



ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(7): 2731-2740
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www.thepharmajournal.com

Received: 06-04-2022

Accepted: 14-06-2022

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Genetic variability studies in tamarind (*Tamarindus indica* L.)

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Abstract

An investigation entitled "Genetic Variability Studies in Tamarind (*Tamarindus indica* L.)" was conducted at Main Garden, Department of Horticulture, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola during the year 2018-20 with objectives to estimate the extent of genotypic and phenotypic variability among tamarind genotypes. To study genotypic, phenotypic and environmental correlation for yield and yield contributing characters of tamarind genotypes. The experimental evidences point out that, analysis of variance revealed that highly significant difference among the genotypes for all the traits studied. The mean performance of 22 genotypes showed wide variation. The study on genetic variability parameters observed high PCV and GCV estimates for the character rag weight, Yield/plant, stem girth, pulp weight, pod weight, shell weight, seed weight, inflorescence length, number of pod/kg, non-reducing sugar, number of seed/pod, seed: pulp ratio. High heritability accompanied with high expected genetic advance was recorded for length of pod, pod width, pod weight, no. of pods/kg, shell weight, rag weight, pulp weight, seed weight, pulp: shell ratio, seed: pulp ratio, no. of seed/pod, inflorescence length, stem girth, non-reducing sugar, yield per plant (kg). It is clear that, these traits were highly heritable showing the presence of additive gene action. Thus, it is indicating better scope for improvement of these traits by an effective selection programme. On the basis of yield and yield contributing characters the genotype viz., MGNT7, MGNT5, MGT1/1 and AGT-3 were found promising for future improvement programme. Hence, these genotypes may be given consideration while formulating selection indices for the improvement of yield and pod qualities of tamarind. Qualitative parameters revealed a wide range of variation for the characters under investigation.

Keywords: Qualitative parameters, biochemical attributes, genotypic coefficient of variance, phenotypic coefficient of variance

Introduction

Tamarind (*Tamarindus indica* L.), is a multipurpose tropical fruit tree used primarily for its fruits, which are eaten fresh or processed, used as a seasoning or spice, or the fruits and seeds are processed for non-food uses. The species has a wide geographical distribution in the subtropics and semiarid tropics and is cultivated in numerous regions (El-Siddig *et al.*, 2006)^[14]. It is grown throughout India and being a cross pollinated species vast diversity is available in the states of Maharashtra, Andhra Pradesh, Chhattisgarh, Tamil Nadu, Gujarat, Rajasthan and North Eastern Indian states. (Malik *et al.*, 2010)^[22]. Tamarind belongs to the dicotyledonous family Fabaceae (Leguminosae) and has a somatic chromosome number of 2n=24. It is thought that Linnaeus gave the specific epithet *indicus* because the name tamarind itself was derived from Arabic which combined Tamar meaning 'date' with Hindi meaning 'of India'. The full Arabic name was Tamar-u' l-Hind and the word date included because of the brown appearance of tamarind pulp (El-Siddig *et al.*, 2006)^[14].

Although tamarind is an ancient domesticate, little attempt has been directed to its genetic improvement. This is understandable because tree improvement research that combines developmental and operational phases is time consuming and the large scale cultivation of tamarind is still in its early stages. Indigenous farmers have however selected planting materials from natural populations based on desirable and observable characteristics but such phenotypic selection means the growing stocks are virtually wild (El-Siddig *et al.*, 2006)^[14]. Since the variation in pod length and pod width was found to be genotypically similar for other traits the potential for improvement depends on sampling the genetic variability available within and between populations. Hence, knowledge of genetic variation and structure of a species and genetic parameters of important traits are essential to develop effective improvement and conservation strategies.

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The genetic improvement goals are straightforward based on the available material. They are faster growth and higher yielding lines for selection for different uses. Since normal crossing is not an option, more trait specific work is needed so that provenance trials can lead to selections which combine the desirable characters and then to cultivars developed from them. These should be developed to fit the different land-use systems of Agro-forestry, orchards/plantations as well as certain stress conditions inherent in a number of wastelands which need to be rehabilitated (El-Siddig *et al.*, 2006) [14]. Tamarind was recorded over a century ago as a variable species especially for pulp colour and sweetness. Since there is such extensive variation in characters such as foliage, flower and pod production and timber quality, there is a considerable scope to improve the species. Improvement holds the key for boosting productivity and yield of the orchards and involves development of genotypes possessing desirable characters like fast growth, good tree form, high yield and resistance or tolerance to major pests, diseases and drought (Radhamani *et al.*, 1998).

Present investigation is carried out to find out genetic variability on the basis of yield and yield attributes of different genotypes will helpful to conserve valuable germplasm and could be protected from being eroded. And its further utilization in tamarind improvement programme. The genetic variability and its components are the genetic fractions of observed variability that provides measures of transmissibility of the variation and response to selection. The knowledge of pattern of inheritance of various traits or characters is important consideration while determining the most appropriate breeding procedure applicable to any crop. The breeder's choice of the material for any improvement work consequently depends on the amount genetic variability present. The phenotype is often not true indicator of the genotype. As such, the variation existing in the natural population is the phenotypic variability which is the result of the genotypic value. The effect of environment and genotype environment interaction. There is a considerable genetic variation exists in tamarind with regard to quantitative character as well as traits contributing to quality of fruits. The size of fruits i.e. length as well as weight of fruits etc are the yield contributing characters while pulp contain and fiber contain determine the quality of the fruit. In view of the above facts, the present studies in tamarind with 22 genotypes were undertaken.

Material and Methods

The present studies entitled "Genetic variability studies in tamarind (*Tamarindus indica* L.)" was carried out on tamarind trees during the year 2018-20 at Main Garden Department of Horticulture, Dr. Panjabrao Deshmukh Krishi Vidyaapeeth, Akola. Material used and methods adopted during the course of investigations were outlined and the genotype coded as MGT1/1, MGT2/3, MGT3/2, MGT4/1, MGT7/3, MGNT1, MGNT2, MGNT3, MGNT4, MGNT5, MGNT6, MGNT7, MGNT8, MGNT9, MGST1, AGT1, AGT2, AGT3, Akola Smruti, Prathisthan-5/1, PKM-1 6/2,

DTH-1 8/1. Whereas, MGT - Main Garden Tamarind, MGNT - Main Garden Nursery Tamarind, MGST - Main Garden Storage Tamarind, AGT - Agronomy Tamarind One plant of each treatment selected, marked, and kept under observations for recording various observations. The observations recorded were as per the keys explained by Anon., 1980, Kaulgud *et al.* (1997), Rodríguez-Medina *et al.* (2010) and Patil (2014). Since the study is based on single plant observation, the samples for observations were collected from each direction i.e. East, West, South and North and each of these directions were considered as one replication. Further, the observed characteristics were subjected to RBD analysis. The data obtained from the present investigation will be analyzed as per the procedure suggested by Panse and Sukhatme (1978). Estimation of genetic variability parameters like Genotypic, phenotypic and environmental coefficient of variation, Heritability (h^2), Genetic Advance (GA), Expected Genetic Advance (GA).

