

Original Research Article

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Study on Diversity of Pummelo (*Citrus grandis* Osbeck.) based on Core Quantitative Characters in West Bengal

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ABSTRACT

The study on diversity of pummelo (*Citrus grandis* Osbeck) was undertaken to assess the variability of collected genotypes from fourteen district of West Bengal in the year of 2016-17. One hundred twenty four genotypes were selected based on assessment of traits provided by the farmers (fruit bearing frequency, maturity, fruit yield) as well as in-situ observation of trees and fruit's characters with an objective for selecting genotypes from divergent clusters and utilizing them in a hybridization programme is likely to produce desirable segregates in subsequent generations that may lead to desirable improvement in pummelo for quality traits. The analytical works were conducted in the laboratory of Fruits Science of Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia, West Bengal. The data obtained were analyzed by different method like- Hierarchical cluster analysis, descriptive analysis, Principal Component Analysis and Biplot. The genotypes were grouped based on ten core quantitative characters of fruits into fifty six clusters. It is observed that all the clusters were distant each other and among them cluster 49 was the largest one consisting of 55 pummelo genotypes followed by cluster 43 and cluster 52 with three genotypes. The co-efficient of variation was high (>20) for five measured or quantitative characters like fruit weight, fruit rind thickness, seed weight, acidity, and ascorbic acid. Principal component analysis of ten core quantitative characters of pummelo showed four components with cumulative variance of 69.357 per cent. Highly loaded characters (>0.5), obtained from PCA for quantitative variables in the first two components, were fruit weight, fruit diameter, fruit length, rind thickness, seed number and seed weight. So, considering all the characters it may be concluded that NPC2, NDC5, NPC12, HWC3, NPC11, PRC4, HGC1, NDC4, NPC1, BKC12, NPC10, HWC5, PMC1, CBC8, BKC8, BWC7, NPC12, PRC7 etc. can be utilized in genotype selection or crop improvement programme.

Keywords

Pummelo,
Genotypes,
Quantitative
characters,
Variability, TSS

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Introduction

Pummelo (*Citrus grandis* Osbeck), a tropical fruit plant species, major monoembryonic species of citrus, originated from South East Asia and it is also called as shaddock (Uzun and Yesiloglu, 2012). Pummelo is easily grown in inferior, marginal and backyard orchard. It is considered as an excellent tree for waste land development in arid and semi-arid region. Pummelo fruit is a fat, sodium and cholesterol free. This makes pummelo a very good source for dieters. It is a good source of vitamin C and calories. Besides its use as a table fruit, the fruit and other parts of pummelo plant can also be exploited for different purposes. Its therapeutic and nutritive values along with its taste and flavour have placed it in the regular dietary list of the people living in advanced countries (Mukhopadhyay, 2004).

In spite of tremendous potentiality for commercial exploitation, pummelo plants are yet to be given due importance in India. An urgent need for pummelo conservation is necessary as there is a tendency of declining varietal diversity due to loss of natural habitat. Therefore, the problem of decreasing variability in pummelo needs a particular attention in preventing further loss of plant species that has not been fully uncovered (Wen *et al.*, 2010). No standard variety of pummelo is found in India except Nagpur Chakotra (Rajput and Haribabu, 2004). However, the diverse eco-geographical distribution in India and the occurrence of spontaneous mutation and natural hybridization have given rise to a wide range of variability in citrus. In West Bengal, diverse populations of pummelo also exist in the different agro-ecological zones with a lot of variations in plant and fruit characters. There is direct need for conservation of crop. Variation and selection are the two fundamental aspects of any plant improvement

programme. Characterization of citrus genetic resources was first attempted by Bonavia (1890), who described the citrus germplasm available in India. In India many good quality pummelo are available in home gardens and descriptive orchards. Characterization of pummelo using morphological traits will help in selecting genetically potential genotypes for their cultivation, marketing and their use in plant breeding programmes. Few attempts on genetic diversity of pummelo have been done earlier (Chomchalow *et al.*, 1987; Phan *et al.*, 2002; Liu *et al.*, 2006 a). Very few works have been done in India including West Bengal (Murthy *et al.*, 1989; Maiti *et al.*, 2001). Thus, considering the above facts it has been decided to undertake this research programme entitled “Study on diversity of pummelo (*Citrus grandis* Osbeck.) based on core quantitative characters in West Bengal”.

