-III (49.15).

4.3.5.3 Cluster mean values of pod traits in tamarind genotypes

The cluster means obtained using Tocher's method for different traits are presented in the Table 14. Among four clusters, cluster-I had highest shell per cent (25.12 %) and lowest pulp weight (6.18 g), number of seeds (6.33), pulp per cent (38.65 %), pulp to shell ratio (1.60) and pod yield per tree (25.54 kg/tree).

Cluster-II had maximum pulp per cent (43.49 %), pulp to shell ratio (2.16) and minimum pod length (11.28 cm), pod width (2.21 cm), pod girth (1.39 cm), shell weight (3.01 g), seed weight (4.92 g), Vein weight (0.53 g), pod weight (14.94 g), shell per cent (20.12 %), Vein per cent (3.55 %).

Cluster III had highest pod width (2.38 cm), shell weight (4.40 g), seed weight (6.22 g) and seed per cent (33.16 %). Cluster IV had maximum pod length (15.09 cm), pod girth (1.48 cm), pulp weight (7.84 g), Vein weight (1.16 g), number of seeds (8.50), pod weight (18.96 g), Vein per cent (6.07 %), pod yield per tree (115.20 kg/tree) and minimum in seed per cent (31.79 %).

4.4 Molecular characterization of tamarind genotypes through SRAP and ISSR markers

Molecular characterization is a useful technique for the identification of the genetic relation between various genotypes in tamarind and also detection of genetic polymorphism. The aim of the study was to investigate the genetic diversity among the tamarind genotypes based on the analysis of molecular markers.

4.4.1 DNA isolation

Genomic DNA was extracted from different tamarind genotypes by modified CTAB method as mentioned in materials and methods. The extraction method yielded good amount of DNA. The quality and quantity of isolated DNA samples were tested and it was found good by agarose gel electrophoresis.

4.4.2 SRAP analysis

Sequence Related Amplified Polymorphism analysis was carried out using 25 primer combinations among which, 10 primer combination yielded maximum number of bands that were consistent, strong, intense and clear. These were selected for fingerprinting and diversity analysis.

Molecular analysis of 12 superior tamarind genotypes G-16, G-17, G-22, G-24, G-25, G-26, G-27, G-30, G-32, G-33, and G-34 by using 10 primer combinations of SRAP revealed a total of 67 scorable bands which were used to estimate the genetic variation in different genotypes. These bands were well cleared, readable and reproducible polymorphic bands. Among total 67 bands, 43 bands were polymorphic, 14 were unique bands and 10 were monomorphic bands. The number of bands produced from each primer varied from 3-13 with an average of 6.7 bands per primer (Table-15).

Among ten primer combinations, Em15 + Me13 produced maximum number of bands (13 bands) followed by primer Em15 + Me14 (12 bands). The highest polymorphic bands are produced by primer combination Em15 + Me13 (8 bands), Em15 + Me14 (8 bands) followed by Em13 + Me12 (5 bands), Em14 + Me15 (5 bands) and Em15 + Me12 (4 bands), while Em11 + Me15, Em12 + Me15, Em13 + Me13 and Em14 + Me12 produced 3 polymorphic bands each.

The primer combination of Em14 + Me12 and Em15 + Me12 produced highest polymorphism of 100 per cent followed by Em14 + Me15 (71.42 %), while Em14 + Me11 produced least polymorphism of 33.33 per cent.

The genotype G-24 had two unique bands produced by primers Em13 + Me12 and another one by Em14 + Me15, while G-22 had four unique bands produced by two different primers Em13 + Me12 (2 unique bands) and Em14 + Me11 (2 unique bands). Whereas, the genotype G-16 had three unique bands produced by Em13 + Me12 (1 unique band), Em13 + Me13 (1 unique band) and Em15 + Me14 (1 unique band). The genotype G-32 had three unique bands produced by three different primers (Em13 + Me13, Em15 + Me13 and Em15 + Me14) and G-34 had two unique bands produced by two different primers (Em14 + Me15 and Em15 + Me14) (Table-16) (Plate-3).

High PIC value was reported in primer combination Em14 Me11 and lowest was found in primer Em11+Me15 (0.34). The average polymorphism information content value reported by using ten SRAP primer combinations was 0.70 (Table-15).

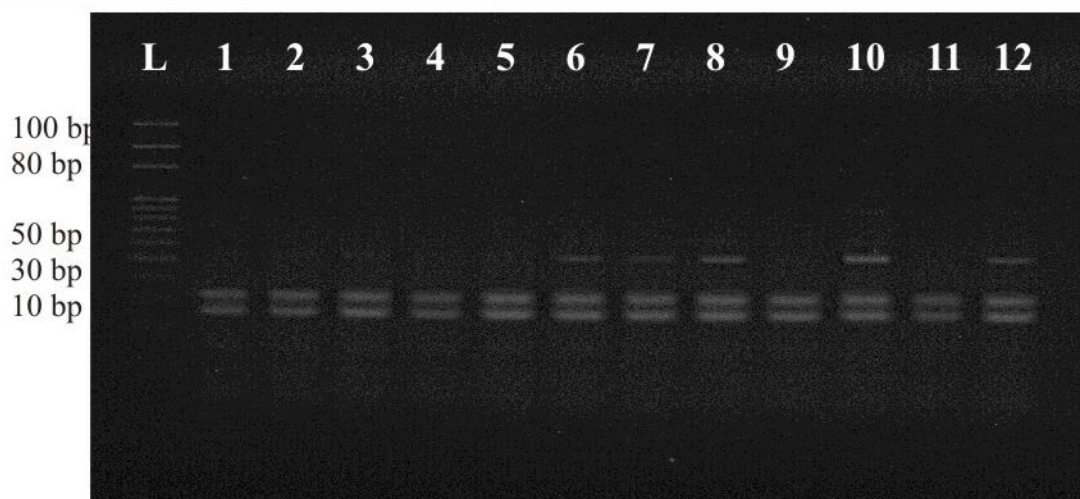
Table 15. Estimates of polymorphism rates in tamarind genotypes with different SRAP primer combinations

Sl. No.	Primer combinations	Number of bands produced	Number of polymorphic bands	Unique bands	Number of monomorphic bands	Per cent of polymorphism	P.I.C Value
1	Em11 + Me15	6	3	0	3	50.00	0.34
2	Em12 + Me15	5	3	0	2	60.00	0.48
3	Em13 + Me12	9	5	4	0	55.55	0.83
4	Em13 + Me13	5	3	2	0	60.00	0.81
5	Em14 + Me11	3	1	2	0	33.33	0.99
6	Em14 + Me12	3	3	0	0	100.00	0.73
7	Em14 + Me15	7	5	2	0	71.42	0.77
8	Em15 + Me12	4	4	0	0	100.00	0.63
9	Em15 + Me13	13	8	1	4	61.53	0.59
10	Em15 + Me14	12	8	3	1	66.66	0.85
		67	43	14	10		0.70

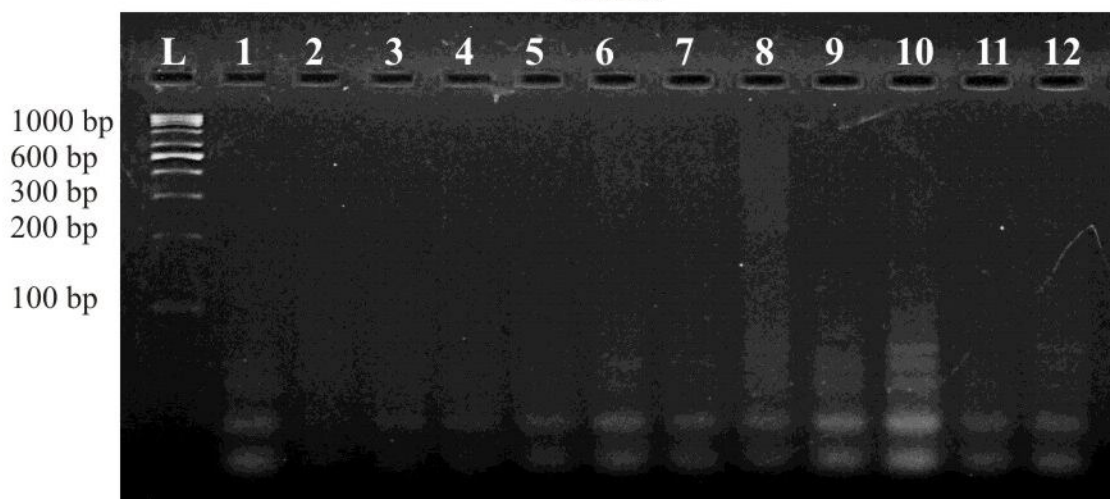
P.I.C: Polymorphism Information Content

Table 16. Unique bands produced by SRAP primer combinations in selected tamarind genotypes

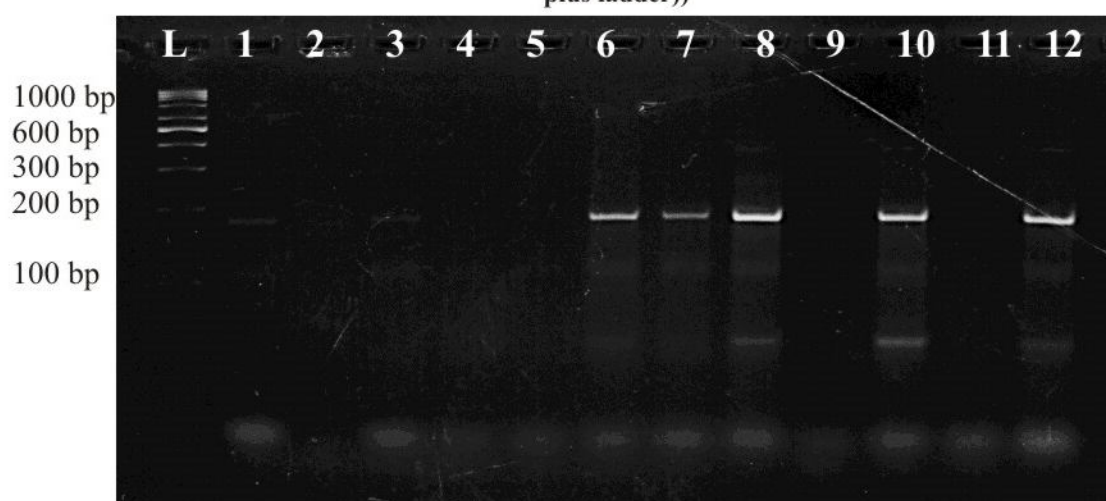
Sl. No.	Primer combination	Number of unique bands produced	Number of unique bands	Genotypes
1	Em13 + Me12	4	1	G-24
			1	G-22
			1	G-16
			1	G-22
2	Em13 + Me13	2	1	G-16
			1	G-32
3	Em14 + Me11	2	1	G-22
			1	G-22
4	Em14 + Me15	2	1	G-34
			1	G-24
5	Em15 + Me13	1	1	G-32
6	Em15 + Me14	3	1	G-16
			1	G-34
			1	G-32