Results and Discussion

The experimental results obtained from the present investigation regarding on both qualitative and quantitative morphological characters in tamarind (*Tamarindus indica* L.) are statistically analyzed, presented and discussed under the following subheadings.

Analysis of variance

The analysis of variance was carried out for all the characters under study to know whether the genotype included differed significantly among themselves. Analysis of variance for all the characters presented in the Table 1. The results revealed that, mean square due to genotypes were significant for all the characters studied for indicating the presence of sufficient genetic variability.

Mean performance of genotypes

The mean data for different quantitative traits across the tamarind genotypes are presented in the Table 1. Selection of desirable genotypes is of prime importance in plant breeding and genotype is normally selected based on its phenotype. As such, a survey of phenotypic variability becomes desirable. Variation in the mean performance of 22 tamarind genotypes and significant mean difference for the traits were observed. There was significant variation recorded among the genotypes with respect to stem girth due to genetic and environmental variation of tamarind genotypes. Stem girth of tamarind genotypes recorded a mean value 111.72 cm. The genotype MGNT4 (278 cm) exhibited significantly maximum stem girth which was followed by genotype MGNT5 (168 cm). However, minimum stem girth (49 cm) was showed by genotype MGT7/3. Similar results are also supported by Rao *et al.* (2010) [35] revealed that, the stem girth was highest (62.1 cm) in PKM-1 followed by V-29 (59.4 cm) during 2009. The results showed that, the significant difference were observed in inflorescence length. Mean inflorescence length of 13.69 cm was recorded across genotype.

Table 1: Analysis of variance of means for different characters

Sr. No.	Character	Mean sum of square		
		Replication	Treatments	Error
1	Length of pod (cm)	0.014	12.93**	0.034
2	Thickness of pod (cm)	0.006	0.114**	0.0028

3	Pod width (cm)	0.001	0.441**	0.0025
4	Pod weight (g)	0.088	105.5**	0.0840
5	No. of pods/Kg	6.132	2106.6**	3.9421
6	Shell weight pod ⁻¹ (g)	0.044	6.374**	0.0069
7	Rag weight pod ⁻¹ (g)	0.058	0.306**	0.0028
8	Pulp weight pod ⁻¹ (g)	0.077	30.23**	0.0360
9	Seed weight pod ⁻¹ (g)	0.043	6.105**	0.0023
10	Pulp recovery (%)	0.024	125.6**	0.0976
11	Pulp: shell ratio	0.010	0.406**	0.0088
12	Seed: pulp ratio	0.036	0.146**	0.00652
13	No. of seed/pod	2.700	7.884**	0.2856
14	Inflorescence length (cm)	0.057	74.03**	0.0309
15	Stem girth (cm)	0.030	11310.9**	0.0937
16	Tartaric acid (%)	0.011	7.409**	0.037
17	TSS (⁰ Brix)	0.020	41.98**	0.0318
18	Total sugar (%)	0.050	36.34**	0.0398
19	Reducing sugar (%)	0.018	11.63**	0.0438
20	Non-reducing sugar (%)	0.026	25.93**	0.0331
21	Acid: sugar ratio	0.044	0.016**	0.0211
22	Yield per plant (Kg)	4.567	3513.4**	5.964

Maximum inflorescence length was recorded in the genotype MGT1/1 (24.37cm) which was followed by genotype MGNT5 (21.12cm). Whereas, minimum inflorescence length was noticed in genotype AGT1 (8.1cm). Similar studies pertaining to important floral characters have been reported by Chavan *et al.* (1999) and Singh *et al.* (2008) in tamarind. The pod length exhibited significant difference among the genotypes of tamarind. Out of the 22 genotypes, genotype MGNT5 expressed maximum pod length (14.23 cm) and which was followed by genotype MGNT7 (13.5cm). However, it was minimum in genotype DTH1 (7.1 cm) with overall mean of 9.72 cm. These findings are in agreement with the results of Gangaprasad (1993) ^[15], Hanamashetti (1996) ^[16], Prabhushankar and Melanta (2004) ^[29] and Divakara *et al.* (2012) ^[13] in tamarind. There was significant variation recorded among the genotypes with respect to pod thickness. Maximum pod thickness was noted in genotype MGNT7 (1.83 cm) followed by genotype AGT3 (1.72 cm). Whereas, the lowest value (1.20 cm) was recorded in genotype MGNT1. Mean pod thickness was 1.46 cm. Similar results were also obtained in tamarind by Gangaprasad (1993) ^[15], Prabhushankar and Melanta (2004) ^[29]. Pod width significantly influenced by the different tamarind genotypes during the experimentation. The maximum pod width was recorded in genotype MGNT5 (3.11 cm) followed by genotype AGT3 (2.97 cm) with mean value of 2.35 cm. However, minimum value for pod width (1.90 cm) was observed in genotype DTH1. These findings are in accordance with the findings Gangaprasad (1993) ^[15], Prabhushankar and Melanta (2004) ^[29] and Divakara *et al.* (2012) ^[13] in tamarind. The pod weight differs significantly among the genotypes of the tamarind. Pod weight of tamarind genotypes recorded a mean value of 13.4 g. The genotype MGNT5 exhibited significantly maximum pod weight (27.05 g) which was followed by genotype MGNT7 (24.4 g). However minimum pod weight (6.1g) was showed by genotype DTH1. The pod weight and the pod yield per tree are related factors. The higher pod weight resulted in higher pulp, shell weight. Significant variations of pod weight in the present investigation have also been reported by Gangaprasad (1993) ^[15], Hanamashetti (1996) ^[16], and Divakara *et al.* (2012) ^[13] in tamarind. Das and Dinesh (2004) ^[10] in papaya, Singh and Singh (2004) ^[41] in mango, Prakash *et al.* (2010) ^[31]

in jamun.

