

# Studies on Genetic Variability of Pummelo (*Citrus grandis* L.) in East Siang District of Arunachal Pradesh, India

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**Abstract**—An extensive surveyed was conducted in different parts of East Siang District, Arunachal Pradesh during 2014-16 to study the available genetic variability, with the help of suitable genetic parameter in pummelo (*Citrus grandis* L.) through exploiting 40 genotypes based on their 47 important physico-chemical character. The experimental result showed that individual fruit weight ranged from 343.07 g ( $T_{33}$ ) to 2403.23 g ( $T_{36}$ ); fruit diameter 10.03 cm ( $T_{33}$ ) to 18.17 cm ( $T_{36}$ ); fruit length 11.03 cm ( $T_{33}$ ) to 21.40 cm ( $T_4$ ); juice content 109.33 ml ( $T_7$ ) to 706 ml ( $T_{20}$ ); rind thickness 1.10 cm ( $T_{40}$ ) to 3.13 cm ( $T_2$ ); seed/fruit 17.67 ( $T_{32}$ ) to 129.67 ( $T_{18}$ ); fruit yield 67.67 ( $T_{11}$ ) to 630.20 Kg/tree ( $T_{36}$ ); TSS 8.47 ( $T_8$ ) to 12.90<sup>o</sup>Brix ( $T_{27}$ ); Ascorbic acid 20.82 ( $T_{34}$ ) to 53.98 mg/ 100g ( $T_{25}$ ); acidity 0.37 % to 1.27 %; reducing sugar 1.99 % to 6.81 %; total sugars 4.60 % to 9.45 % and sugar: acid ratio from 5.96 to 20.38. The PCV and GCV were recorded highest for yield per plant (49.04 %, 49.01 %) respectively. Similarly PCV and GCV were recorded lowest in fruit segments (8.19 %). High heritability coupled with high genetic gain was observed for in yield per plant. The correlation coefficients and path coefficient among the different characters were worked out at both phenotypic and genotypic levels. Yield per plant showed significant and positive correlation with fruit weight, fruit diameter, fruit length, fruit juice content and vitamin C. The path coefficient analysis revealed that fruit juice content had maximum positive direct effect on yield per plant followed by fruit diameter, vitamin C, number of fruit segment and acidity. The 40 genotypes were separated in 7 major cluster groups.

## 1. INTRODUCTION

Pummelo (*Citrus grandis* L.) belong to the family Rutaceae. It is one of the most distinctive and easily recognized species of the genus *Citrus*. The word pummelo is derived from *Pomum melo*, the melon-apple (Hume, 1937). It is believed to have originated in south-east Asia (Verdi, 1988) probably Thailand and Malaysia from there it spread to China, India and Persia.

The pummelo tree may be 16 to 50 ft (5-15 m) tall, with a somewhat crooked trunk (10-30 cm) thick, technically leaves are (5-20 cm) long, (2-12 cm) wide, leathery, dull-green, glossy above, dull and minutely hairy beneath; the petiole broadly winged to occasionally wingless. The flowers are fragrant, borne singly or in clusters of 2 to 10 in the leaf axils; 4 to 5 petals, yellowish-white in bundles of 4 to 5 and anthers are orange in colour. The fruit shape ranges from nearly round to oblate or pear-shaped; (10-30 cm) wide; the peel, clinging or more or less easily removed, greenish yellow or pale-yellow, minutely hairy, dotted with tiny green glands, (1.25-2 cm) thick, the albedo soft; pulp pink or white; is divided into 11 to 18 segments, very juicy to fairly dry; the flavour varies from mildly sweet and bland to sub-acid or rather acid, sometimes with a faint touch of bitterness. Pummelo is a cross-pollinated crop and therefore they have numerous seeds. Like other citrus fruits, the pummelo usually ripen in winter.

In contrast to most citrus, pummelo is one of the major mono-embryonic species and cross pollinated, thus it is a true zygotic seedling that exhibits great genetic diversity that manifests in the variability of quantitative and qualitative attributes due to natural hybridization, which is considered pre-requisite for any crop improvement programme.

Therefore, the aim of present study was to determine the components of variability, character associated and path analysis for yield and yield contributing traits in pummelo.