Gel profile of tamarind genotypes using Em11+Me15 SRAP primer combination. (Lane 1-12 represents the genotypes in the same order as listed in table 19. L – ladder (100 bp ladder))

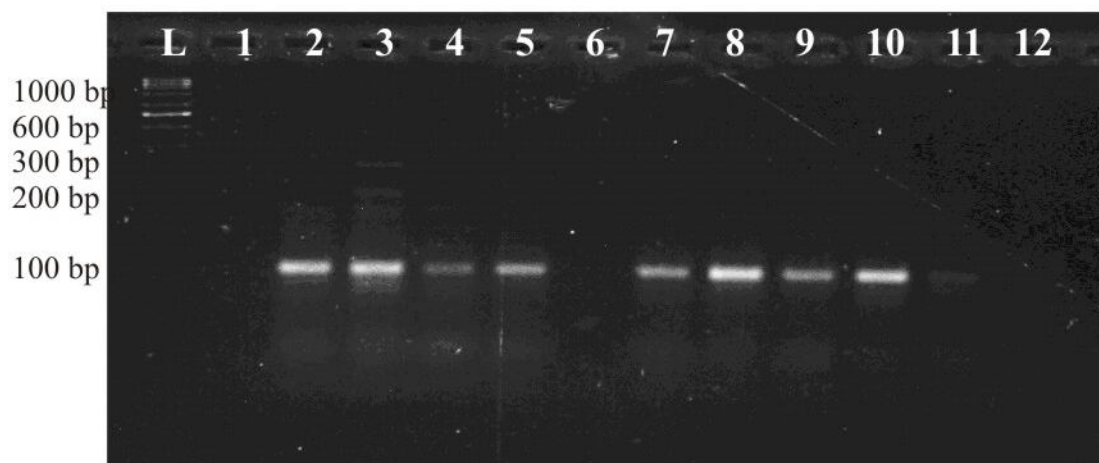


Gel profile of tamarind genotypes using Em12+Me15 SRAP primer combination. (Lane 1-12 represents the genotypes in the same order as listed in table 19. L – ladder (1 kb plus ladder))

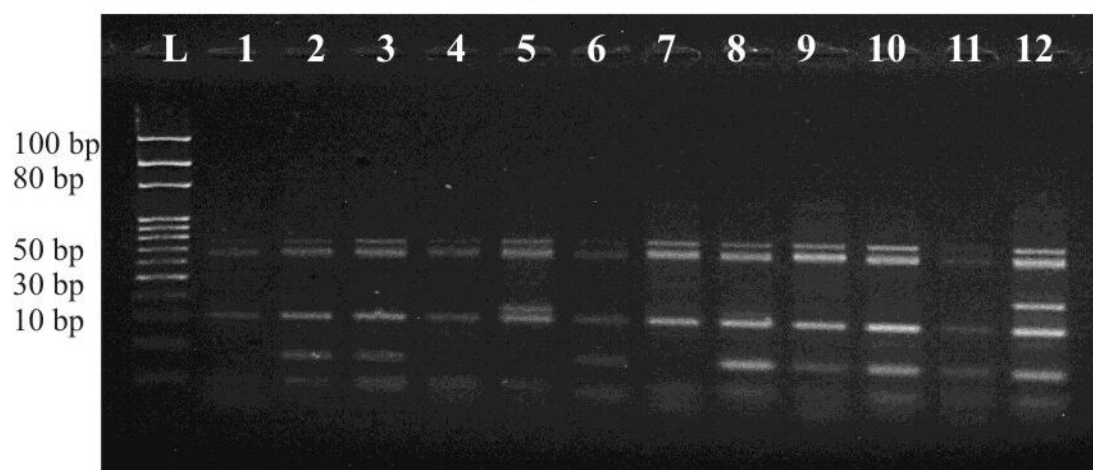


Gel profile of tamarind genotypes using Em13Me12 SRAP primer combination. (Lane 1-12 represents the genotypes in the same order as listed in table 19. L – ladder (1 kb plus ladder))

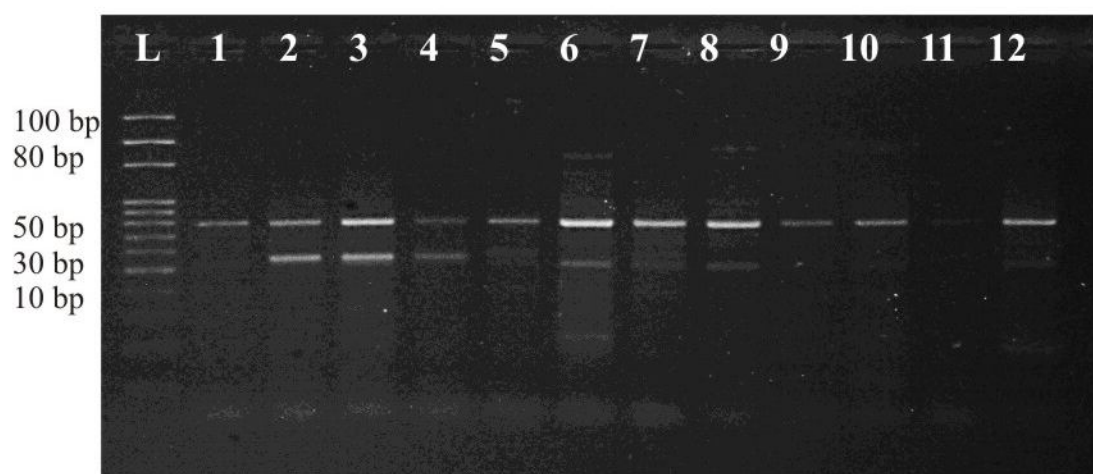
Plate 3a. Gel profile of superior tamarind genotypes using different SRAP primer combinations



Gel profile of tamarind genotypes using Em14+Me11 SRAP primer combination. (Lane 1-12 genotypes the varieties in the same order as listed in table 19. L – ladder (1 kb plus ladder))

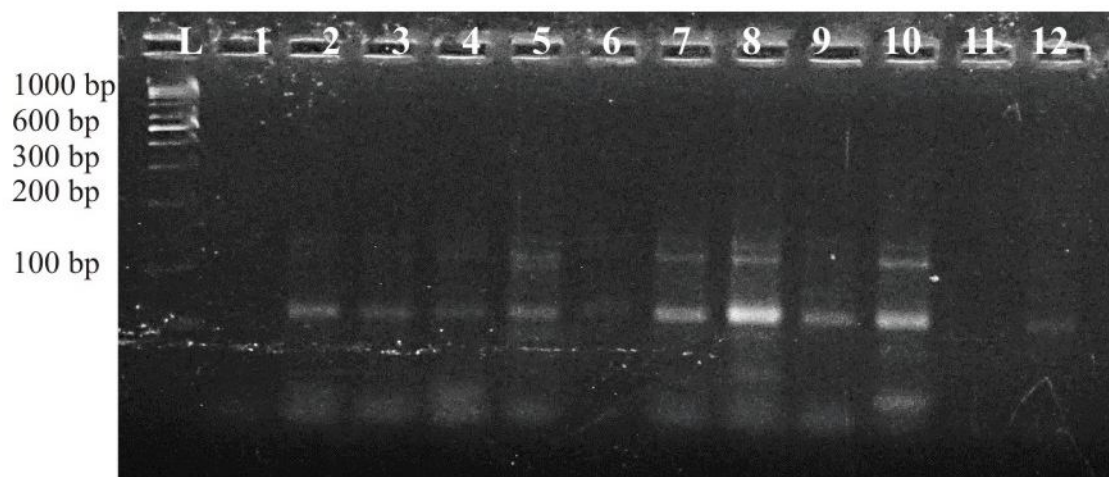


Gel profile of tamarind genotypes using Em15+Me13 SRAP primer combination. (Lane 1-12 genotypes the varieties in the same order as listed in table 19. L – ladder (100 bp ladder))



Gel profile of tamarind genotypes using Em15Me14 SRAP primer combination. (Lane 1-12 genotypes the varieties in the same order as listed in table 19. L – ladder (100 bp ladder))

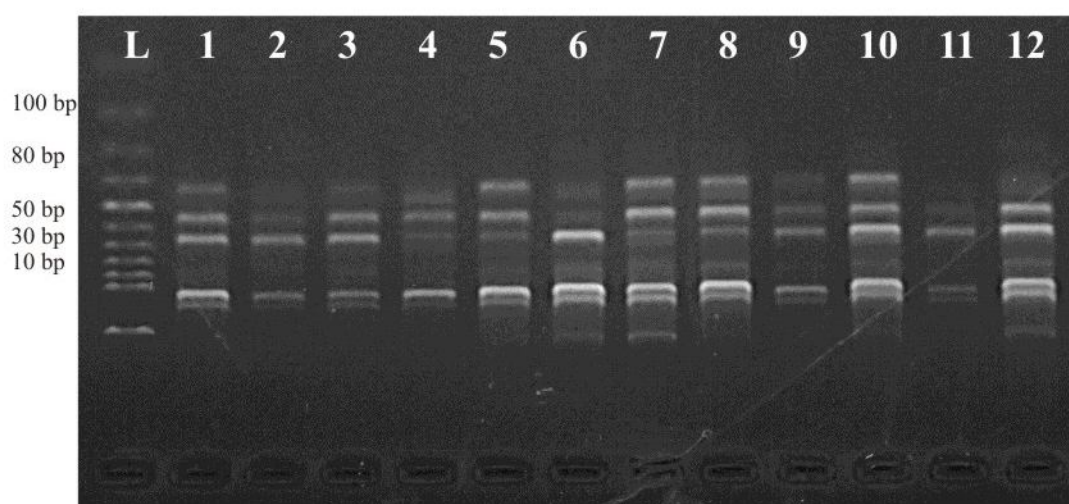
Plate 3b. Gel profile of superior tamarind genotypes using different SRAP primer combinations



Gel profile of tamarind genotypes using Em14Me15 SRAP primer combination. (Lane 1-12 represents the genotypes in the same order as listed in table 19. L – ladder (1 kb plus ladder))



Gel profile of tamarind genotypes using UBC 811 ISSR primers. (Lane 1-12 represents the genotypes in the same order as listed in table 19. L – ladder (100 bp ladder))



Gel profile of tamarind genotypes using UBC 810 ISSR primers. (Lane 1-12 represents the genotypes in the same order as listed in table 19. L – ladder (100 bp ladder))

Plate 3c. Gel profile of superior tamarind genotypes using different SRAP and ISSR primers

4.4.3 ISSR marker analysis

Six ISSR primers were used for characterization of 12 different superior tamarind genotypes.