The genotype exhibited significant variation among them. Significantly maximum number of pod kg⁻¹ was observed in genotype DTH1 (120) followed by genotypes MGT2/3 (117) with a mean value of 77.46. The minimum number of pod kg⁻¹ was recorded in genotype MGNT5 (42) followed by genotype MGNT7 (43). The higher number of pod kg⁻¹ obtained may be due to more vegetative growth which resulted in to high rate of photosynthesis and also the difference in pod weight kg⁻¹ may be due to difference in pulp to weight, shell weight, rag weight, number of seed pod⁻¹ and seed weight among the difference genotype. Similar variation in number of pod kg⁻¹ was reported by Hanamashetti (1996) ^[16] and Mastan *et al.* (1997) ^[23] in different tamarind genotypes. There was significant variation recorded among the genotypes with respect to shell weight per pod. Maximum shell weight pod⁻¹ was noted in genotypes MGNT5 (6.6 g) followed by genotype MGNT7 (6.1 g). Whereas, lowest shell weight pod⁻¹ (1.75 g) was recorded in genotype DTH1 with mean of 3.40g. The variation in shell weight pod⁻¹ of different tamarind genotypes under study may be attributed to the difference in size of fruit. Similar variation with respect to shell weight pod⁻¹ of different tamarind genotypes were observed by Mastan *et al.* (1997) ^[23], Shivanandam (1980) ^[38], Hanamashetti and Sulikeri (1997) ^[18] in different tamarind genotypes. There was significant variation recorded among the genotypes with respect to rag weight. Mean rag weight was 0.36 g. Maximum rag weight was noted in genotype MGNT7 (1.25 g) followed by genotype MGNT5 (0.95 g). Whereas, minimum value (0.10 g) was recorded in genotype MGT2/3 and DTH1. The difference in rag weight among the genotypes may be due to the difference in the rate of development of vascular tissue in fruit (Hanamashetti, 1997) ^[18]. Similar results in tamarind have also been reported by Prabhushankar *et al.* (2004) ^[30] and Divakara *et al.* (2012) ^[13]. The results indicated that, significant differences were observed in pulp weight. The data revealed that, the maximum pulp weight was recorded in genotype MGNT5 (13.85 g) and followed by genotype MGT1/1 (9.8 g). However, it was minimum in genotype DTH1 (2.45 g). Mean pulp weight across 22 genotypes was 5.78g. Fruit length, breadth and weight are measures of fruit size, the larger the fruit the more is the pulp weight (Karale *et al.*, 1999). Significant variation in pulp weight trait studied in

the present investigation have also been reported in tamarind by Benjamin *et al.* (1999)^[2] Prabhushankar *et al.* (2004)^[29] and Divakara *et al.* (2012)^[13]. There was significant variation recorded among the genotypes with respect to seed weight. Maximum seed weight was noted in genotype MGNT7 (7.35 g) followed by genotype MGNT5 (5.65 g). Whereas, the minimum value (1.8 g) was recorded in genotype DTH1 with mean of 3.85g. The difference in seed weight may be attributed to the difference in the number and size of seeds (Shivanandam, (1980; Hanamahetti, 1996)^[38, 16]. Similar results were observed by Gangaprasad (1993)^[15] and Divakara *et al.* (2012)^[13] in tamarind and Prakash *et al.* (2010)^[31] in jamun.

There was significant difference among the genotypes in respect to number of seed per pod. The maximum number of seed pod⁻¹ was recorded with the genotype MGT7/3 and MGNT7 (8.00) which was found to be at par with genotype MGNT5 (7.5). However, the minimum number of seeds pod⁻¹ was recorded in genotype DTH1 (3.00). Mean number of seed was 5.42. There was significant variation recorded among the genotypes with respect to pulp recovery. Among the different tamarind genotypes, pulp recovery was significantly maximum in genotype PKM-1 (53.19%) which was at par with MGT1/1 (52.83%). Whereas, the minimum pulp recovery was observed in genotype MGNT1 (32.9%) with mean of 42.13%. Prabhushankar *et al.* indicated that, clones like PKM-1, Urigam, No-33, P-11 and NB-15 were very important with respect to excellent pulp recovery. There was significant variation recorded among the genotypes with respect to pulp: shell ratio. Maximum pulp: shell ratio was noted in genotype PKM-1 (2.23) which was found at par with genotype MGNT6 (2.13). Mean pulp: shell ratio was 1.66. Whereas, lowest value (1.12) was recorded in genotype MGNT1. The genotypes exhibited the significant variation in seed: pulp ratio. Maximum seed: pulp ratio was noted in genotype MGNT1 (1.00) which was at par with genotype MGT7/3 (0.99), MGNT9 (0.97). The lowest Seed: pulp ratio was observed in genotype MGT1/1 (0.36). Overall mean of Seed: pulp ratio was 0.71. The similar variation in seed: pulp ratio in tamarind genotype was noticed by Singh and Nandini (2011)^[43] and Rajan *et al.* (2009)^[34] in mango.

There was significant wider variability in the pod yield was recorded due to the variability in the age. Maximum yield per plant (153.4 kg) was recorded in genotype AKT-10, followed by genotype MGNT7 (125kg). Whereas, it was minimum (15 kg) in the genotype MGT2/3 and MGT7/3 with mean of 42.14 kg. The genetic makeup of the plant plays as a vital role in the productivity of plant. The yield is known to be a polygenic character besides care and management of orchard, age of plant and season are the important factor influence in the yield. Similar trends also observed in respect of yield as obtained by Prabhushankar *et al.* (2004)^[30], Rao *et al.* (2010)^[35], Hanamashetti *et al.* (1996)^[16] also observed the similar trends of yield in different tamarind genotypes.

