The Pharma Innovation Journal 2023; 12(6): 5020-5026

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2023; 12(6): 5020-5026

www.thepharmajournal.com
Received: 23-04-2023
Accepted: 30-05-2023

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Genetic diversity analysis of loquat (*Eriobotrya japonica* Lind L.) Germplasm through morphological traits

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Abstract
The present investigation was carried out from seeded origin of wild germplasm of loquat in Jammu subtropics areas during the year 2019-20at SKUAST-J, Jammu and Kashmir (UT), India**.** During the investigation, one hundred loquat genotypes was explored of different location to estimate the extent of genetic diversity by morphological and biochemical characterization using NBPGR descriptor. The genotypes evaluated during the investigation recorded significant amount of variability for various descriptive and quantitative characteristics. Fruit length ranged from 2.84 to 4.61 cm, fruit width 2.25 to 3.86 cm, fruit weight 10.87 to 26.87 g, seed length 11.59 to 23.78 mm, seed width 10.03 to 18.90 mm, seed weight 2.27 to 5.89 g, number of seeds per fruit 1.66 to 4.33, pulp percent 50.81 to 66.86 percent, fruit yield 24.31 to 43.96 kg/tree and juice percent 57.21 to 84.98 percent. Majority of genotypes showed high juice percent. Total soluble solids ranged from 10.03 to 11.62 ºBrix, titratable acidity 1.02 to 1.61 percent, TSS acid ratio 6.66 to 10.43, total sugars 7.99 to 8.83%, reducing sugars 4.70 to 5.81 percent and non-reducing sugars 2.57 to 3.40%. Phenotypic coefficient of variability was slightly higher in magnitude than genotypic coefficient of variability and broad sense heritability was high for all the characters. Genetic advance as percentage of mean varied from 4.54% (total sugars) to 43.69% (number of seeds per fruit). Correlation coefficients revealed that fruit weight showed positive phenotypic and genotypic correlation with fruit yield, seed length, juice percent and pulp percent. Five major components were detected using principle component analysis exhibiting 74.88%of total variance. On the basis of cluster analysis all the genotypes were divided into seven clusters having 304.13 to 2915.52 inter-cluster distance and 462.21 to 823.93 intra-cluster distance.

Keywords: Loquat, genetic diversity, seedling origin and fruit quality

Introduction
Loquat (*Eriobotrya japonica* Lindl.) is an important subtropical evergreen fruit tree, belongs to family Rosaceae, subfamily Maloidenae and is a pome fruit, which originated in China (Huang *et al*., 2007) [12]. Presently it is being cultivated in China, Japan, India, Pakistan, Madagascar, Mauritius Island, United States, Brazil and Australia (Hussain *et al*., 2007) [13]. Loquat is becoming an important industry in China as well as Spain, Japan, India, Pakistan and Turkey (Janick, 2007) [16]. In India it is grown nearly throughout the country up to an elevation of 1525 m above mean sea level and is mostly confined to Uttar Pradesh, Delhi, Himachal Pradesh and Punjab and up to small extent in Assam, Maharashtra, Nandi hills of Tamil Naidu and Mysore. It is mainly propagated through seed in these areas and shows wide range of variability. Loquat has adapted well to the Mediterranean climate and produced in the same areas where citrus is cultivated (Badenes *et al*., 2000) [2]. However, it has more specific environmental requirements than citrus (Caballero and Fernandez, 2003) [3].

It is used worldwide for having immense medicinal potential, nutritional importance and aesthetic value (as a decorative tree) especially near houses. Besides being sweet and juicy it is very nutritious. It contains vitamins (A, B, and C), minerals (phosphorus and calcium) and Sugars (Karadeniz, 2003) [18]. The edible part of fruit contains 87.4% water, 10.2% carbohydrates, 0.7% proteins, 0.3% fat, 0.% minerals, 0.9% fibre, 0.03% calcium, 0.02% phosphorus and 0.7 mg iron/100 g (Singh and Rajput, 1963) [29]. Loquat is mainly self-compatible, but in few varieties self-incompatibility has only been found (Chen and Chu, 2008) [5]. The traditional propagation from seed has provided a range of varieties adaptable to different environments and planting regions. *Ex situ* germplasm collections have been established in China, Japan and Spain.