Molecular analysis of superior tamarind genotypes by using 6 primers ISSR revealed a total of 35 scorable bands which were used to estimate the genetic variation in different genotypes. These bands were well cleared, readable and reproducible polymorphic bands. Among total 35 bands, 25 bands were polymorphic, 4 were unique bands and 6 were monomorphic bands. The number of bands produced from each primer varied from 1-10 with an average of 5.8 bands per primer (Table-17) (Plate-4).

Among six primers, UBC 810 produced maximum number of bands (10 bands) followed by UBC 855 (9 bands) and P 817 (6 bands). The highest polymorphic bands are observed in primer UBC 855 (9 bands) followed by primer UBC 810 (6 bands). Whereas, primer P 817 produced 4 polymorphic bands and the least polymorphic bands were observed in UBC 811 (1 band).

The primer UBC 811 and UBC 855 produced maximum per cent of polymorphism of 100 per cent followed by P 817 (66.66 %) and the least polymorphism per cent was observed in primer UBC 826 (50.00 %).

The genotype G-32 had showed four unique bands produced by primers UBC 826 (2 unique bands) and UBC 840 (2 unique bands) (Table 18). The highest PIC value was reported in primer UBC 826 (0.94) and the lowest PIC value was reported in primer P 817 (0.36). The average PIC value reported by using six ISSR primers was 0.54.

4.4.4 Analysis of genetic diversity by using SRAP and ISSR markers

4.4.4.1 Cluster analysis and genetic similarity matrix

SRAP and ISSR bands were scored from gel profile by assigning binary values '1' for the presence of bands and '0' for the absence of band. Such data generated from

Table 17. Estimates of polymorphism rates in tamarind genotypes with ISSR primers

Sl. No.	Primer combinations	Number of bands produced	Number of polymorphic bands	Unique bands	Number of monomorphic bands	Per cent of polymorphism	P.I.C Value
1	UBC 811	1	1	0	0	100.00	0.75
2	UBC 826	4	2	2	0	50.00	0.94
3	UBC 810	10	6	0	4	60.00	0.38
4	UBC 855	9	9	0	0	100.00	0.49
5	P 817	6	4	0	2	66.66	0.36
6	UBC 840	5	3	2	0	60.00	0.79
		35	25	4	6		0.54

P.I.C: Polymorphism Information Content

Table 18. Unique bands produced by ISSR primers in selected tamarind genotypes

Sl. No.	Primers	Number of unique bands produced	Number of unique bands	Genotypes
1	UBC 826	2	1	G-32
			1	G-32
2	UBC 840	2	1	G-32
			1	G-32

all the general profiles were used for statistical analysis. The similarity matrix was computed using Jaccard similarity coefficient. The pooled SRAP and ISSR data was utilized for cluster analysis using NTSYC-PC ver.2.1 software for different tamarind genotypes.

4.4.4.2 Similarity matrix and dendrogram generated by SRAP and ISSR markers

The similarity matrix coefficient ranged from 30 to 74 per cent genetic variation within different tamarind genotypes for 10 SRAP and 6 ISSR markers. The scoring data showed that, the highest similarity of 74 per cent was observed between G-24 and G-16 followed by G-25 and G-26 (73%), while the least similarity of 30 per cent was observed between genotypes G-24 and G-33 (Table-19).

4.4.4.3 Dendrogram

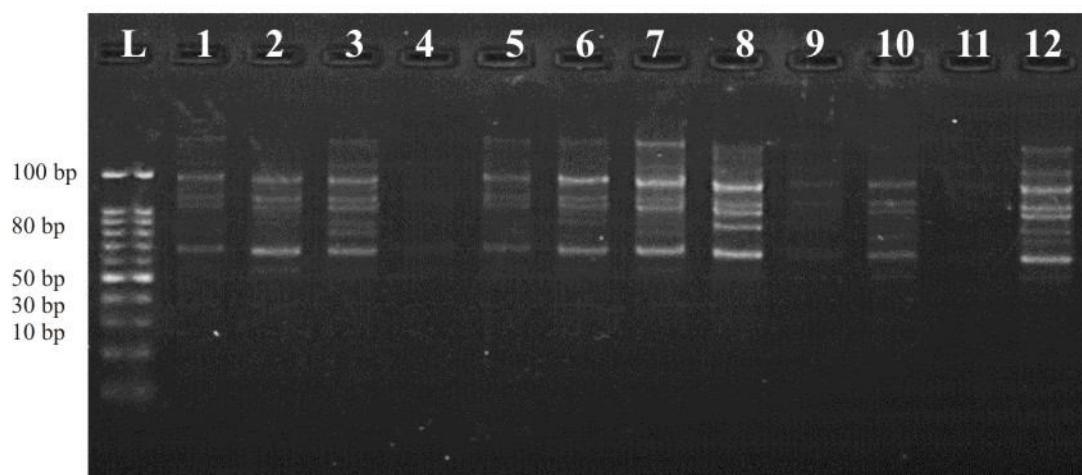
The dendrogram was established using Jaccard similarity Coefficient. Cluster analysis based on a total of 102 bands with 68 polymorphic bands using 10 SRAP and 6 ISSR primers have been disclosed in Figure-3.

Superior tamarind genotypes were grouped into two clusters. Cluster I constituted with other genotypes except G-33 genotype whereas, cluster II constituted with only one genotype G-33.

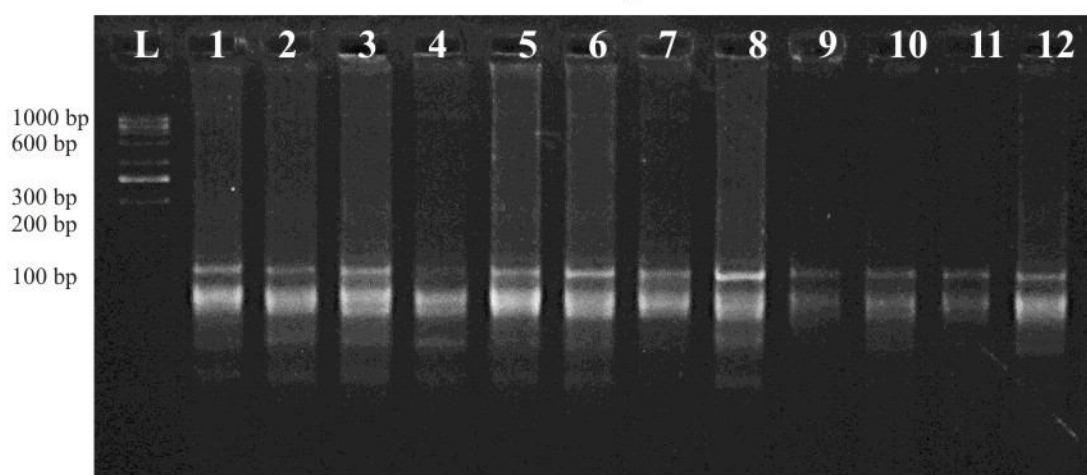
The cluster I in dendrogram was further divided into two sub clusters, sub cluster I again divided into two groups, group I consists of seven genotypes G-27, G-34, G-30, G-26, G-25, G-16 and G-24 whereas, group II consists of genotype G-17. Sub cluster II had three genotypes G-35, G-22, G-32.

4.4.4.4 Similarity matrix among tamarind genotypes

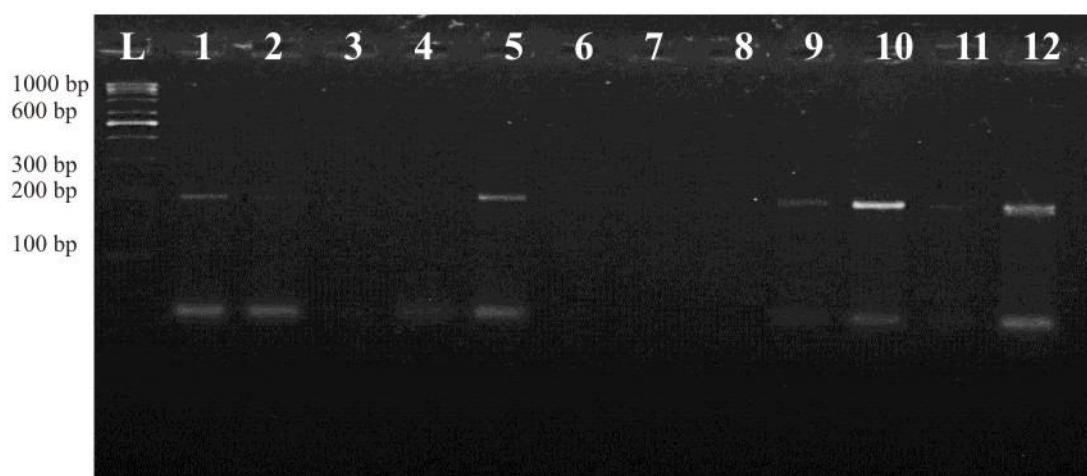
In dendrogram, the major cluster I divided into two sub clusters, sub cluster I is further divided into two groups; group I and group II. Group I had seven genotypes G-27, G-34, G-30, G-26, G-25, G-16 and G-24. The similarity index among the genotypes of this group was 0.66 (G-27 and G-34), 0.60 (G-27 and G-30), 0.73 (G-25 and G-26), 0.74 (G-16 and G-24) and in group II G-17 had similarity index of 0.50. Sub cluster II had similarity index of 0.62 (G-22 and G-32).