Materials and Methods

The study of pummelo diversity was conducted at fourteen districts of West Bengal during 2016-17. The different pummelo districts in which survey was conducted for identification of superior genotypes were North 24 Parganas (NPC), Nadia (NDC), Burdwan (BWC), Purulia (PRC), Hooghly (HGC), Bankura (BKC), South 24 Parganas (SPC), Birbhum (BBC), Howrah (HWC), Murshidabad (MDC), Malda (MLC), Paschim Medinipur (PMC), Uttar Dinajpur (UDC) and Cooch behar (CBC). The diversity was observed mostly in home gardens. The analytical works were conducted in the laboratory of Fruits Science of Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia, West Bengal. To know the pummelo diversity available in the different districts, primary information was collected from the Sub divisional and District Horticulture Office, Horticulture Research and Development Farm and Krishi Vigyan Kendra. Accordingly different areas were

surveyed and first hand information was collected from farmers to identify their preferred phenotypes. Individual plant was selected based on assessment of traits provided by the farmers (fruit bearing frequency, maturity, fruit yield) as well as in-situ observation of trees (general health) and fruits (fruit shape, fruit size, peel thickness, pulp colour etc.). One hundred twenty four genotypes were selected covering fourteen districts for studying diversified characters of pummelo. All the plants were more or less uniform age and vigour.

The pummelo collections were named on the basis of above said code used for different districts. Ten core quantitative fruit characters (Fruit weight, Fruit diameter, Fruit length, Rind thickness, Rind thickness, Segment number, Seed weight, Acidity, TSS and Ascorbic acid) from 'citrus descriptor' (IPGRI, 1991) were considered for characterization of these pummelo germplasm. Three fully mature, healthy and disease free fruits from each replication were collected randomly from different direction for recording different observations. The physical and chemical characters of fruits were recorded after thorough washing with tap water to remove adhering impurities. Fruit and seed weight was measured by using electronic (digital) balance whereas fruit rind thickness was measured by slide calliper.

Total soluble solids content of fruits was determined with the help of a hand refractometer. Acidity and ascorbic acid content of fruit were estimated by following the standard methods (AOAC, 1984). Descriptive statistics were used to describe the basic features of the data in a study for quantitative characters. The data obtained were analysed statistically by Hierarchical cluster analysis following single linkage (nearest neighbourhood) method (Gronau and Moran, 2007). The data obtained

were further analysed by the method of Principal Component Analysis and Biplot (Metsalu and Vilo, 2015).

Results and Discussion

The results of descriptive analysis presented in table 1, clearly revealed a wide range of variability in nine quantitative or measured fruit characters among different pummelo collections.

The co-efficient of variation was high (>20) for five measured or quantitative characters like fruit weight, fruit rind thickness, seed weight, acidity, and ascorbic acid. Again, among nine characters, the co-efficient of variation was higher in seed characters like seed weight (64.0), acidity (66.84) and Ascorbic acid (45.47). Higher co-efficient of variation revealed higher variability which indicated that superior clones can be identified from the existing variation. Singh *et al.*, (2015b) observed much less co-efficient of variation (3.455-17.032) among pummelo clones with higher in peel thickness and 100 seed weight.

Hierarchical cluster analysis following single linkage divided 124 pummelo collections into 56 clusters with allowed distance 2.015 considering ten core quantitative characters. Results (Table 2 and Fig. 1) showed that all the clusters were distant each other and cluster 49 was the largest one consisting of 55 pummelo genotypes followed by cluster 43 and cluster 52 with three genotypes.

On the other hand, cluster 21, cluster 28, cluster 29, cluster 50, cluster 51, cluster 53, cluster 54, cluster 55 and cluster 56 consisted of 2 pummelo genotypes in each and remaining clusters comprised of single member or genotype. Liu *et al.*, (2006 b) obtained 6 groups by UPGMA analysis using 33 pummelo cultivars and 29 core characteristics.