Among these collections, the Chinese collections possess highest diversity. There are more than 1000 accessions described in the various Chinese germplasm collections (Zheng, 2007) [41].

Genetic diversity and the relationships among different varieties of loquat are of great importance for the conservation of genetic resources, breeding, national and international exchange of germplasm (He *et al*., 2011) [11]. Research on genetic diversity of loquat based on pomological traits and molecular markers have been widely carried out (Cai 2000; Soriano *et al*. 2005; Dong 2008; Qiao 2008; Gisbert *et al*. 2009 and Yang 2009) [4, 33, 6, 27, 9, 39]. These studies significantly enhanced understanding about the distribution and structure of genetic diversity in loquat germplasm around the world.

Materials and Methods

Survey was done during the year 2019-20 at different loquat growing areas of district Jammu, Samba and Kathua of Jammu and Kashmir (UT). In order to examine the degree of genetic diversity and collection of superior germplasm from different areas of Jammu Sub-tropics of Jammu and Kashmir (UT) and to understand the genetic diversity among these with morphological characteristics. During the survey to get the first hand information local inhabitants were consulted about seedling origin genotypes grown in the area at various places. After repeated visits and observation, one hundred (100) loquat genotypes with diverse characters were selected at fruit maturity stage. Plants of different loquat genotypes with distinct characters available at all these sites were selected and permanently tagged. Codes were allotted to each genotype on the basis of their location. Regular visits were made during the period of flowering, fruit setting, fruit maturity and ripening stages during the years of study. Morphological characterization of loquat accessions was based on the list of loquat descriptors NHBR. sixteen quantitative descriptors were then examined: fruit shape, fruit stalk thickness, pulp texture, seed colour, fruit weight (g), fruit length (cm), fruit width (cm), seed weight (g), seed length (mm), seed width (mm), number of seeds/fruit, juice percent, pulp percent, fruit yield (kg/tree), total soluble solids, titratable acidity, TSSacid ratio, total sugars (%), reducing sugars (%) and non-reducing sugars (%.).

Data Analysis

The data recorded was statistically analysed with the help of WINDOSTAT statistical package (version 9.3). Analysis of variance, cluster analysis based on Tocher's method using squared Euclidean distance was performed using the statistical software Windostat and Statistical Package for Agricultural Research (SPAR) version 7.0 programme. The genetic divergence was calculated according to Mahalanobis D^2 statistics (1936).The data recorded during the investigation was also subjected to the statistical analysis through principal component analysis. The divergence was studied using Kaufman and Rosseau (1990) [20].

Results and Discussion

Mean performance for the sixteen quantitative characters are presented in Table 1, 2. Mean performance of various genotypes for the sixteencharacters under study indicated that wide range of variability was present among the genotypes. This indicated the presence of sufficient variability in the genetic material under study and it was good enough to carry out further analysis.

Fruit weight ranged from 10.87 g to 26.87 g, fruit length ranged from 2.84 cm to 4.61 cm, fruit width 2.25 cm to 3.86 cm, seed length 11.59 mm to 23.78 mm, seed width 10.03 to 18.90 mm, seed weight 2.27 g to 5.89 g, number of seeds per fruit 1.66 to 4.33, pulp percent (50.81%) to (66.86%), juice percent (57.21%) to (84.98%) and yield 24.31 kg/tree to 43.96 kg/tree. The data clearly show in table No. 1 the wide variability with respect to physical characters. The inherent ability of a genotype to utilize the available resources efficiently might be result to achieve bigger size of fruits. Selections showed variability in their fruit characters especially in size of fruits Ahmad (2008) [1]. Singh (2010) [32] while characterizing loquat genotypes in Punjab observed that fruit length varied from 3.00 to 4.45cm, fruit width 2.88 to 3.35 cm and fruit weight 15.78 to 24.38 g, almost similar type of variation for various fruit characters have also been shown by Hussain *et al.* (2011a) [14] and Hussain *et al*. (2011b) [15]. Considerable variations were found in seed characters. Regarding the seed size, observations were recorded on seed length and seed width. The seed length ranged from 11.59 to 23.78 mm, seed width 10.03 to 18.90 mm. Karadeniz *et al.* (2007) [19] who stated that seed length ranged from (15.40 to 23.32 mm) and width ranged from (6.47 to 16.96 mm). These results are also in agreement with the findings of Singh, (2010) [32] who found that seed length and width in different loquat genotypes ranged from 10.60 to 10.83 cm and 10.08 to 10.35 mm, respectively.