Biochemical attributes

There was significant variation among the tamarind genotypes with respect to tartaric acid content of pods. Maximum tartaric acid was recorded in genotype PKM-1 (15.45%), which was followed by genotypes AGT2 (13.78%), MGNT4 (13.76%). Significantly lowest tartaric acid was observed in genotypes MGNT7 (8.49%) and AGT3 (9.66%), respectively. Mean value of tartaric acid was 12.36 percent. Hanamashetti

(1996)^[16] reported that, the difference in the tartaric acid content is related to the difference in the genotype and varies from season to season. Shankaracharya (1998)^[37] revealed that the tartaric acid ranged between of 8-18 percent, which is in accordance with average tartaric acid content of the genotypes. Tamarind needs to be more acidic and higher the acid content better is the quality (Prabhushankar *et al.*, 2004)^[29]. Significant variation in tartaric acid content studied in the present investigation has also been reported by Prabhushankar and Melanta (2004)^[29], Prabhushankar *et al.* (2004)^[30] and Divakara (2009)^[12] in tamarind. Total soluble solids of pulp recorded significant difference among the different tamarind genotypes. It was found that, the genotype AKT-10 (70.83^oB) recorded a higher TSS which was followed by genotype MGT4/1 (70.44^oB), MGT1/1 (69.73^oB), MGT2/3 (68.77^oB). The lower TSS was recorded in genotypes MGNT8 (61.13^oB) with mean value of 65.55^oBrix. The difference in TSS content of the pulp may be due to difference in sugar content of fruits (Prabhushankar *et al.*, 2004)^[30]. Similar results in tamarind were observed by Karale (2001)^[20] and Divakara (2009)^[12], Singh and Srivastava (2000)^[40] in jackfruit and Prakash *et al.* (2010)^[31] in jamun. The total sugars differed significantly among the genotypes of the tamarind. Mean total sugars were 31.28 percent across the tamarind genotypes. Genotype MGT4/1 exhibited significantly highest total sugars (36.91%) which was at par with genotypes MGNT7 (36.82%). However, lowest total sugars (26.82%) were showed by genotype MGNT8 and PKM-1. The pulp composition of tamarind is variable depending on locality and varieties (Gunaseena and Hughes, 2000)^[14]. Total sugars variations in pulp may be attributed to the season and tartaric acid content of the pulp. These results are in accordance with the findings of Divakara (2009)^[12] in tamarind, Singh and Srivastava (2000)^[40] in jackfruit, Kumar *et al.* (2009)^[34] in bael, Prakash *et al.* (2010)^[31] in jamun, Bihari and Suryanarayan (2011)^[5] in guava, Wani *et al.* (2012)^[45] in pomegranate. The reducing sugars content of fruit differed significantly among the all tamarind genotypes under study. The mean value of reducing sugar was 22.54 percent. The maximum reducing sugars (25.76%) was recorded in genotype AKT-10 and followed by genotype MGNT7 (25.39%). While, the lowest reducing sugars was noted in genotype MGNT8 (19.92%). Wide range of variation recorded among various types of tamarind in terms of physico-chemical characters offers good scope for further selection (Kennedy *et al.*, 1998)^[21]. Similar studies in tamarind have been reported by Divakara (2009)^[12], Kumar *et al.* (2009)^[34] in bael, Bihari and Suryanarayan (2011)^[5] in guava. There was significant variation across the genotypes regarding non-reducing sugars. Mean non reducing sugar was 8.73 percent among the tamarind genotypes. Genotype MGT4/1 exhibited highest non reducing sugars (14.49%) which were at par with genotype MGST1 (12.52%). However, genotype AGT3 noted lowest non reducing sugars (5.16%). Similar conclusions were made by Divakara (2009)^[12] in tamarind, Kumar *et al.* (2009)^[34] in bael, Bihari and Suryanarayan (2011)^[5] in guava.

Acid: sugar ratio

There was significant difference were observed with respect to acid: sugar ratio of tamarind genotypes. Mean acid: sugar ratio was 0.39. The maximum acid: sugar ratio 0.57 was recorded in genotype PKM-1 followed by genotype MGNT8 (0.50). However, minimum ratio for acid: sugar (0.23) was

observed in genotype MGNT7. Similar results are also supported by Rajmanickam and Rajmohan (2008) [33] in Banana.

Genetic variability parameters

The data for different genetic variability parameters viz. phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), environmental coefficient of variation (ECV), heritability (h^2), genetic advance (GA), expected genetic advance (EGA) across the tamarind genotypes presented in table 3. The range values of different

characters reflect the extent of phenotypic variability available in tamarind. This alone will not be sufficient to assess the utility of germplasm in breeding programmes because, the observed variability includes the genotypic, environmental and genotype X environmental interaction components. Therefore, further partitioning of variability into genetic and environmental components if necessary to judge the ability of this material. The heritable portion of the observed phenotypic variation can be ascertained by studying the components of variation i.e. phenotypic and genotypic coefficients of variation.

Table 2: Mean performance of different quantitative traits of 22 tamarind genotypes

Genotypes	Stem Girth (cm)	Inflorescence length(cm)	Length of pod (cm)	Thickness of pod (cm)	Pod Width (cm)	Pod weight (gm)	No of pods/Kg	Shell weight pod ⁻¹ (g)	Rag weight pod ⁻¹ (g)	Pulp weight pod ⁻¹ (g)	Seed weight pod ⁻¹ (g)	Pulp Recovery (%)
MGT1/1	82	24.37	11.29	1.6	2.79	18.5	50	4.65	0.5	9.8	3.6	52.83
MGT2/3	54	10.52	7.9	1.25	1.97	8.5	117	2.1	0.1	3.35	2.95	39.4
MGT3/2	57	9.55	9.2	1.53	2.32	12.6	79	3.4	0.3	5.3	3.6	42
MGT4/1	90	9.27	11.63	1.42	2.6	16.1	62	3.9	0.45	7.45	4.35	46.27
PT 5/1	58	8.25	9.3	1.4	2.3	12.3	80	3.35	0.35	5	3.65	40.4
MGT7/3	49	10.47	10.2	1.28	2.58	14.1	70	3.35	0.25	5.3	5.25	37.4
DTH 8/1	105	12.77	7.1	1.3	1.9	6.1	120	1.75	0.1	2.45	1.8	40
AGT-1	58	8.1	9.55	1.47	2.35	15	66	3.75	0.4	5.9	4.95	39.3
AGT-2	80	15.17	9.64	1.58	2.16	15.6	63	4.45	0.25	5.8	5.15	37
AGT-3	101	17	11.14	1.72	2.97	11.9	71	2.85	0.3	5.65	2.85	47.47
AKT-10	127	12.5	9	1.32	2	10.5	76	2.6	0.2	4.1	3.6	38.9
MGNT-1	156	15.1	8.2	1.2	2	9.2	108	2.7	0.2	3	3.3	32.9
MGNT-2	115	14.12	8.3	1.6	2.46	11.6	86	2.75	0.35	5.1	3.4	43.9
MGNT-3	110	10.15	9.7	1.51	2.5	11.65	75	2.65	0.3	5.3	3.4	45.49
MGNT-4	278	12.25	7.6	1.3	2	8.15	106	2.4	0.15	2.85	2.75	34.9
MGNT-5	168	21.12	14.23	1.70	3.11	27	42	6.6	0.95	13.85	5.65	51.2
MGNT-6	148	13.27	9.45	1.30	2.08	8.2	87	1.8	0.2	3.85	2.35	46.95
MGNT-7	137	19.25	13.5	1.83	2.65	24.4	43	6.1	1.25	9.7	7.35	39.7
MGNT-8	127	18.32	10.5	1.47	2.25	14.9	67	4.15	0.4	5.8	4.15	38.92
MGNT-9	140	16.37	7.7	1.31	2.09	8.9	112	2.2	0.1	3.35	3.25	37.6
MGST1	158	12.57	9.48	1.55	2.27	12.5	69	3.3	0.35	5.15	3.3	41.2
PKM-1	60	10.8	9.42	1.50	2.46	17.2	55	4.1	0.55	9.15	4.1	53.19
Mean	111.72	13.69	9.72	1.46	2.35	13.4	77.46	3.40	0.36	5.78	3.85	42.13
SE (m)	0.153	0.087	0.093	0.026	0.025	0.144	0.992	0.041	0.023	0.093	0.022	0.156
C.D. 5%	0.432	0.248	0.264	0.075	0.070	0.409	2.805	0.117	0.067	0.263	0.063	0.441