Table.1 Variability study of different quantitative characters of pummel

Characters	Minimum	Maximum	Mean	Std. Deviation	CV (%)
Fruit weight (g)	462.50	1906.60	923.28	301.09	32.61
Fruit diameter (cm)	8.03	18.23	13.39	2.00	14.96
Fruit length (cm)	9.90	21.30	13.86	2.39	17.25
Rind thickness (cm)	0.67	3.83	1.69	0.62	36.96
Segment number	10.30	18.60	14.51	1.70	11.72
Seed weight (g)	0.00	0.68	0.25	0.16	64.00
Acidity (%)	0.32	1.63	0.98	0.66	66.84
TSS (^o brix)	6.00	11.20	8.33	0.95	11.45
Ascorbic acid (mg/100 ml juice)	16.50	78.00	33.52	15.24	45.47

Table.2 Clusters of pummelo genotypes based on ten core quantitative characters using single linkage clustering methods on squared Euclidean distance matrix

Cluster number	Cluster members (Allowed distance = 2.015)
1	NDC1
2	HGC1
3	NDC4
4	NPC13
5	HWC5
6	NPC2
7	HWC1
8	BKC3
9	PRC7
10	MDC1
11	NPC10
12	NDC5
13	BKC2
14	BWC1
15	BKC8
16	NDC7
17	NDC9
18	SPC5
19	PRC4

20	SPC6
21	BKC1, BWC2
22	MLC3
23	HGC8
24	NPC4
25	NDC12
26	NPC1
27	SPC1
28	UDC2, BKC10
29	CBC8, BWC5
30	MDC4
31	BKC9
32	NPC8
33	UDC1
34	BWC13
35	HWC2
36	BKC13
37	BBC3
38	NDC2
39	BKC7
40	HWC3
41	SPC4
42	UDC4
43	BKC11, HGC4, HWC4
44	CBC1
45	PKC4
46	MDC2
47	NDC3
48	BWC6
49	PMC1, BWC8, PMC2, NPC3, BWC15, PRC5, BKC4, BWC3, NPC15, MLC4, PRC11, HGC7, PRC10, NDC8, BWC12, BKC6, PRC12, BWC10, BKC5, BWC9, NPC16, BBC4, HGC2, HGC3, CBC6, HGC5, NPC6, NDC11, CBC5, NDC9, CBC2, MLC7, MLC2, MDC3, UDC3, HWC6, PRC2, PRC1, PMC3, PRC8, PRC6, CBC10, CBC7, PRC3, NPC5, BWC11, CBC4, PMC5, BBC6, NPC14, CBC9, MLC6, SPC3, BBC5, BBC1
50	NPC12, NPC7
51	NDC10, NDC6
52	SPC2, CBC3, BBC2
53	BWC14, BWC7
54	BKC12, NPC11
55	MLC5, MLC1
56	PRC9, BWC4

Fig.1 Dendrogram (by single linkage) of different pummelo genotypes using ten quantitative characters