Total soluble solids ranged from 10.03 to 11.62 ^{0}Brix with mean value of 10.69 ^{0}Brix. Similar results were found by Polat *et al.* (2005) [24] in loquat while studying the pomological characters found that total soluble solids ranged from (9.59 to 11.77 ^{0}Brix). Durgac *et al*. (2006) [7] investigated the growth performances, phenological and pomological characteristics of different loquat genotypes and found that total soluble solids ranged from (9.09 to 11.77 ^{0}Brix). Maximum total soluble solids was found (11.62 ^{0}Brix) which was lower than that reported by Wu, (2001); Karadeniz and Senyurt (2007) [19]; Xie *et al.* (2007) [38]; Polat and Caliskan (2011) [25]; Elsabagh and Haeikl (2012) [8] and Kaur (2018a) [21] having total soluble solids of (13.80 ^{0}Brix), (18.50 ^{0}Brix), (14.30 ^{0}Brix), (14.20 ^{0}Brix), (13.22 ^{0}Brix) and (20.85 ^{0}Brix) respectively. The titratable acidity ranged from 1.02%to 1.61%. The variation in fruit acidity may be due to different rates of conversion of organic acids into soluble sugars by different genotypes. These values were similar to the results reported by Kaur (2018a) [21] and Singh (2010) [32]. TSS/acid ratio was found in the range of 6.66 to 10.43. Singh (2010) [32] found that TSS/acid ration in different genotypes ranged from 7.19 to 11.00. The total sugar content ranged from 7.99 to 8.83%whereas, the mean total sugar content among different genotypes was 8.36%. Regarding reducing sugars the highest mean value for reducing sugars (5.81%) was recorded in the fruits of LQJ-56 and the lowest amount of reducing sugars (4.71%) was recorded in the fruits of LQJ-4.71, whereas, the highest mean value for non-reducing sugars (3.40%) was recorded in the fruits of LQJ-73 and the lowest amount of non-reducing sugars (2.57%) was recorded in the fruits of LQJ-61. Such variability may be due to variability in rainfall or maturity level at the time of harvesting. These results are in line with the findings of Singh (2010) [32] and Toker *et al*. (2013) [36]. Seymour *et al.* (1993)

[31] noted that the major sugar differences among the loquats were found for glucose, fructose, and sorbitol; these variations are important for the formation of different flavors. The reducing sugars glucose and fructose together with sucrose constitute the majority of the soluble solids (Nunes *et al*., 1995) [23]. As far as the environment is concerned, prevailing temperature and rainfall distribution over growing areas definitely had affected the growth and composition of fruits especially during late stage of fruit development. The major sugar substances that contribute to sweetness are glucose and fructose that play a major role in taste (Stevens *et al*., 1977) [35].

Parameters of variability

The magnitude of phenotypic and genotypic coefficient of variability were found highest for number of seeds per fruit which were 23.29%and 22.22%respectively, followed by fruit weight (19.57%and 19.42%), seed weight (19.57%and 18.24%), seed width (17.70%and 17.68%), yield per tree (13.49%and 12.72), seed length (12.34%and 12.30%), fruit width (10.90%and 10.77%), fruit length (10.77%and 10.60%), titratable acidity (9.61%and 9.40%), TSS/acid ratio (9.50%and 9.23%), juice percent (9.44%and 9.36%), pulp percent (6.94%and 6.75%), non-reducing sugars (6.22%and 6.21%), reducing sugars (4.91%and 4.88%), Total soluble solids (4.16%and 4.09%) respectively whereas, lowest phenotypic and genotypic coefficient of variability were observed in total sugar (2.23%and 2.22%, respectively). The character number of seeds exhibit higher phenotypic coefficient value than genotypic value indicating that a greater amount of genetic variability is present for this character which provides greater scope for genotype.