Gel profile of tamarind genotypes using UBC 855 ISSR primers. (Lane 1-12 represents the genotypes in the same order as listed in table 19. L – ladder (100 bp ladder))



Gel profile of tamarind genotypes using P 817 ISSR primers. (Lane 1-12 represents the genotypes in the same order as listed in table 19. L – ladder (1 kb plus ladder))



Gel profile of tamarind genotypes using UBC 840 ISSR primers. (Lane 1-12 represents the genotypes in the same order as listed in table 19. L – ladder (1 kb plus ladder))

Plate 4. Gel profile of superior tamarind genotypes using different ISSR primers

Table 19. Similarity coefficient in different superior tamarind genotypes using SRAP and ISSR markers

	G-27	G-26	G-25	G-17	G-34	G-16	G-30	G-24	G-35	G-22	G-33	G-32
G-27	1.00											
G-26	0.61	1.00										
G-25	0.62	0.73	1.00									
G-17	0.50	0.60	0.51	1.00								
G-34	0.66	0.56	0.59	0.53	1.00							
G-16	0.57	0.60	0.63	0.44	0.57	1.00						
G-30	0.60	0.56	0.66	0.53	0.70	0.63	1.00					
G-24	0.54	0.58	0.63	0.49	0.57	0.74	0.71	1.00				
G-35	0.50	0.49	0.49	0.48	0.56	0.46	0.51	0.46	1.00			
G-22	0.47	0.49	0.44	0.48	0.48	0.56	0.54	0.56	0.57	1.00		
G-33	0.43	0.38	0.31	0.38	0.35	0.32	0.33	0.30	0.41	0.35	1.00	
G-32	0.55	0.46	0.49	0.38	0.49	0.55	0.55	0.59	0.47	0.62	0.33	1.00

G : Genotype

4.4.4.5 Association of some phenotypic characters with SRAP and ISSR cluster

A dendrogram based on cluster results of different superior tamarind genotypes revealed that they are distributed in dendrogram based on pod length, pod width, pod girth, pod weight, pulp weight, shell weight, seed weight, vein weight, number of seeds and pod yield per tree.

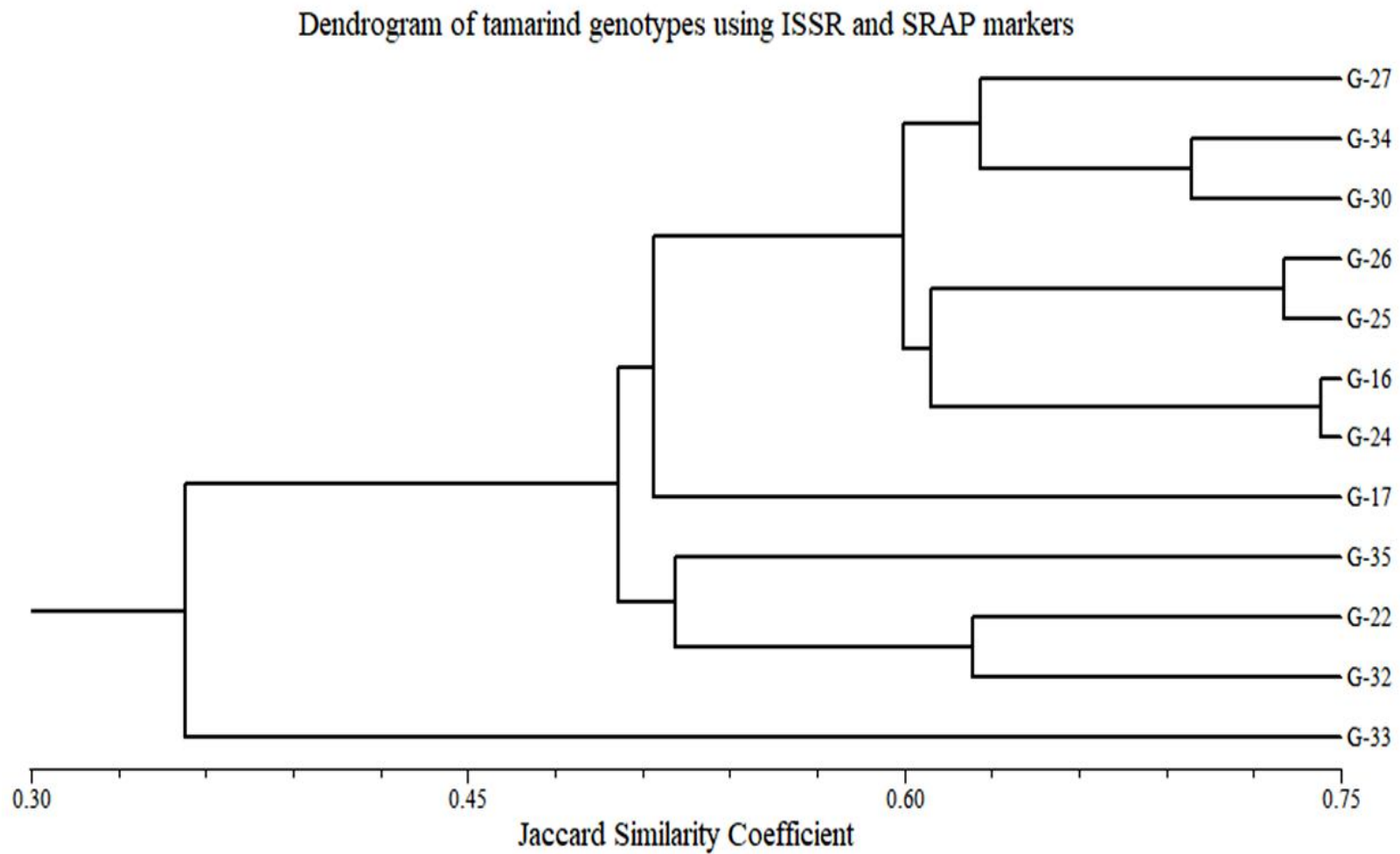


Fig. 3. Dendrogram showing genetic relationship among superior tamarind genotypes using SRAP and ISSR marker

5. DISCUSSION

The amount of genetic dissimilarity present in the available genotype leads to the extent of advancement of any crop. Hence, the chance of choosing superior genotypes rises with increase in the scale of genetic variability in the available germplasm (Simmonds, 1962). The observations recorded with respect to nature and extent of genetic diversity, coefficient of variation, genetic advance, heritability and per cent contribution of character to diversity would be valuable in founding standard procedure for selection of economically important desirable parameters of the selected genotypes.

The present investigation entitled “Assessment of genetic variability for productivity and quality traits in Tamarind (*Tamarindus indica* L.)” had led to some important observations. The salient features of the observation recorded have been discussed and interpreted below.

5.1 Morphological characters of plant growth and yield traits

5.1.1 Vegetative traits

The results for plant height showed vast difference among 61 genotypes studied, that was varied from lowest 3.01 m (G-7) to highest 7.63 m (G-64). The variation in regard to plant height is due to difference in the genetic makeup of the various genotypes and due to the differential consumption of resources from the soil. Such factors cause morphological and heritable evolutionary variations in the population. This was supported by following references Hanamashetti (1996), Divakara and Rathakrishnan (2011).

A wide divergence was reported in regard of trunk diameter among the several genotypes, while the minimum trunk diameter was reported by genotype G-58 (0.38 m) and the maximum trunk diameter was reported by genotype G-16 (1.50 m). The variation was due to the distinct feature of the different tamarind genotypes. These findings are inline with supporting reference of Hanamashetti (1996) and Rao and Subramanyam (2010).

The data with respect to plant spread reported that, G-22 showed maximum plant spread of 7.02 m in East-West direction and minimum was found in G-40 (3.02) genotype whereas, G-25 (7.98) showed maximum plant spread in North-South direction and minimum was observed in genotype G-7 (3.30 m). This variation due to the presence of more number of primary and secondary branches which depends genetic makeup of genotypes. Similar findings were reported by Kotecha and Kadam (2002), Divakara (2008) and Tania *et al.* (2018).

Significant variation was found with respect to crown size among all the genotypes. Maximum crown size was observed in genotype G-25 (7.48 m) and G-40 genotype reported minimum crown size of 3.26 m. The difference was due to variation in the plant spread. Similar findings were reported by Kotecha and Kadam (2002), Divakara (2008), Rao and Subramanyam (2010) and Agasimani *et al.* (2019).

The data depicted in table 1 showed the maximum trunk diameter was reported by genotype G-16 (1.50 m) whereas, minimum trunk diameter was reported by genotype G-58 (0.38 m). The variation was due to the genetic makeup of the different tamarind genotypes. These results were in line with the findings reported by Hanamashetti (1996), Divakara and Rathakrishnan (2011), Pooja *et al.* (2018).

The number of days taken for flowering in all tamarind genotypes ranged from 65 days to 80 days from harvesting. The pods of all tamarind genotypes attend maturity in one-week interval hence, the number of days taken for harvesting of pods in all tamarind genotypes ranged from 262 days to 278 days from flowering. Similar findings were reported by Tania *et al.* (2018).

5.1.2 Yield traits

The results obtained in regard to pod length revealed that, it was significantly varied from 7.42 cm (G-54) to 15.49 cm (G-26). The variation in length of the pod among different genotypes may be due to genetic makeup of each genotype. These findings are inline with earlier reference coated by Divakara (2008), Fandohan *et al.* (2011), Sharma *et al.* (2015) and Pooja *et al.* (2018).

Among different tamarind genotypes reported, the pod width was varied from 1.84 cm (G-4) to 3.33 cm (G-51). There was a significant difference in regard with pod

width which may be due to genotypic difference in between the selected genotypes and the similar findings with respect to pod width were reported by Kotecha and Kadam (2002), Divakara (2008), Rao and Subramanyam (2010) and Agasimani *et al.* (2019)

The girth of the pod was varied significantly among several genotypes recorded. The maximum pod girth reported was 1.72 cm (G-33) and minimum was 1.15 cm (G-57). The difference in regard with pod girth might be due to genetic makeup of the genotype and also may be due to variation in thickness of the seed. The findings reported are in similar with earlier reporters by Prabhushankar *et al.* (2004), Fandohan *et al.* (2011) and Mayavel *et al.* (2018).