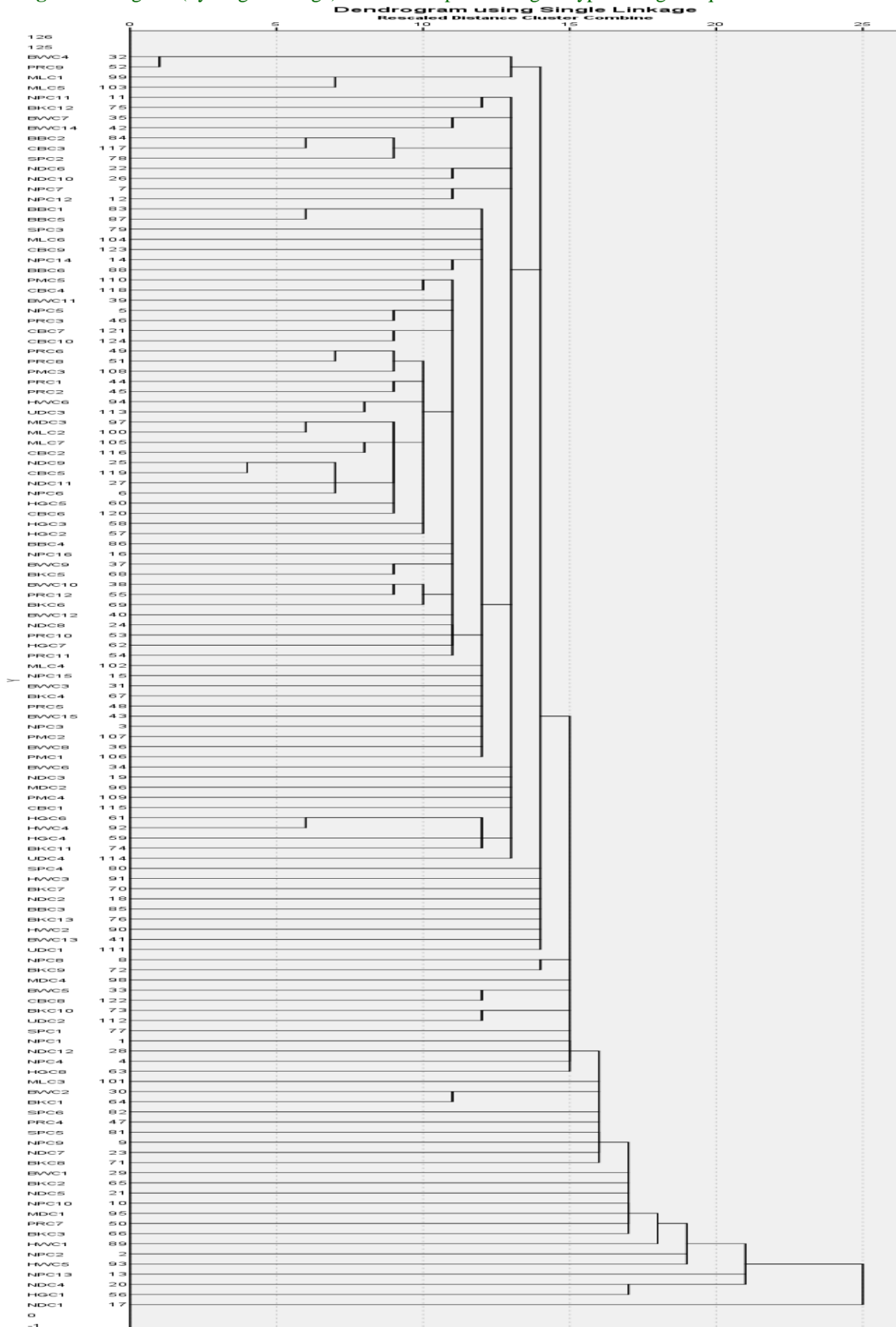


Fig.2 Loading biplot of PCA (F1 Vs F2) for quantitative characters