Table 2: Cont...

Genotypes	Pulp: Shell ratio	Seed: Pulp ratio	No of seed pod ⁻¹	Yield per Tree (Kg)	Tartaric Acid (%)	Titrateable Acidity(%)	TSS (°Brix)	Total sugar (%)	Reducing Sugar (%)	Non-Reducing sugar (%)	Acid: Sugar ratio
MGT 1/1	2.1	0.36	4.65	26	11.77	12.90	69.73	34.39	22.14	12.15	0.34
MGT 2/3	1.59	0.88	5	15	12	13.04	68.77	31.02	22.7	8.32	0.38
MGT 3/2	1.55	0.67	6	25	13.45	14.49	67.45	32.61	20.11	12.5	0.41
MGT 4/1	1.91	0.58	5.75	32	11.31	12.45	70.44	36.91	22.42	14.49	0.3
PT 5/1	1.49	0.73	5	30	12.40	13.57	65.89	30.84	23.08	7.76	0.4
MGT 7/3	1.58	0.99	8	15	13.70	14.40	63.89	33.64	24.57	9.07	0.4
DTH 8/1	1.4	0.73	3	45	12.45	13.55	66.45	32.24	25.02	7.22	0.38
AGT-1	1.57	0.83	6	48.5	13.17	14.67	65.00	31.58	22.15	9.43	0.41
AGT-2	1.3	0.88	7	37.5	13.78	15.08	64.78	28.87	22.98	5.89	0.47
AGT-3	1.98	0.5	4.15	32	9.66	12.27	63.53	29.25	24.09	5.16	0.33
AKT-10	1.57	0.87	6	153.4	12.88	14.33	70.83	33.64	25.76	7.88	0.38
MGNT-1	1.12	1	6	30.9	10.60	11.43	65.86	28.81	23.16	5.65	0.36
MGNT-2	1.85	0.66	5	21	13.02	14.26	59.64	27.38	20.48	6.9	0.47
MGNT-3	2	0.64	4.15	20	11.37	12.77	66.70	30.18	21.4	8.78	0.37
MGNT-4	1.18	0.96	4	48	13.76	14.20	67.09	29.62	22.05	7.57	0.46
MGNT-5	2.09	0.4	7.5	78	12.50	13.69	66.35	31.12	21.03	10.09	0.4
MGNT-6	2.13	0.61	3.65	50	11.94	13.09	64.73	30.56	21.13	9.43	0.39
MGNT-7	1.59	0.75	8	125	8.49	10.75	62.83	36.82	25.39	11.43	0.23
MGNT-8	1.39	0.71	6.6	30	13.57	14.45	61.13	26.82	19.92	6.9	0.5

MGNT-9	1.52	0.97	4	20	13.23	15.84	68.40	28.97	22.42	6.55	0.45
MGNT1	1.56	0.64	5.4	18	11.60	13.87	58.33	36.15	23.63	12.52	0.32
PKM-1	2.23	0.44	4.4	27.3	15.45	17.20	64.39	26.82	20.38	6.44	0.57
Mean	1.66	0.71	5.42	42.16	12.36	13.74	65.55	31.28	22.54	8.73	0.40
SE (m)	0.047	0.012	0.267	1.232	0.096	0.7	0.089	0.031	0.033	0.028	0.007
C.D. 5%	0.133	0.036	0.755	3.482	0.272	2.2	0.252	0.089	0.093	0.081	0.020

Table 3: Genetic parameters of different quantitative traits of tamarind genotypes

Sr. No.	Characters	Range	Mean	S.E (M)	CD at 5%	PCV (%)	GCV (%)	ECV (%)	h ²	GA	EGA (%)
1	Length of pod (cm)	7.1-14.2	9.72	0.093	0.264	18.55	18.45	11.92	99.78	3.679	37.81
2	Thickness of pod (cm)	1.20-1.83	1.46	0.026	0.075	12.0	11.44	30.67	95.33	0.327	22.43
3	Pod width (cm)	1.90-3.11	2.35	0.025	0.070	14.22	14.07	21.13	99.08	0.674	28.65
4	Pod weight (g)	6.1-27	13.4	0.144	0.409	38.37	38.31	20.16	100	10.55	78.80
5	No. of pods/Kg	42-120	77.46	0.992	2.805	29.70	29.60	25.56	99.66	47.05	60.74
6	Shell weight pod ⁻¹ (g)	1.75-6.6	3.40	0.041	0.117	37.13	37.06	29.45	99.89	2.593	76.17
7	Rag weight pod ⁻¹ (g)	0.10-1.27	0.36	0.023	0.067	74.13	72.78	14.1	98.21	0.557	147.1
8	Pulp weight pod ⁻¹ (g)	2.45-13.8	5.78	0.093	0.263	47.54	47.43	31.28	99.85	5.646	97.46
9	Seed weight pod ⁻¹ (g)	1.8-7.35	3.85	0.022	0.063	31.96	31.94	11.25	100.1	2.542	65.75
10	Pulp recovery (%)	32.9-53.1	42.13	0.156	0.441	13.31	13.29	9.74	100	11.52	27.34
11	Pulp: shell ratio	1.12-2.23	1.66	0.047	0.133	19.72	18.90	15.65	95.93	0.622	37.30
12	Seed: pulp ratio	0.36-1.0	0.71	0.012	0.036	26.80	26.56	13.56	98.88	0.389	54.23
13	No. of seed pod ⁻¹	3-8	5.42	0.267	0.755	27.27	25.42	19.86	93.38	2.64	48.83
14	Inflorescence length (cm)	8.1-24.37	13.69	0.087	0.248	31.43	31.40	11.28	100	8.853	64.64
15	Stem girth (cm)	49-278	111.7	0.153	0.432	47.6	47.5	4.27	99.78	109.5	98.04
16	Tartaric acid (%)	8.49-15.45	12.36	0.096	0.272	11.2	11.1	11.58	99.10	2.768	22.63
17	TSS (⁰ Brix)	58.33-70.8	65.55	0.089	0.252	4.95	4.94	12.27	99.79	6.661	10.16
18	Total sugar (%)	26.8-36.9	31.28	0.031	0.089	9.64	9.64	7.20	100	6.208	19.84
19	Reducing sugar (%)	19.9-25.7	22.54	0.033	0.093	7.57	7.56	10.29	99.89	3.509	15.56
20	Non-reducing sugar (%)	5.16-14.4	8.73	0.028	0.081	29.16	29.15	9.66	100	5.243	60.03
21	Acid: sugar ratio	0.23-0.57	0.40	0.007	0.020	16.6	16.2	3.71	97.59	0.127	32.55
22	Yield per plant (Kg)	15-153.4	42.16	1.232	3.482	73.5	73.2	6.04	99.59	60.79	150.4