Significant variation was found with respect to pulp weight per pod among different genotypes. The maximum pulp weight was observed in genotype G-51 (15.22 g) and minimum in genotype G-1 (3.06 g). The difference in pulp weight per pod was due to variation in pod length, pod girth and pod thickness. The supportive results have also been described by Hanamashetti *et al.* (2003), Divakara (2008), Pooja *et al.* (2018) and Rajamanickam (2019).

The data regarding shell weight reported significant variation among different genotypes. The shell weight per pod was ranged from 2.60 g (G-19) to 6.84 g (G-56), it was attributed to the variation in pod size and thickness of the shell. The similar findings with respect to shell weight per pod were also depicted by Ganacharya (2005), Divakara (2008), Rao and Subramanyam (2010) and Rajamanickam (2019).

Significant variation was found with respect to vein weight among all the genotypes. Genotype G-44 (1.44 g) reported highest vein weight and lowest vein weight was noticed in genotype G-62 (0.22 g). The variation might be due to difference in the rate of development of vascular tissues in the pod and presence of number of veins per pod. The findings obtained were in close conformity with the results reported by Challapilli (1992), Mastan *et al.* (1997), Divakara (2008) and Agasimani *et al.* (2019).

The genotypes varied significantly in regard with total number of seeds per pod among several genotypes. The number of seeds per pod was varied from 3.50 (G-2 and G-58) to 10.25 (G-46). The difference in seed number might be due to variation in pod length, ovule fertility, arrangement of seeds inside the pod and also may be due to seed

size. Similar divergence with respect to number of seeds were reported by several workers Ganacharya (2005), Rao and Subramanyam (2010) and Tadas *et al.* (2015).

The seed weight per pod reported significant difference among several genotypes. The weight of the seeds per pod varied from 2.60 g (G-4) to 9.13 g (G-46). The disparity in seed weight may be attributed due to difference in the size and number of seeds present in individual genotypes. The findings were supported with the results reported by Prabhushankar *et al.* (2004), Ganacharya (2005), Fandohan *et al.* (2011) and Pooja *et al.* (2018).

The pod weight reported was differed significantly among several genotypes. The highest pod weight reported was 29.31 g (G-51) and minimum was 9.81 g (G-57). The wide variation in regard to pod weight was attributed to the difference in pod length, number of seeds, pod width, seed weight, pulp weight, shell weight and vein weight among the several genotypes. The variation was similarly reported by Divakara (2008), Rao and Subramanyam (2010), Sharma *et al.* (2015) and Mayavel *et al.* (2018).

The genotypes studied recorded high significant with respect to pulp per cent per pod, which was ranged from 28.56 per cent (G-1) to 51.95 per cent (G-51). The variation in pulp per cent among several genotypes might be due to length, thickness, width and pulp content of the pod, it may be also due to distinct feature of different genotypes. Similar results in regard with pulp per cent in tamarind was also reported by Sivakumar (2000), Kotecha and Kadam (2002) and Sharma *et al.* (2015).

The data depicted in results showed significant diversity in regard to shell per cent and it was varied from 18.14 per cent (G-51) to 34.29 per cent (G-57) per cent. The difference in shell per cent might be due to variation in pod size, shell thickness and shell weight. It is also due to inherent genetic makeup of individual genotype. The findings obtained were in close conformity with the results reported by Sivakumar (2000), Divakara (2008), Hanamashetti *et al.*, (2003), Agasimani *et al.* (2019) and Pooja *et al.* (2018).

Significant variation was found with respect to seed per cent among all the genotypes. The maximum seed per cent was observed in genotype G-19 (39.87 %) and minimum in genotype G-60 (23.09 %). The variation might be due to difference in

length of the pod, ovule fertility, seed number and seed weight. The results obtained were in agreement with the findings reported by Hanamashetti and Sulikeri (1997), Mastan *et al.* (1997) and Divakara (2008).

The vein per cent showed significant variation among different genotypes with the highest vein per cent of 7.68 per cent (G-42) and lowest vein per cent of 2.02 per cent (G-62). The variation might be due to difference in the rate of development of vascular tissues in the pod, vein weight per pod and also due to distinct feature of the different genotypes. Similar findings are reported by Hanamashetti and Sulikeri (1997), Mastan *et al.* (1997) and Divakara (2008).

Significant variation was found with respect to pulp: shell ratio among all the genotypes. The maximum pulp: shell ratio was observed in genotype G-51 (2.86) and minimum in genotype G-1 (0.85) (Table 4). The variation might be due to difference in the pulp content and shell content per pod and also due to genetic makeup of individual genotype.

The pod yield per tree showed significant variation among different genotypes. The highest pod yield per tree was found in G-25 (115.20 kg/tree) and minimum was reported in G-7 (9.8 kg/ tree) genotype. The difference was due to the presence of more number of primary and secondary branches. Pod yield per tree also governed by inherent genotypic makeup of each genotype and also depends on environmental conditions. These findings are in close conformity with findings reported by Gangaprasad (1993), Hanamashetti and Sulikeri (1997), Sharma *et al.* (2015) and Pooja *et al.* (2018).

The wide variation was reported in regard to pod shape among various tamarind genotypes. The different pod shapes recorded were straight, Semi-curved and 'C' shape. Among 61 genotypes, twenty-four showed straight pods, thirty-five genotypes showed Semi-curved pods and 'C' shape pods were found in two genotypes. Such variation in pod shape in seedling progenies was also reported by Hanamashetti *et al.*, (2003), Agasimani *et al.* (2019) and Pooja *et al.* (2018).

Genotypes varied significantly with respect to pulp colour. The different pulp colour recorded were dark brown, brown and blackish brown. Among 61 genotypes,

dark brown pulp was observed in forty-two genotypes, brown pulp was observed in sixteen genotypes and blackish brown pulp was observed in three genotypes. These results are inline with the results of Prabhushankar *et al.* (2004),

5.1.3 Quality traits of pulp

The significant variation was reported among genotypes with respect to total soluble solids. The maximum TSS was recorded in genotypes G-32 (44.5) whereas, minimum TSS was observed in G-33 and G-41 (27.5). This difference in TSS value was due to variation in the sugar content of the pulp. Similar findings were reported by Prabhushankar *et al.* (2004), Joshi *et al.* (2013), Tadas *et al.* (2015) and Tania *et al.* (2018).

The results showed significant diversity in regard to tartaric acid. The maximum tartaric acid content was reported by genotype G-33 (21.14 %) whereas, minimum per cent of tartaric acid was reported in genotype G-2 (7.14 %). The variation was due to difference in the sugar content of the pulp and inherent genetic makeup of each genotype. These findings were similar with the results obtained by Divakara (2008), Tadas *et al.* (2015), Agasimani *et al.* (2019) and Rajamanickam (2019)

Ascorbic acid showed significant variation among all the tamarind genotypes. The highest ascorbic acid recorded was 12.69 observed in genotypes G-27, G-30 and G-62 whereas, the minimum ascorbic acid was recorded by genotypes G-31 (4.62). the variation was due to perpetual synthesis of glucose-6-phosphate throughout the growth and development of fruits which is thought to be the precursor of ascorbic acid and it also depends on effect of genetic difference among the genotypes. Similar findings were reported by Ishola *et al.* (1990), Sharma *et al.* (2015) and Pooja *et al.* (2018).

The total sugar showed significant variation among different tamarind genotypes. The highest total sugar was found in G-32 (41.67) whereas, minimum total sugar was reported in G-33 (25.44). The variation was due to difference in acidity content of the pulp and within and between genotypes. These findings are closely

associated with the findings reported by Joshi *et al.* (2013), Tania *et al.* (2018) and Pooja *et al.* (2018).

5.2 Genetic variability parameters

The genotypic coefficient of variation, phenotypic coefficient of variation, heritability and Genetic advance over per cent mean are valuable tools for assessing the extent of diversity present in the available genotypes. Among all the studied characters, phenotypic coefficient of variability were higher in magnitude than genotypic coefficient of variability which signify that these character are influenced by environmental elements. Coefficients of variability varied in magnitude from character to character which exhibit the existence of diversity in the available genotypes (Fig. 4).

Tamarind trees are cross-pollinated and seed propagated and show high degree of variability. The GCV and PCV were reported maximum for pulp weight, shell weight, seed weight, Vein weight, number of seeds, pod weight, vein weight, pulp to shell ratio, and pod yield per tree. These findings were corroborate with the results obtained by Mastan *et al.* (1997), Biradar (2001), Patil (2004), Divakara (2008) and Agasimani *et al.* (2019),

Moderate GCV and PCV was reported in pulp per cent, shell per cent, pod length and pod width. Similar results were observed by Divakara (2008). Whereas, low GCV and moderate PCV was found in pod girth indicating that the traits show less variability and not suitable for direct selection. which is in corroborate with the findings reported by Hanamashetti (1996), Mastan *et al.* (1997), Ganacharya (2005) and Divakara (2008).

The broad sense heritability and genetic advance over per cent mean estimations were reported to be high in traits like pod length, pod width, pulp weight, shell weight, seed weight, vein weight, number of seeds, pod weight, shell per cent, vein per cent, pulp to shell ratio and pod yield per tree. High GCV, PCV along with high heritability and GAM indicating that, presence of additive gene action and these traits show more

variability and likely to provide high direct selection response. Whereas, moderate GAM with high heritability was reported in pod girth, pulp per cent and shell per cent (Fig. 5.). Similar results were reported by Mastan *et al.* (1997), Biradar (2001), Divakara (2008) and Agasimani *et al.* (2019).