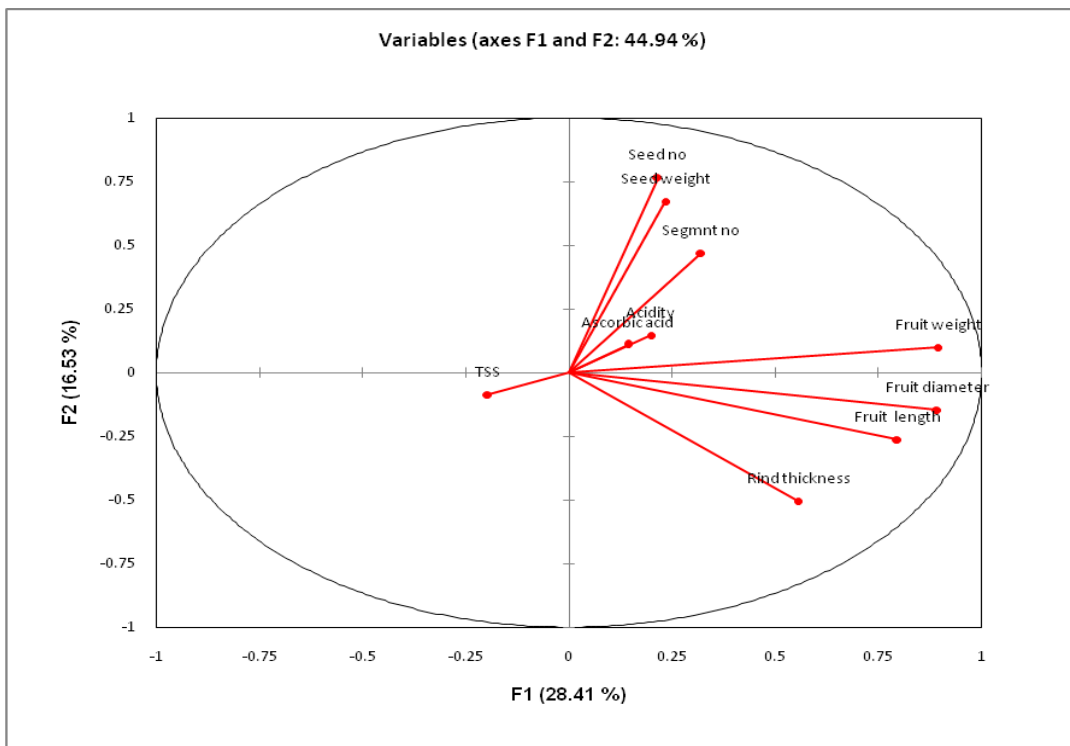
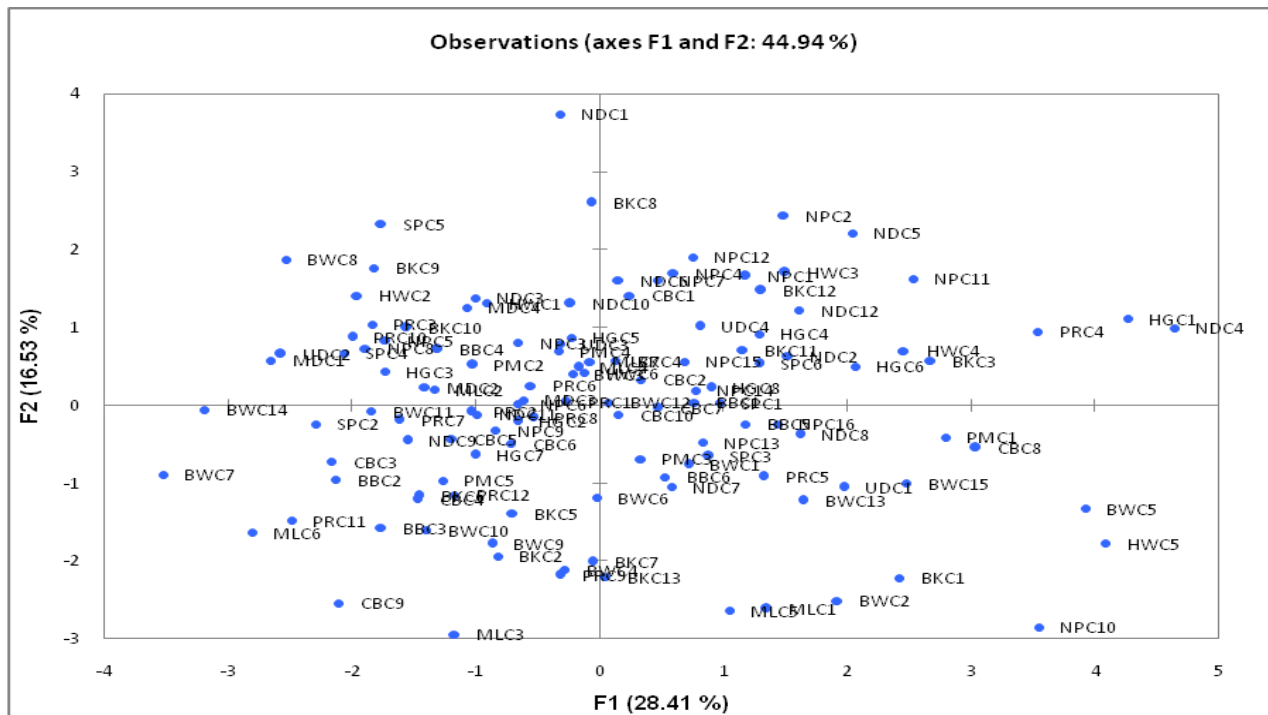