Estimates of heritability in broad sense varied from 86.80%in seed weight to 99.80%in seed width. Highest heritability of (99.80%) was recorded in seed weight, followed by non-reducing sugars (99.60%), seed length (99.30%), total sugars and reducing sugars followed same amount (98.60%), followed by fruit weight (98.50%), juice percent (98.30%), fruit width (97.60%), fruit length (97.00%), Total soluble solids (96.70%), titratable acidity (95.80%), pulp percent (94.70%), TSS/ acid ratio (94.40%), number of seeds (91.00%), yield per tree (88.90%) whereas, minimum heritability among all traits were observed in seed weight (86.80%). The high heritability indicates that the traits understudy had great scope for genetic improvement. Rajan *et al.* (2009) also observed high heritability for different characters in several fruit crops. Moderate to low estimates indicate a limited scope of improvement through selection.

Genetic advance as percentage of mean varied from 4.54% (total sugars) to 43.69%(number of seeds/fruit). Highest genetic advance as percentage of mean was found for total sugars (43.69%). Moderate genetic advance as percentage of mean was found for fruit weight (39.70%), seed width (36.39%), seed weight (35.01%), seed length (25.25%), yield per tree (24.72%), fruit width (21.93%), fruit length (21.52%) and was found low for juice percent (19.13%), titratable acidity (18.97%), TSS/acid ratio (18.49%), pulp percent (13.54%), reducing sugars (9.98%), Total soluble solids (8.29%) and total sugars (4.54%). Similar findings were also reported by several workers (Rajan *et al.* 2009, Srivastava *et al.* 2014) [34] who reported high heritability with high genetic gain for different attributes in other fruits crops.

Phenotypic correlation

Fruit length showed positive and significant correlation with fruit width (0.798), fruit weight (0.712), seed length (0.487), seed width (0.393), pulp percent (0.405) and juice percent (0.390). Fruit width showed positive correlation with fruit weight (0.569), seed length (0.567), seed weight (0.531), pulp percent (0.315) and juice percent (0.344). Fruit weight showed positive correlation with seed length (0.324), pulp percent (0.525) and juice percent (0.462). Seed length showed positive correlation with seed weight (0.774) and negative correlation with number of seeds (-0.230). Seed weight showed positive correlation with number of seeds per fruits (0.651). Number of seeds per fruit showed negative correlation with total soluble solids (-0.221). Pulp percent showed positive correlation with juice percent (0.633). Total soluble solids showed positive correlation with TSS acid ration (0.298), total sugars (0.756) and reducing sugars (0.592). Titratableacidity showed negative correlation with TSS acid ration (-0.895) and showed positive correlation with total sugars (0.201). Total sugars showed positive correlation with reducing sugars (0.672). Reducing sugars showed negative correlation with non-reducing sugars (-0.678).

Principal component analysis

Principal component analysis showed that the 1st five principal components possessed Eigen value >1.0 and PC6 possessed Eigen value <1.0. PC1, PC2 and PC3 contributed total variance of 30.45%, 14.80%, and 11.69 respectively with total variance (56.96%) showing maximum factor loading by seed length, seed width, TSS, non-reducing sugar, fruit length, fruit weight, yield per tree and juice percent by the first three PC's.