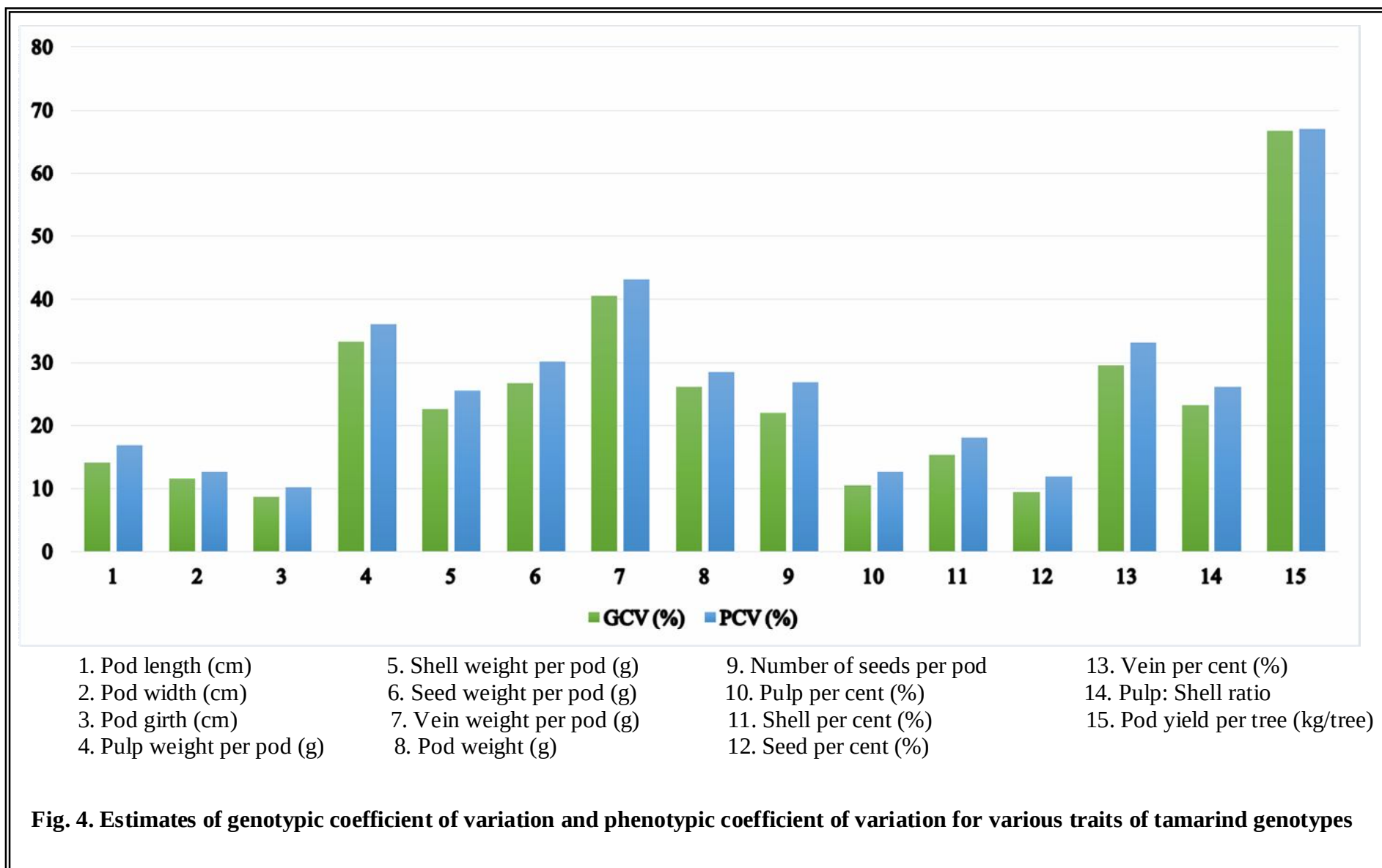
5.3 Correlation analysis

Correlation studies specify the degree of inter-relationship of plant traits for improvement of yield and yield attributing characters in any breeding programme. Hence, comprehension of the inter-relationship between fruit yield per plant and yield attributing characters is vital importance for effective selection and improvement of any yield characters.

Correlation is a estimates of degree of relationship between two traits. In the present study both genotypic and phenotypic correlation were performed for yield per plant and its attributing characters. Generally genotypic correlation is higher than phenotypic correlation for most of characters analysed. Genotypic correlation indicate the inherent association between genes controlling any two traits thus helps in effective selection scheme.

Pod yield per plant showed highly significant and positive association with pod length, number of seeds, pod weight, seed weight, vein weight per pod, pulp weight, pod width, shell weight. Significant positive association with pulp per cent, vein per cent pod girth and positively non-significant association with seed per cent at both phenotypic and genotypic levels which indicates that these traits suggest effective selection for increased yield. Similar results are reported by Bhogave *et al.* (2018) and Mayavel *et al.* (2018).

Pod length showed positive and highly significant association with pod weight, seed weight, pulp weight, shell weight, pod width, number of seeds, vein weight and pod girth. Whereas, significant and positive association with pulp per cent and non-significant positive association with vein per cent at both genotypic and phenotypic levels. These results are also in line with the work of Divakara (2008), Algabal *et al.* (2012), Singh and Nandini (2014) and Mayavel *et al.* (2018).



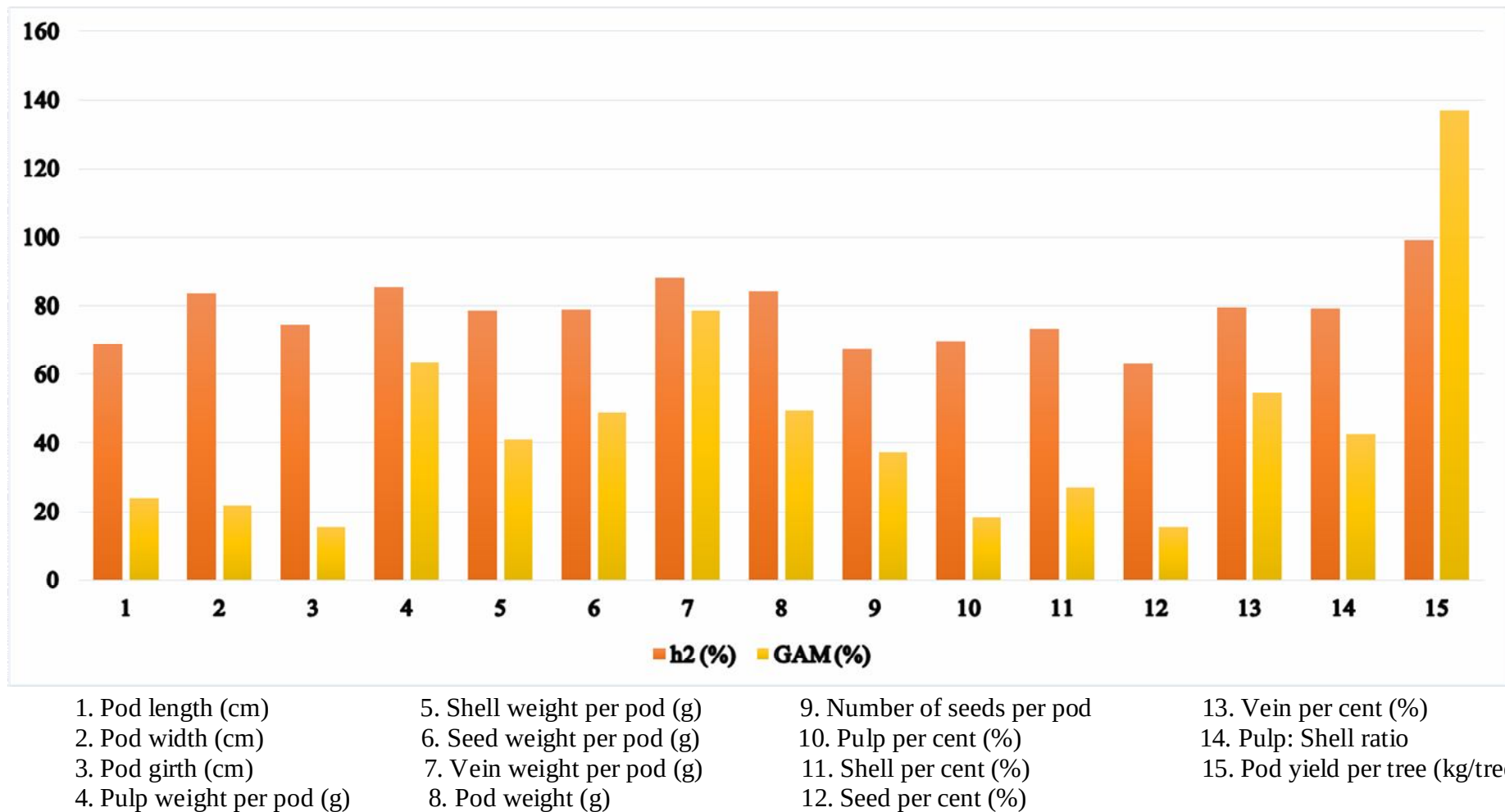


Fig. 5. Estimates of heritability and genetic advance over mean for various traits of tamarind genotypes

Pod width showed highly significant and positive association with pulp weight, pod weight, seed weight, shell weight, pulp per cent, pod girth, vein weight, number of seeds at both genotypic and phenotypic levels. Similar outcome in regard to correlation studies on pod width was reported by Divakara (2008) and Bhogave *et al.* (2018).

Pod girth exhibited highly significant and positively correlated with pod weight, pulp weight, shell weight, vein weight, seed weight, number of seeds, pulp per cent. There was non-significant and positive correlation of vein per cent at both phenotypic and genotypic levels. The results obtained were similar to the findings reported by Divakara (2008) and Algabal *et al.* (2012).

Pulp weight was highly significant and positive association with pod weight, seed weight, pulp per cent, shell weight, number of seeds, vein weight. Shell weight had highly significant and positively correlated with pod weight, seed weight, vein weight, number of seeds whereas, non-significantly and positively correlated with shell per cent followed by pulp per cent at both phenotypic and genotypic levels. Similar findings are reported by Divakara (2008), Bhogave *et al.* (2018) and Agasimani *et al.*, (2019).

There was highly significant and positive association of seed weight with pod weight, number of seeds, vein weight and seed per cent whereas, non-significant and positive association between seed weight and pulp per cent. Vein weight showed highly significant and positive correlation with vein per cent followed by pod weight, number of seeds whereas, non-significant and positive association with pulp per cent at both genotypic and phenotypic levels. These results are in line with the work reported by Algabal *et al.* (2012), Singh and Nandini (2014) and Pooja *et al.* (2018).