Phenotypic coefficient of variation (PCV)

The estimates of phenotypic coefficient of variation (PCV) was high for pod weight (38.37%), number of pods/kg (29.70%), shell weight pod⁻¹ (37.13%), rag weight pod⁻¹ (74.13%), pulp weight pod⁻¹ (47.54%), seed weight pod⁻¹ (31.96%), seed: pulp ratio (26.80%), number of seed pod⁻¹ (27.27%), inflorescence length (31.43%), stem girth (47.6%), non-reducing sugar (29.16%), yield/plant (73.5%). The value of phenotypic coefficient of variation was moderate for length of pod (18.55%), thickness of pod (12%), Pod width (14.22%), pulp recovery (13.31%), pulp: shell ratio (19.72%), tartaric acid (11.2%), acid: sugar ratio (16.6%). Low phenotypic coefficient of variation was estimated for TSS (4.95%), total sugar (9.64%), reducing sugar (7.57%).

Genotypic coefficient of variation (GCV)

The estimates of genotypic coefficient of variation (GCV) was high for pod weight (38.31%), numbers of pods/kg (29.60%), shell weight pod⁻¹ (37.06%), rag weight pod⁻¹ (72.78%), pulp weight pod⁻¹ (47.43%), seed weight pod⁻¹ (31.94%), seed: pulp ratio (26.56%), number of seed pod⁻¹ (25.42%), inflorescence length (31.40%), stem girth (47.5%), non-reducing sugar (29.15%), yield plant⁻¹ (73.2%). The value of genotypic coefficient of variation was moderate for length of pod (18.46%), thickness of pod (11.44%), pod width (14.07%), pulp recovery (13.29%), pulp: shell ratio (18.90%), tartaric acid (11.1%), acid: sugar ratio (16.2%). Low genotypic coefficient of variation was estimated for TSS (4.94%), total sugar (9.64%), reducing sugar (7.56%). Genetic variation is the inherent or genetic variability which remains unaltered by environmental conditions. Genotypic coefficient of variation is the indicator of such variation in the genotype

for a particular trait. High GCV values suggesting that, these characters can be improved by selection. Low GCV estimates showing high impact of environmental factors on the expression of these traits.

Environmental coefficient of variation (ECV)

The estimates of environmental coefficient of variation was high for thickness of pod (30.67%), pod width (21.13%), pod weight (20.16%), number of pods/kg (25.56%), shell weight/pod (29.45%), pulp weight pod⁻¹ (31.28%). The value of environmental coefficient of variation was moderate for length of pod (11.92%), rag weight pod⁻¹ (14.1%), seed weight pod⁻¹ (11.25%), pulp: shell ratio (15.65%), seed: pulp ratio (13.56%), number of seed pod⁻¹ (19.86%), inflorescence length (11.28%), tartaric acid (11.28%), TSS (12.27%), reducing sugar (10.29%). Low environmental coefficient of variation was estimated for pulp recovery (9.74%), stem girth (4.27%), total sugar (7.20%), non-reducing sugar (9.66%), acid: sugar ratio (3.71%), yield plant⁻¹ (6.04%). Since most of the economic characters are complex in inheritance and are greatly influenced by several genes interacting with various environmental conditions, the study of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is not only useful for comparing the relative amount of phenotypic and genotypic variations among different traits but also very useful to estimates the scope for improvement by selection. The reliability of a parameter to be selected for breeding programme among other factors is dependent on the magnitude of its coefficient of variations (CV) especially the GCV. However, the difference between genotypic and phenotypic coefficient of variability indicate the environmental influence. While a lower value of CV

generally depicts low variability among the tested sample; high proportion GCV to the PCV is desirable in breeding works (Bello, 2012) ^[1]. Environmental variation is the non-heritable variation which is entirely due to the environmental effects and varies under different environmental conditions. High ECV suggests high contribution of environmental factors in determining this trait. Selection for such traits may be misleading. Low ECV showing better stability of genotypes for these characters under varied climatic conditions.

The magnitude of phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) in all traits under study suggesting the role of environment for the expression of traits besides its genetic makeup. On the basis of higher phenotypic as well as genotypic coefficient of variation was recorded for pod weight, number of pods/kg, shell weight pod⁻¹, rag weight pod⁻¹, pulp weight pod⁻¹, seed weight pod⁻¹, seed: pulp ratio, number of seed pod⁻¹, inflorescence length, stem girth, non-reducing sugar, yield plant⁻¹. Thus, the selection of these traits will be worthwhile for improvement in tamarind. The other researchers worked on variability in tamarind and other fruit crops made similar observations were Hanamashetti (1996) ^[16], Kennedy *et al.* (1998) ^[21], Divakara (2008, 2009) ^[11, 12], Divakara *et al.* (2012) ^[13], Singh and Nandini (2014) ^[43] in tamarind, Singh and Mishra (2010) ^[44] in bael, Sharma *et al.* (2011) ^[36] in cashewnut, Mohammed *et al.* (2014) ^[25] and Rajamanickam and Rajmohan (2014) in banana, Bhat and Dhillon (2015) ^[3] in pear, Mishra *et al.* (2015) ^[24] in strawberry.