Non- hierarchical Euclidean cluster analysis

Genetic divergence was assessed by MahalanobisD^2statistic. Although, D^2 is a quantitative measure of genetic divergence, the clustering pattern of genotypes obtained with this method is arbitrary. The non- hierarchical Euclidean cluster analysis for genetic divergence of fruit, seed and bio-chemical characters divided the genotypes into seven clusters. Cluster II and Cluster IV contained the maximum number of genotypes (35) in each cluster, whereas the lowest number of genotypes (01) was found in the cluster III, Cluster V and Cluster VII. The maximum intra-cluster distance was observed in cluster VI (823.93) followed by cluster IV (653.33), cluster II (547.69) and cluster I (462.21). Cluster VI and VII showed maximum inter cluster distance of (2915.52) followed by cluster III and VII (253.22), cluster III and V (2321.09), cluster V and VI (2217.17) and cluster IV and cluster VI (2068.07) whereas, minimum inter-cluster distance was observed between cluster V and VII (304.13). Among different clusters, the maximum mean value for fruit weight (20.04 g) was observed in cluster V whereas, minimum fruit weight (15.9 g) was observed in cluster VII. Contribution of different traits towards divergence among physical and biochemical traits shows that fruit yield per tree contributes highest toward total divergence and pulp percent contributed lowest towards total divergence.

Cluster mean analysis

The maximum number of genotypes was found in cluster II (35) and cluster IV (35) whereas, minimum number of

genotypes was observed in cluster III, V and VI with one genotype. Among different clusters, the maximum mean fruit weight was observed in cluster V (20.04 g) followed by cluster VI (19.73 g) and the maximum fruit yield was observed in cluster cluster II (34.42 kg/tree) followed by cluster VI (35.33 kg/tree). These results are in agreement with the results of (Yosoulkanian *et al.*, 2016) [40]. Cluster means of different traits results in identifying the diverse parents for hybridization and these divergent parents are likely to broaden genetic base (variability) and make available transgressive segregants with high heterotic effects (Gomathinayagam and Rao, 1997) [10] and (Qian and He, 1991) [26]. Sardana *et al.* (1997) [30] observed that cluster means and genotypic coefficient variation reveal interesting picture about nature of diversity.

Percent contribution of various characters towards genetic divergence: A comparison of contribution of different characters towards divergence is utmost thing in selecting and choice of parent (Ramaya and Senthikumar, 2008) [28]. Fruit yield per tree gave maximum contribution towards diversity (42.77%) followed by fruit width (34.30%), seed length (8.16%), total sugar (4.61%), fruit weight (3.64), juice percent (2.32%), seed weight (1.92%), titratable acidity (0.81%), fruit length (0.67%), TSS (0.63%), number of seeds per fruit (0.16%) and pulp percent (0.02%).

Table 1: Descriptive statistics for variability in fruit and seed characteristics of loquat genotypes

Character	Minimum	Maximum	Mean ±SE	Critical difference (C.D) at 0.5%	S.D
Fruit weight (g)	10.87	26.87	18.71±0.26	0.73	3.64
Fruit length (cm)	2.84	4.61	3.73±0.04	0.11	0.40
Fruit width (cm)	2.25	3.86	3.17±0.03	0.08	0.34
Seed weight (g)	2.27	5.89	4.15±0.17	0.47	0.78
Seed length (mm)	11.59	23.78	18.63±0.11	0.31	2.30
Seed width (mm)	10.03	18.90	14.69±0.06	0.19	2.60
Number of seeds per fruit	1.66	4.53	2.97±0.12	0.33	0.67
Pulp (%)	50.81	66.86	57.73±0.53	1.48	3.94
Juice (%)	57.21	84.98	70.01±0.49	1.37	6.58
Yield (kg/tree)	24.31	43.96	34.98±0.96	2.52	4.54

Table 2: Descriptive statistics for variability in bio-chemical traits of loquat genotypes

Character	Minimum	Maximum	Mean ±SE	(C.D) at 0.5%	S.D
Total soluble solids (^{O}B)	10.03	11.63	10.69±0.04	0.13	0.44
Titratable acidity (%)	1.02	1.61	1.24±0.01	0.04	0.12
TSS acid ratio	6.66	10.43	8.62±0.11	0.31	0.80
Total sugars (%)	7.99	8.83	8.36±0.01	0.03	0.19
Reducing sugars (%)	4.71	5.81	5.28±0.01	0.05	0.26
Non-reducing sugars (%)	2.57	3.40	2.92±0.007	0.01	0.18