Number of seeds showed highly significant and positive correlation with pod weight, seed per cent. There was non-significant and positive association with pulp per cent and vein per cent. Pod weight showed highly significant and positive correlation with pulp per cent and had negative association with shell per cent. There was non-significant and positive association with seed per cent and vein per cent at both genotypic and phenotypic levels. The results obtained are in close conformity with the findings of Bhogave *et al.* (2018) and Mayavel *et al.* (2018).

5.4 Path coefficient analysis

Yield is a complex trait and is composed of dependent and independent characters which contribute directly as well as indirectly through each other. selection based on only correlation study for high yield would be misleading. Since a trait may not be directly associated with yield may be depend on other traits. Through path analysis, it is possible to find out the direct and indirect influence of component characters on the yield. This technique was developed by Wright (1921) and demonstrated by Dewey and Lu (1959) helps in dividing correlation coefficient into direct and indirect association of different characters on the yield.

In the present study, path analysis between the components of pod yield per plant in tamarind was calculated. As the only genotypic correlations are inherent, so the path analysis is discussed only at genotypic level.

In the current research, among 14 traits chosen for path analysis which revealed that, seed weight, pod length, number of seeds and vein weight had maximum positive direct effect on pod yield per tree (Table 10). Similar findings were reported by Divakara (2008), Pooja *et al.* (2018) and Agasimani *et al.* (2019). So direct selection of plant based on any of these independent traits leads to improvements of genotypes for tamarind pod yield per tree. Whereas, maximum negative direct effect on pod yield per tree was observed by pulp weight, pod weight, pod girth, pod width, seed per cent, shell weight. Similar findings were reported by Singh and Nandini (2014), Agasimani *et al.* (2019) and Mayavel *et al.* (2018).

5.5 Genetic divergence

Mahalanobis D^2 statistics is a good diagnostic multivariate method that is used for getting quantitative diversity estimates between biological populations. To generate new variability and desired recombinants, genetically divergent parents are necessary. In the present study, the 61 genotypes of tamarind were grouped into 4 clusters based on pod parameters which indicated that the considerable genetic divergence was noticed among genotypes.

Among the traits Pod yield per tree contributed maximum for genetic diversity followed by, Vein weight, pod width, seed weight, pulp to shell ratio, pulp per cent, pod girth, pulp weight, seed per cent, number of seeds, shell weight, shell per cent, Vein per cent, pod length and pod weight.

Intra-cluster distances revealed, cluster-I with genotypes shared maximum intra-cluster distance ($D^2 = 120.25$) followed by cluster-III ($D^2 = 62.55$) and remaining intra-cluster distance revealed zero divergence. However, present research was noticed that there is comparatively high intra-cluster distance in cluster I indicated that the occurrence of enough quantity of diversity within genotypes. Hence there is scope for selection within the clusters.

The maximum inter cluster distance based on pod parameters was noticed between cluster-I and cluster-IV (1811.48) indicating that wide range of genetic diversity was present between the clusters, followed by cluster-II and cluster-IV (654.69). whereas, minimum inter cluster distance was found between cluster-II and cluster-III (49.15), indicated that, genotypes of these clusters were genetically close. Similar findings were reported by Samiullah (1993), Hanamashetti *et al.* (2003), Singh and Nandini (2011) and Bhogave *et al.* (2018).

The cluster means for different traits of tamarind was obtained using Tocher method. Among four clusters, cluster-I had mean value highest for shell per cent and lowest for pulp weight, number of seeds, pulp per cent, pulp to shell ratio and pod yield per tree. Cluster-II had mean value maximum for pulp per cent, pulp to shell ratio and minimum for pod length, pod width, pod girth, shell weight, seed weight, Vein weight, pod weight, shell per cent, Vein per cent. Cluster III had mean value highest for pod width, shell weight, seed weight and seed per cent. Cluster IV had mean value maximum for pod length, pod girth, pulp weight, Vein weight, number of seeds, pod weight, Vein per cent, pod yield per tree and minimum for seed per cent.

It was revealed that, considerable difference for cluster mean was found for all the traits among clusters, this shows that, each cluster has its uniqueness that separated it from other traits. The superior genotypes for breeding programme can also be selected on the basis of cluster mean and inter cluster distance. Similar results were reported by Hanamashetti (1996) and Bhogave *et al.* (2018).

5.6 Molecular characterization of superior tamarind genotypes

Molecular tools will be useful for addressing the questions regarding genetic relationship among individuals, population structure as well as mapping loci and tracking quantitative traits. SRAP (sequence-related amplified polymorphism) markers have been developed which is used to amplify coding region of DNA with primer targeting open reading frames. These markers have proven to be robust and highly variable. SRAP and ISSR markers have been used in this study to assess the genetic diversity of large germplasm collections.

Genetic diversity of 12 tamarind genotypes was studied using 10 SRAP and 6 ISSR primers. Molecular analysis of superior tamarind genotypes by using 10 primer combinations of SRAP revealed a total of 67 scorable bands, in which 43 bands were polymorphic, 14 were unique bands and 10 were monomorphic bands. The number of bands produced from each primer varied from 3 to 13 with an average of 6.7 bands per primer.

The primer combination of Em14 + Me12 and Em15 + Me12 produced highest polymorphism of 100 per cent followed by Em14 + Me15 (71.42 %) while, Em14 + Me11 produced least polymorphism of 33.33 per cent. Similar trend of polymorphism was reported by Nandini *et al.* (2011) and Gangaprasad *et al.* (2013) in tamarind crop.

The genotype G-24 had two unique bands produced by primers Em13 + Me12 and another one by Em14 + Me15, while G-22 had four unique bands produced by two different primers Em13 + Me12 (2 unique bands) and Em14 + Me11 (2 unique bands). Whereas, the genotype G-16 had three unique bands produced by Em13 + Me12 (1 unique band), Em13 + Me13 (1 unique band) and Em15 + Me14 (1 unique band). The genotype G-32 had three unique bands produced by three different primers (Em13 + Me13, Em15 + Me13 and Em15 + Me14) and G-34 had two unique bands produced by two different primers (Em14 + Me15 and Em15 + Me14). Similarly, Kumar *et al.* (2015) reported with 10 RAPD primers of 58 polymorphic bands with unique bands in three genotypes. The detection of unique band out of polymorphic bands was also reported by other authors such as Nandini *et al.* (2011) and Agasimani *et al.* (2019).

Six ISSR primers were used for characterization of 12 different superior tamarind genotypes. Molecular analysis of superior tamarind genotypes by using 6

ISSR primers revealed a total of 35 scorable bands, in which 25 bands were polymorphic, 4 were unique bands and 6 were monomorphic bands. The number of bands produced from each primer varied from 1 to 10 with an average of 5.8 bands per primer. Similar findings were reported by Sarmiento *et al.* (2017) by using ISSR primer.

The primer UBC 811 and UBC 855 produced maximum per cent of polymorphism (100 %) followed by P 817 (66.66 %) and the least polymorphism was observed in primer UBC 826 (50.00 %). The genotype G-32 had showed four unique bands produced by primers UBC 826 (2 unique bands) and UBC 840 (2 unique bands). Similar trend of polymorphism was reported by Nandini *et al.* (2011) and Gangaprasad *et al.* (2013) in tamarind crop by using RAPD markers.

Genetic diversity between 12 superior genotypes were determined on the basis of Jaccard Similarity Coefficient. The maximum similarity of 74 per cent was reported between G-24 and G-16 followed by G-25 and G-26 (73%), while the least similarity of 30 per cent was observed between genotypes G-24 and G-33. Similar results were recorded by Yang-Shiyu *et al.* (2008), Nandini *et al.* (2011), Nandini and Ratan (2012) and Agasimani *et al.* (2019) in tamarind crop by using other markers.

5.5.2 Comparison of morphological and molecular data

While considering morphological characters, it was found distinctness among the cultivars, but when observed with different characters separately they showed similarity in one of the most important morphological features for discrimination of genotypes. Compared with other genotypes, G-33 showed regular bearing habit while other genotypes showed slightly irregular bearing habit. The first sub group of sub cluster I had the genotypes like G-34, G-30 and G-27 which are derived in the same cluster and having similar pod length, shell per cent and seed per cent, were grouped together. In sub group II, genotype G-26 and G-25 were grouped into one cluster having similarity in traits like plant trunk diameter, pod width, pod girth and number of seeds. In sub group III genotype G-16 and G-24 were clustered with more similarity in traits like crown size, pod width, pod girth and pod weight. In sub cluster II contains G-22, G-32 and G-35 having similarity traits such as trunk diameter, pod width, and seed per cent. Similar results were reported by Nandini *et al.* (2011), Kumar *et al.* (2015) Sarmiento *et al.* (2017) and Agasimani *et al.* (2019) by using RAPD markers.

Table 20. List of top five superior tamarind genotypes for yield and quality parameter

Sl. No.	Genotypes	Pod length (cm)	Pod weight (g)	Pod yield/tree (Kg/tree)	Tartaric acid (%)	TSS (°Brix)
1	G-16	13.38	18.56	76.00	10.22	38.50
2	G-25	15.08	18.96	115.20	19.14	29.00
3	G-26	15.49	22.53	83.30	12.85	40.00
4	G-32	11.28	14.94	64.50	11.74	44.50
5	G-33	13.75	17.98	69.30	21.14	27.50

Future line of work

- Due to perennial nature of the crop further evaluation of genotypes by using new breeding technologies are required to develop good varieties and good planting material.
- Identification of tamarind genotypes which are suitable for preparation of processed products like tamarind sweet pickle, juice, jam *etc.*, is required.
- The elite trees could be selected for molecular characterization through different markers like SSR and SCAR markers.