Heritability

Heritability is a measure of the phenotypic variance attributes to genetic causes and has predictive function in plant breeding. It provides information on the extent to which a particular morphogenetic character can be transmitted to successive generations. Knowledge of heritability influences the choice of selection procedures used by the plant breeder to decide which selection methods would be most useful to improve the character and to determine the relative importance of genetic effects (Bello, 2012) ^[1]. Higher estimates of heritability was observed for length of pod (99.78%), thickness of pod (95.33%), width of pod (99.08%), pod weight (100%), number of pod/kg (99.66%), shell weight pod⁻¹ (99.89%), rag weight pod⁻¹ (98.21%), pulp weight pod⁻¹ (99.85%), seed weight pod⁻¹ (100.1%), pulp recovery (100%), pulp: shell ratio (95.93%), seed: pulp ratio (98.88%), number of seed pod⁻¹ (93.38%), inflorescence length (100%), stem girth (99.78%), tartaric acid (99.10%), TSS (99.79%), total sugar (100%), reducing sugar (99.89%), non-reducing sugar (100%), acid: sugar ratio(97.59%), yield plant⁻¹ (99.59%). Since most of economic characters are complex in their inheritance and are greatly influenced by environmental conditions, the study of heritability and genetic advance is very useful to estimates the scope of improvement by selection (Bhat and Dhillon, 2015) ^[3]. Heritability magnitude indicates the reliability with which the genotype will be recognized by its phenotypic expression. High heritability indicates that the traits under study had great scope for genetic improvement. The heritability estimates were high for characters like for length of pod, thickness of pod, width of pod, pod weight, number of pod per kg, shell weight pod⁻¹, rag weight pod⁻¹, pulp weight pod⁻¹, seed weight pod⁻¹, pulp recovery, pulp: shell ratio, seed: pulp rati, number of seed pod⁻¹, inflorescence length, stem girth, tartaric acid, TSS, total

sugar, reducing sugar, non-reducing sugar, acid: sugar ratio, yield plant⁻¹. Many workers have observed high heritability for different characters in several fruit crops Kennedy *et al.* (1998) ^[21], Divakara (2008, 2009) ^[11, 12], Singh and Nandini (2014) ^[43] in tamarind, Sharma *et al.* (2011) ^[36] in cashewnut, Rajan *et al.* (2009) ^[34] and Nayak *et al.* (2013) ^[26] in mango, Rabha *et al.* (2013) ^[32] in citrus, Jambhale *et al.* (2014) ^[19] in papaya, Mohammed *et al.* (2014) ^[25] and Rajamanickam and Rajmohan (2014) in banana, Bhat and Dhillon (2015) ^[3] in pear. Moderate to low estimates indicates that improvement through would be limit.

Genetic advance

Since heritability is also influenced by environment, the information on heritability alone may not help in pin-pointing characters for enforcing selection. Nevertheless, the heritability estimates in conjunction with the predicted genetic advance will be more reliable (Johnson *et al.* 1955). Heritability gives information on the magnitude of inheritance of quantitative characters, while genetic advance will be helpful in formulating suitable selection procedures. If high heritability is associated with high genetic advance, the variation could be due to additive gene effects (Panse and Khargonkar, 1957) ^[28]. Similarly, high heritability coupled with low genetic advance and vice versa indicates that the variability is due to non-additive interaction of genes (dominance or epistasis). The high estimate of genetic advance was registered for number of pod/ kg (47.05%), stem girth (109.5%), yield plant⁻¹ (60.79%). Medium genetic advance was estimated for pod weight (10.55%), pulp recovery (11.52%). The value of genetic advance was low for length of pod (3.67%), thickness of pod (0.32%), pod width (0.67%), shell weight pod⁻¹ (2.59%), rag weight pod⁻¹(0.55%), pulp weight pod⁻¹ (5.64%), seed weight pod⁻¹ (2.54%), pulp: shell ratio (0.62%), seed: pulp ratio (0.38%), number of seed/pod(2.64%), inflorescence length(8.85%), tartaric acid(2.76%), TSS(6.66%), total sugar(6.20%), reducing sugar(3.50%), non-reducing sugar(5.24%), acid: sugar ratio(0.12%). The estimate of genetic advance for different traits analysis was high for number of pod/kg, stem girth and yield/plant which revealed that these characters had additive gene effect and therefore, have more roles in proficient selection. The moderate estimate of genetic advance was exhibited by number of pod weight and pulp recovery while rest traits showed low genetic advance which indicates that these characters had non additive gene effect that offer limited scope for selection. Many workers have observed varying magnitude of genetic advance for different characters in several fruit crops like Hanamashetti (1996) ^[16], Kennedy *et al.* (1998) ^[21], Divakara (2008, 2009) ^[11, 12], Singh and Nandini (2014) ^[43] in tamarind, Sharma *et al.* (2011) ^[36] in cashewnut, Bhat and Dhillon (2015) ^[3] in pear.

Expected genetic advance

The estimates of expected genetic advance was high for length of pod (37.81%), thickness of pod (22.43%), width of pod (28.65%), pod weight (78.80%), number of pod/kg (60.74%), shell weight pod⁻¹ (76.17%), rag weight pod⁻¹ (147.1%), pulp weight pod⁻¹ (97.46%), seed weight pod⁻¹ (65.75%), pulp recovery (27.34%), pulp: shell ratio (37.30%), seed: pulp ratio (54.23%), number of seed pod⁻¹ (48.83%), inflorescence length (64.64%), stem girth (98.04%), tartaric acid (22.63%), non-reducing sugar (60.03%), acid: sugar ratio(32.55%), yield plant⁻¹ (150.4%). Moderate expected

genetic advance was estimated for TSS (10.16%), total sugar (19.84%), reducing sugar (15.56%).

The estimates of variability unless heritability estimates accompanied with high genetic advance have less utility in drawing conclusion regarding identification of useful characters for selection programme and in prediction of possibilities of yield improvement. The joint interpretation of these parameters would provide a better insight of gain expected through phenotypic selection (Burton, 1952). In the present study, high heritability estimates accompanied with high genetic advance as percent of mean were observed for length of pod, thickness of pod, width of pod, pod weight, number of pod/kg, shell weight pod⁻¹, rag weight pod⁻¹, pulp weight pod⁻¹, seed weight pod⁻¹, pulp recovery, pulp: shell ratio, seed: pulp ratio, number of seed pod⁻¹, inflorescence length, stem girth, tartaric acid, non-reducing sugar, acid: sugar ratio, yield plant⁻¹ which revealed that, these characters had additive gene effect and, therefore, have more roles in proficient selection. Many researchers have observed high heritability and expected genetic advance as percent of mean for different characters in several fruit crops Hanamashetti (1996) [16], Kennedy *et al.* (1998) [21], Divakara (2008, 2009) [11, 12], Singh and Nandini (2014) [43] in tamarind, Sharma *et al.* (2011) [36] in cashewnut, Bhat and Dhillon (2015) [3] in pear.