Fig.3 Scoring biplot of PCA (F1 Vs F2) for pummelo genotypes based on quantitative characters



Principal component analysis of ten core quantitative characters of pummelo resulted four components with cumulative variance of 69.357 per cent (Table 3). Components with Eigen value more than 1 were considered only. The Eigen value was high in F1 (2.841) and low in F4 (1.157). The component matrix F1 alone contributed 28.415 per cent of total variance with positive loading of fruit weight (0.894), fruit diameter (0.893), fruit length (0.796), rind thickness (0.556) and acidity (0.199) in contrast to total soluble solids (TSS) which was negatively loaded. The component F2 explained 16.53 per cent of total variance having positively loaded variables of seed number (0.776), seed weight (0.671), segment number (0.469), acidity (0.146) and ascorbic acid (0.109). The negatively loaded variables in this component were rind thickness, fruit length and fruit diameter. The component F3 explained 12.85 per cent of total variance. The highly and positively loaded characters in this component were ascorbic acid (0.734), acidity (0.480), segment number (0.303) in contrast to seed weight and TSS. Component F4 with 11.57 of total variance loaded positively with higher value of TSS (0.708) and acidity (0.614) as compared to segment number which was negatively loaded (Table 3).

Loading of ten core quantitative characters and component scores of pummelo genotypes were presented (Fig. 2 and Fig. 3) keeping X-axis as F1 (component-1) and Y-axis as F2 (component-2). The first and fourth quadrants of loading plot were distributed with six and three characters, respectively, whereas it was single character in third quadrant (Fig. 2). Similarly, one hundred and twenty four pummelo genotypes were scattered among four quadrants of scoring plot (Fig. 3).

The six characters viz. seed numbers, seed weight, segment number, acidity, ascorbic acid and fruit weight were confined in 1st quadrant of loading plot.

So, the genotypes remained in the 1st quadrant of scoring plot (NPC2, NDC5, NPC12, HWC3, NPC11, PRC4, HGC1, NDC4, NPC1, BKC12 etc.) had higher mean values for these characters.

Again 4th quadrant of loading plot was confined with three characters viz. fruit diameter, fruit length and rind thickness. Genotypes, corresponding to the 4th quadrant of scoring plot (NPC10, HWC5, BWC5, BKC1, BWC15, PMC1, CBC8, BWC2, UDC1, BWC13, MLC1, MLC5, NDC8, PRC5 etc.), were higher in fruit diameter, fruit length and rind thickness.

Likewise, genotypes present in the 3rd quadrant (MLC3, CBC9, MLC6, BWC7, BWC14, SPC2, CBC3, BBC2, PRC11, BBC3, BWC10, BWC9, BKC2 etc.) were rich in TSS content (Fig. 2 and 3). Singh *et al.*, (2015b) observed almost similar cumulative variance (68.30%) from first four principal components where acidity, fruit weight, fruit length and fruit width were the most important characters.

The diagram 'Biplot' was used to clarify the relation between genotypes and variables. Results indicated that fruit characters distributed in loading plot contributed a considerable role to the differentiation of pummelo genotypes confined into loading plot.

From the above results, it is concluded that there is a profound diversity among pummelo collections and few genotypes (HGC1, PRC4, NDC4, NDC5, NPC10, HWC5, PMC1, CBC8, BEC5, BKC8, BWC7, NPC12, PRC7 etc.) may be exploited for various attributes based on consumers acceptance as well as few may be important breeding material for development of improved varieties after further evaluation.

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