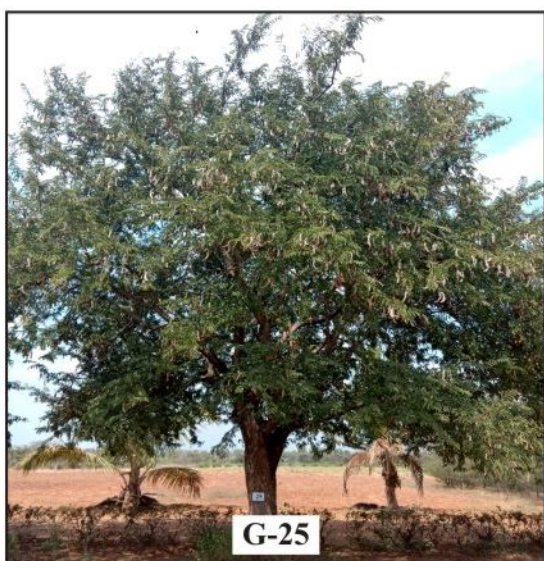


Plate 5a. High yielding superior tamarind genotypes



Plate 5b. High yielding superior tamarind genotypes

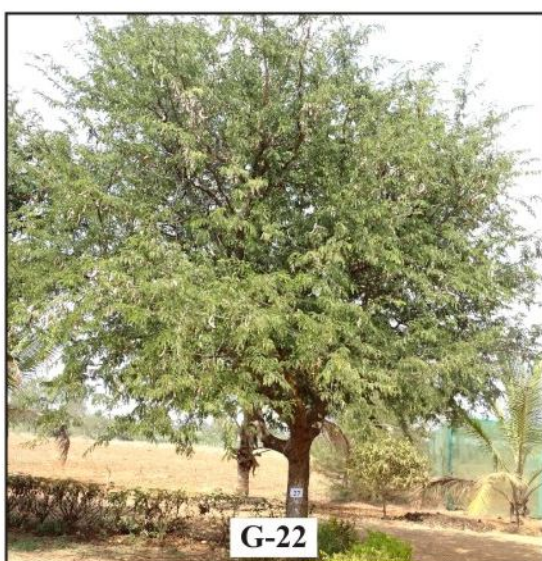


Plate 5c. High yielding superior tamarind genotypes

6. SUMMARY AND CONCLUSIONS

The present investigation was undertaken to evaluate 61 tamarind genotypes which are 20 years old planted at horticulture research experimental station, Hidkal Dam, Belagavi district, Karnataka. Molecular characterization of superior tamarind genotypes has been done at Kittur Rani Channamma College of Horticulture, Arabhavi, Belgaum district, Karnataka. The results of the experiment were analysed statistically and summarized as below.

6.1 Genetic variability for yield and quality traits in tamarind genotype

There was highly significant variation among all the 61 tamarind genotypes with respect to growth and yield parameters. Maximum tree height was reported in G-64 while, minimum in G-7 and minimum trunk diameter was reported by genotype G-58. Whereas, maximum trunk diameter was reported by genotype G-16. Maximum crown size was observed in genotype G-25 and G-40 genotype reported minimum crown size.

Among 61 tamarind genotypes, Maximum pod length was reported in G-26 while, minimum pod length in G-54 and highest pod width was noticed in G-51 whereas, minimum in G-4. Pod girth was maximum in G-33 while, minimum pod girth was reported in G-57 and pulp weight was reported highest in genotype G-51 while, lowest pulp weight was reported in G-1. Maximum shell weight was recorded by G-56 and minimum was recorded by G-19. Seed weight was recorded highest in G-46 and lowest seed weight was observed in G-4. Pod weight was observed maximum in G-51 and minimum pod weight was noticed in G-57. Maximum pod yield per tree was reported by G-25 and lowest pod yield per tree was reported in G-7.

Significant variation was found with respect to quality parameters, pod shape and pulp colour in 61 tamarind genotypes. Maximum TSS, total acidity, ascorbic acid and total sugar was reported in G-32, G-33, G-27 and G-32 genotypes respectively.

Among 61 genotypes, 24 showed straight pods, 35 genotypes showed Semi-curved pods and 'C' shape pods were found in two genotypes. Dark brown pulp was observed in 42 genotypes, brown pulp was observed in 16 genotypes and blackish brown pulp was observed in 3 genotypes.

The GCV and PCV were reported maximum for pulp weight, shell weight, seed weight, Vein weight, number of seeds, pod weight, vein weight, pulp to shell ratio, and pod yield per tree. Moderate GCV and PCV was reported in pulp per cent, shell per cent, pod length, pod width. Whereas, low GCV and moderate PCV was found in pod girth.

The broad sense heritability and genetic advance over per cent mean estimations were reported to be high in traits like pod length, pod width, pulp weight, shell weight, seed weight, vein weight, number of seeds, pod weight, shell per cent, vein per cent, pulp to shell ratio and pod yield per tree indicating that these characters shows more variability due to additive gene action and likely to provide direct selection response. Whereas, moderate GAM with high heritability was reported in pod girth, pulp per cent and shell per cent.

6.2 Correlation, path coefficient analysis and genetic divergence

Pod yield per plant showed highly significant and positive association with pod length, number of seeds, pod weight, seed weight, vein weight per pod, pulp weight, pod width, shell weight. Significant positive association with pulp per cent, vein per cent pod girth and positively non-significant association with seed per cent at both phenotypic and genotypic levels, which indicates that these traits suggest effective selection for increased yield.

Path analysis which revealed that, seed weight, pod length, number of seeds and vein weight had maximum positive direct effect on pod yield per tree. So direct selection of plant based on any of these independent traits leads to improvements of genotypes for tamarind pod yield per tree. Whereas, maximum negative direct effect on

pod yield per tree was observed by pulp weight, pod weight, pod girth, pod width, seed per cent, shell weight.

Among the traits Pod yield per tree contributed maximum for genetic diversity followed by, Vein weight, pod width, seed weight, pulp to shell ratio, pulp per cent, pod girth, pulp weight, seed per cent, number of seeds, shell weight, shell per cent, Vein per cent, pod length and pod weight.

Intra-cluster distances revealed, cluster-I with genotypes shared maximum intra-cluster distance followed by cluster-III and remaining intra-cluster distance revealed zero divergence. However, present research was noticed that there is comparatively high intra-cluster distance in cluster I indicated that the occurrence of enough quantity of diversity within genotypes. Hence there is scope for selection within the clusters. The maximum inter cluster distance based on pod parameters was noticed between cluster-I and cluster-IV, indicating that wide range of genetic diversity was present between the clusters, followed by cluster-II and cluster-IV. whereas, minimum inter cluster distance was found between cluster-II and cluster-III, indicated that, genotypes of these clusters were genetically close

6.3 Molecular characterization of superior tamarind genotypes

Genetic diversity of 12 superior tamarind genotypes was studied using 10 SRAP and 6 ISSR primers for characterization of different superior genotypes.

In SRAP primer combination, Em14 + Me12 and Em15 + Me12 produced highest polymorphism of 100 per cent followed by Em14 + Me15 (71.42 %), while Em14 + Me11 produced least polymorphism of 33.33 per cent. In ISSR primers, the primer UBC 811 and UBC 855 produced maximum per cent of polymorphism of 100 per cent followed by P 817 (66.66 %) and the least polymorphism per cent was observed in primer UBC 826 (50.00 %)

Genetic diversity between 12 superior genotypes were determined on the basis of Jaccard Similarity Coefficient. The maximum similarity of 74 per cent was reported between G-24 and G-16 followed by G-25 and G-26 (73%), while the least similarity of 30 per cent was observed between genotypes G-24 and G-33. Where the dendrogram shows that G-33 genotype having less similarity among all the genotypes which is regular bearer compare to all other genotypes.

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Appendix I: Metrological data recorded during the experimental period from January 2019 to March 2020 at Horticulture Research Experimental Station, Hidkal Dam.

Month	Temperature °C		Relative humidity (%)	Rainfall (mm)
	Maximum	Minimum		
2019				
January	33.00	12.00	57.50	-
February	32.50	17.50	53.5	-
March	36.60	15.00	47.48	-
April	37.10	15.70	65.9	-
May	40.80	14.10	68.8	11.60
June	35.10	14.18	78.8	203.90
July	31.40	13.00	81.35	65.50
August	30.70	12.60	70.00	234.90
September	39.80	10.40	77.50	59.00
October	38.00	14.50	67.50	299.00
November	31.50	14.50	67.50	7.10
December	32.00	15.00	65.00	12.30
2020				
January	35.00	14.50	64.50	-
February	34.00	17.50	57.00	-
March	37.50	18.50	53.00	-

ASSESSMENT OF GENETIC VARIABILITY FOR PRODUCTIVITY AND QUALITY TRAITS IN TAMARIND (*Tamarindus indica* L.) GENOTYPES

PRIYANKA G. P.

2021

Dr. I. B. BIRADAR
Major Advisor

ABSTRACT

An investigation has been carried for evaluation of 61 tamarind genotypes which are planted at HRES, Hidkal Dam, for growth, yield and quality traits and also molecular characterization was carried out for superior tamarind genotypes.

The analysis of variance was found to be highly significant among genotypes for all the yield parameters. GCV and PCV were moderate to high for all the characters except pod girth, seed per cent. High heritability in association with high genetic advance were observed for pod length, pod width, pulp weight, shell weight, seed weight, vein weight, number of seeds, pod weight, pulp per cent, shell per cent and vein per cent indicating that simple selection would be sufficient for these traits to bring genetic improvement. Pod yield per tree (kg/tree) had highly significant and positive correlation with all the characters studied except seed per cent and shell per cent. Path analysis studies revealed that seed weight, pod length, number of seeds and vein weight had maximum positive direct effect on pod yield per tree. Hence, it would be rewarding to lay stress on these characters in selection programme of the genotypes for increasing yield.

Mahalanobis D^2 study revealed that 61 tamarind genotypes were grouped into 4 clusters, cluster-I has maximum intra-cluster distance indicating the occurrence of enough quantity of diversity within genotypes and the maximum inter-cluster distance was noticed between cluster-I and Cluster-IV indicating the wide range of genetic diversity was present between the clusters. Pod yield per tree had maximum contribution towards genetic diversity.

Molecular characterization of tamarind genotypes using 10 SRAP and 6 ISSR markers showed that the primers Em14+Me12, Em15+Me12, UBC811 and UBC855 produced maximum per cent of polymorphism. The similarity matrix obtained for 12 superior tamarind genotypes was ranged from 30 to 74 per cent. Cluster analysis showed grouping of genotypes into two major clusters, however few genotypes with good characters related to pod and pulp characters are grouped together. The high yielding plants like G-25, G-26, G-16, G-17 and G-33 maybe further utilized for selecting superior genotypes having major plus characters and also further crop improvement programme.

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