Qualitative Characters

The results of qualitative parameters of tamarind genotypes and the frequency distribution of qualitative parameters of tamarind genotypes have been presented in Table 4 and Table 5, respectively. The observations recorded on qualitative traits from each of 22 tamarind genotypes indicated a considerable amount of variation in all the traits. Three different bark colour were observed among genotypes categorized as light brown, brown and thick brown. Brown colour was recorded in sixteen genotypes followed by light brown colour in four genotypes and thick brown colour in two genotypes. Four different branching habit were observed among genotypes categorized as erect sparse, semi erect, drooping and semi drooping. Erect sparse branching habit was observed in ten genotypes followed by semi erect branching habit recorded in six genotypes, semi drooping branching habit observed in four genotypes and drooping branching habit observed in two genotypes. Plant stature were categorized as tall, dwarf and medium. Tall plant stature observed in thirteen genotypes, dwarf plant stature found in three genotypes and medium

plant stature observed in six genotypes the petal colour varied from pale yellow to yellow. Yellow petal colour was recorded in fourteen genotypes. However, eight genotypes have pale yellow petal colour. Early, mid and late flowering were observed among genotypes. Thirteen genotypes were early, three were mid and rest six was late in their flowering time. Pod shape were categorized as straight, slightly curved, moderately curved and deeply curved. Straight pod shape was observed in four genotypes whereas slightly curved pod shape were recorded in twelve genotypes, moderately curved pod shape observed in four genotype namely and deeply curved pod shape recorded in two genotype. Light brown, brown and red brown pulp colour was recorded among twenty-two tamarind genotypes. Brown pulp colour was observed in ten genotypes followed by light brown colour in nine genotypes and three genotypes had red brown pulp colour. Among the genotypes eight genotypes had dull white endocarp colour, seven genotypes had white endocarp colour and seven genotypes has extra white endocarp colour. The marketing price of the pulp is decided on the basis of exocarp colour (light brown with slight shining) and endocarp colour (white or phool patti) of the pulp (Karale, 2001) [20]. The results on similar lines were also reported by Shivanandam (1980) [38], Challapilli (1992) [8], Hanamashetti (1996) [16], Kennedy *et al.* (1998) [21], Biradar (2001) [6], Prabhushankar and Melanta (2004) [30], Rao and Subramanyam (2010) [35], Bhogave *et al.* (2018) [4] in tamarind.

On the basis of findings reported in present investigation the study concluded as Genotypic coefficient of variation in general were greater in magnitude than the corresponding phenotypic ones, High values of GCV and heritability estimates supplemented with greater genetic gains are also indicative of additive gene effects regulating the inheritance of such traits therefore, these characters reflect greater selective value and offer ample scope for selection and phenotypic coefficient of variation was lessened under the influence of environment. Analysis of genetic variability, revealed that the characters pod weight, number of pods/kg, shell weight, rag weight, pulp weight, seed weight, seed: pulp ratio, number of seed pod⁻¹, inflorescence length, stem girth, non-reducing sugar and yield plant⁻¹ (kg) showing high GCV, heritability and expected genetic advance and are least affected by environment and governed by additive gene action. Hence, selection will be effective for improvement of these traits.

Table 4: Qualitative parameters of tamarind genotypes

Genotypes	Bark colour	Branching habit	Plant stature	Colour of petals	Flowering time	Shape of pod	Pulp colour	Endocarp colour
MGT 1/1	Light Brown	Erect Sparse	Tall	Yellow	Early	Moderately curved	Brown	Extra white
MGT 2/3	Brown	Semi Erect	Dwarf	Pale yellow	Late	Slightly curved	Light brown	Dull white
MGT 3/2	Brown	Erect Sparse	Medium	Pale yellow	Late	Moderately curved	Brown	White
MGT 4/1	Brown	Erect Sparse	Tall	Pale yellow	Early	Moderately curved	Light brown	Extra white
PT 5/1	Light Brown	Semi Erect	Dwarf	Pale yellow	Late	Slightly curved	Red brown	White
MGT 7/3	Brown	Semi Erect	Dwarf	Yellow	Late	Slightly curved	Red brown	White
DTH 8/1	light Brown	Erect Sparse	Medium	Pale yellow	Early	Slightly curved	Brown	White
AGT-1	light Brown	Erect Sparse	Medium	Yellow	Early	Slightly curved	Light brown	White
AGT-2	Thick Brown	Erect Sparse	Medium	Yellow	Early	Moderately curved	Light brown	Dull white
AGT-3	Brown	Semi Erect	Tall	Yellow	Early	Deeply curved	Brown	Dull white
AKT-10	Brown	Semi Erect	Medium	Yellow	Mid	Slightly curved	Brown	White
MGNT-1	Thick Brown	Erect Sparse	Tall	Pale yellow	Early	Slightly curved	Brown	White
MGNT-2	Brown	Semi Erect	Tall	Yellow	Early	Straight	Brown	Extra white
MGNT-3	Brown	Erect Sparse	Tall	Yellow	Early	Slightly curved	Light brown	Extra white
MGNT-4	Brown	Semi drooping	Tall	Yellow	Mid	Straight	Light brown	Extra white
MGNT-5	Brown	Semi drooping	Tall	Yellow	Early	Deeply curved	Light brown	Extra white

MGNT-6	Brown	Droping	Tall	Yellow	Early	Straight	Brown	Dull white
MGNT-7	Brown	Semi drooping	Tall	Pale yellow	Late	Slightly curved	Light Brown	Dull white
MGNT-8	Brown	Semi drooping	Tall	Yellow	Early	Slightly curved	Brown	Dull white
MGNT-9	Brown	Droping	Tall	Yellow	Early	Slightly curved	Brown	Dull white
MGST1	Brown	Erect Sparse	Tall	Pale yellow	Late	Straight	Light brown	Dull white
PKM-1	Brown	Erect Sparse	Medium	Yellow	Mid	Slightly curved	Red brown	Extra white

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