Table 3: Estimation of various genetic parameters of loquat genotypes

Character	Coefficient of variation (%)		Heritability % (Broad sense)	Genetic Advance	Genetic Advance (% Mean)
	PCV	GCV			
Fruit length (cm)	10.77	10.60	97.00	0.80	21.52
Fruit width (cm)	10.90	10.77	97.60	0.69	21.93
Fruit weight (g)	19.57	19.42	98.50	7.43	39.70
Seed length (mm)	12.34	12.30	99.30	4.70	25.25
Seed width (mm)	17.70	17.68	99.80	5.34	36.39
Seed weight (g)	19.57	18.24	86.80	1.45	35.01
Number of seeds/fruit	23.29	22.22	91.00	1.30	43.69
Pulp (%)	6.94	6.75	94.70	7.81	13.54
Yield per tree	13.49	12.72	88.90	8.65	24.72
Juice (%)	9.44	9.36	98.30	13.39	19.13
Total soluble solids (^{O}B)	4.16	4.09	96.70	0.88	8.29
Titratable acidity (%)	9.61	9.40	95.80	0.23	18.97
TSS acid ratio	9.50	9.23	94.40	1.59	18.49
Total sugars (%)	2.23	2.22	98.60	0.38	4.54
Reducing sugars (%)	4.91	4.88	98.60	0.52	9.98
Non-reducing sugars (%)	6.22	6.21	99.60	0.37	12.77

Table 4: Principal components for sixteen quantitative traits in loquat genotypes

	PC1	PC2	PC3	PC4	PC5	PC6
Eigene Value (Root)	4.87	2.37	1.87	1.75	1.12	0.85
% Var. Exp.	30.46	14.81	11.69	10.94	6.99	5.32
Cum. Var. Exp.	30.46	45.26	56.96	67.90	74.88	80.20
Factor loadings						
Fruit length (cm)	0.25	0.19	0.37	0.04	0.13	0.16
Fruit width (cm)	0.21	0.00	-0.19	-0.38	0.35	-0.01
Fruit weight (g)	0.00	0.25	0.52	0.07	-0.10	0.34

Seed length (mm)	0.32	-0.01	-0.19	-0.03	-0.47	0.18
Seed width (mm)	0.39	0.01	-0.18	0.04	0.02	-0.18
Seed weight (g)	-0.36	0.02	0.16	-0.02	0.30	-0.12
Number of seeds per fruit	0.37	0.14	-0.09	-0.07	0.09	0.02
Pulp (%)	0.21	-0.07	0.19	-0.26	-0.25	-0.56
Yield per tree	0.30	0.15	0.40	0.04	-0.16	0.11
Juice (%)	-0.09	0.03	0.39	-0.39	-0.07	-0.40
Total soluble solids(^{0}B)	0.36	-0.18	0.03	0.18	0.10	-0.21
Titratable acidity (%)	0.04	-0.32	0.05	0.53	-0.19	-0.08
TSS acidity ratio	0.30	0.10	-0.01	-0.02	0.51	0.16
Total sugars (%)	0.08	-0.27	0.25	0.42	0.35	-0.26
Reducing sugars (%)	0.08	-0.56	0.14	-0.24	-0.05	0.30
Non-reducing sugars (%)	-0.01	0.57	-0.15	0.26	-0.08	-0.25

Table 5: Distribution of different loquat genotypes into clusters based on D^2 statistics

Cluster	Number of genotypes in the cluster	Accession number of the genotypes
I	20	LQJ-65, LQJ-83, LQJ-97, LQJ-48, LQJ-85, LQJ-93, LQJ-94, LQJ-90, LQJ-84, LQJ-95, LQJ-80, LQJ-82, LQJ-55, LQJ-76, LQJ-67, LQJ-58, LQJ-86, LQJ-21, LQJ-71, LQJ-38.
II	35	LQJ-10, LQJ-29, LQJ-54, LQJ-59, LQJ-32, LQJ-81, LQJ-24, LQJ-13, LQJ-42, LQJ-16, LQJ-18, LQJ-09, LQJ-06, LQJ-26, LQJ-03, LQJ-69, LQJ-01, LQJ-51, LQJ-48, LQJ-66, LQJ-12, LQJ-07, LQJ-41, LQJ-08, LQJ-05, LQJ-15, LQJ-14, LQJ-17, LQJ-04, LQJ-22, LQJ-23, LQJ-11, LQJ-02, LQJ-43, LQJ-68.
III	01	LQJ- 100
IV	35	LQJ-92, LQJ-98, LQJ-74, LQJ-88, LQJ-30, LQJ-27, LQJ-45, LQJ-40, LQJ-75, LQJ-96, LQJ-87, LQJ-57, LQJ-63, LQJ-34, LQJ-44, LQJ-39, LQJ-72, LQJ-31, LQJ-37, LQJ-53, LQJ-52, LQJ-91, LQJ-62, LQJ-33, LQJ-35, LQJ-20, LQJ-28, LQJ-79, LQJ-64, LQJ-49, LQJ-25, LQJ-99, LQJ-47, LQJ-36, LQJ-61.
V	01	LQJ- 77
VI	07	LQJ-65, LQJ-83, LQJ-97, LQJ-48, LQJ-85, LQJ-93, LQJ-94, LQJ-90
VII	01	LQJ-56

Table 6: Mean intra (bold) and inter cluster (D^2 Values) distance values

Cluster	I	II	III	IV	V	VI	VII
I	464.21	998.29	701.86	1218.08	1456.25	797.78	1791.7
II		547.69	2045.21	1568.49	789.6	1707.9	1017.93
III			0	1050.48	2321.09	945.33	2537.22
IV				653.33	1251.32	2068.07	1049.74
V					0	2217.17	304.13
VI						823.93	2915.52
VII							0

Table 7: Cluster means for various traits in different clusters of 100 loquat genotypes

Cluster	Fruit length (cm)	Fruit width (cm)	Fruit weight (g)	Seed length (mm)	Seed width (mm)	Seed weight (g)	Number of seeds/ fruit	Pulp (%)	Fruit yield kg/tree	Juice (%)	TSS (^{0}B)	Titrable acidity (%)	TSS acid ratio	Total sugar (%)	Reducing sugars (%)	Non-reducing (%)
I	3.78	3.26	19.70	19.46	15.43	3.99	2.80	56.45	35.2	69.65	10.55	1.23	8.61	8.23	5.02	3.05
II	3.77	3.29	18.06	19.9	16.88	4.01	2.85	57.89	35.42	70.25	10.84	1.26	8.67	8.44	5.44	2.85
II	3.44	2.80	17.58	16.71	12.40	4.94	3.73	55.74	31.6	72.35	10.19	1.16	8.76	8.11	4.80	3.15
IV	3.63	3.02	18.67	17.02	11.91	4.27	3.09	58.67	34.51	70.4	10.65	1.24	8.65	8.37	5.35	2.86
V	4.01	3.34	20.04	17.00	15.29	4.84	3.33	58.79	32.93	73.52	10.78	1.57	6.88	8.74	5.71	2.87
VI	3.96	3.21	19.73	18.87	16.04	4.43	3.45	56.39	35.33	67.98	10.58	1.22	8.73	8.35	4.90	3.28
VII	3.35	2.88	15.90	16.41	13.33	4.86	3.00	55.86	34.59	64.02	11.40	1.50	7.61	8.66	5.81	2.70

Table 8: Percent contribution of individual traits towards total divergence in loquat Genotypes

Source	Contribution (%)
Fruit length (cm)	0.67
Fruit width (cm)	34.3
Fruit weight (g)	3.64
Seed length (mm)	8.16
Seed width (mm)	1.92
Number of seeds per fruit	0.16
Pulp (%)	0.02
Fruit yield kg/tree	42.77
Juice (%)	2.32
Total soluble solids (^{O}Brix)	0.63
Titratable acidity (%)	0.81
Total sugars (%)	4.61

Conclusion

It can be concluded from the present investigation that the fruit weight showed positive phenotypic and genotypic correlation with fruit yield, seed length, juice percent and pulp percent. Five major components were detected using principle component analysis exhibiting 74.88%of total variance. On the basis of cluster analysis all the genotypes were divided into seven clusters having 304.13 to 2915.52 inter-cluster distance and 462.21 to 823.93 intra-cluster distance.

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