## 2. MATERIALS AND METHODS

The present study was conducted during 2014 to 2016 on 40 selected genotypes (Table 1) collected from different location of East Siang district, Arunachal Pradesh. The site is situated in between N 27°56.629' - N 28°10.402' latitude and E 095°07.233' - E 095°26.520' longitudes with an altitude of 132-393 meter above the mean sea level. The prevailing climatic condition of East

Siang district is sub-tropical humid and maximum rainfall occurs between June and September. Pre-monsoon rain starts from the month of May and post-monsoon rain prevails up to October.

**Table 1: Source of Collection, Location and Elevation of 40 Genotypes**

Treatment	Source of collection	Latitude (N)	Longitude (E)	Elevation (m)
T <sub>1</sub>	Boying	N 28°03.251`	E 095°17.249`	317
T <sub>2</sub>	Boying	N 28°03.261`	E 095°17.243`	318
T <sub>3</sub>	Oyan	N 27°52.619`	E 095°18.847`	132
T <sub>4</sub>	Oyan	N 27°52.581`	E 095°18.981`	132
T <sub>5</sub>	Oyan	N 27°52.665`	E 095°18.888`	132
T <sub>6</sub>	Roing	N 28°03.662`	E 095°16.673`	365
T <sub>7</sub>	Roing	N 28°03.702`	E 095°16.631`	370
T <sub>8</sub>	Roing	N 28°03.712`	E 095°16.633`	369
T <sub>9</sub>	Roing	N 28°03.704`	E 095°16.638`	368
T <sub>10</sub>	Tigra	N 28°03.948`	E 095°17.085`	337
T <sub>11</sub>	Tigra	N 28°03.952`	E 095°17.136`	332
T <sub>12</sub>	Tigra	N 28°03.952`	E 095°17.139`	332
T <sub>13</sub>	Rasam	N 28°03.850`	E 095°16.975`	345
T <sub>14</sub>	5-mile	N 28°00.603`	E 095°19.770`	151
T <sub>15</sub>	5-mile	N 28°00.610`	E 095°19.765`	151
T <sub>16</sub>	Takilalung	N 28°01.387`	E 095°15.744`	296
T <sub>17</sub>	Takilalung	N 28°01.258`	E 095°15.716`	283
T <sub>18</sub>	Takilalung	N 28°01.238`	E 095°15.859`	270
T <sub>19</sub>	Takilalung	N 28°01.276`	E 095°15.919`	269
T <sub>20</sub>	Napit	N 28°02.317`	E 095°18.365`	212
T <sub>21</sub>	Napit	N 28°02.317`	E 095°18.326`	215
T <sub>22</sub>	Sipi	N 28°04.115`	E 095°18.143`	250
T <sub>23</sub>	Sipi	N 28°04.121`	E 095°18.135`	250
T <sub>24</sub>	Mebo	N 28°10.174`	E 095°24.843`	393
T <sub>25</sub>	Mebo	N 28°10.399`	E 095°24.355`	377
T <sub>26</sub>	Mebo	N 28°10.373`	E 095°24.266`	371
T <sub>27</sub>	Mebo	N 28°10.402`	E 095°24.280`	375
T <sub>28</sub>	Motum	N 28°04.823`	E 095°26.371`	173
T <sub>29</sub>	Motum	N 28°04.979`	E 095°26.520`	176
T <sub>30</sub>	Sibo	N 28°03.650`	E 095°17.177`	310
T <sub>31</sub>	Sibo	N 28°03.643`	E 095°17.175`	326
T <sub>32</sub>	Sibut	N 28°00.757`	E 095°14.607`	276
T <sub>33</sub>	Sibut	N 28°00.473`	E 095°14.930`	220
T <sub>34</sub>	Sibut	N 28°00.804`	E 095°14.580`	285
T <sub>35</sub>	Sibut	N 28°00.808`	E 095°14.584`	285
T <sub>36</sub>	Ledum	N 27°56.629`	E 095°08.956`	317
T <sub>37</sub>	Ledum	N 27°56.473`	E 095°07.739`	323
T <sub>38</sub>	Ledum	N 27°56.556`	E 095°07.686`	334
T <sub>39</sub>	Ledum	N 27°56.455`	E 095°07.238`	340
T <sub>40</sub>	Ledum	N 27°56.254`	E 095°07.233`	340

The primary selection criterion was based on fruits and yield attributes of the genotypes. Individual genotypes were marked in the field. The data were recorded at the time of fruit maturity during October-December of the each year, *i.e.*, 2014, 2015 & 2016 and data was pooled for analysis. Three fruits from each genotype were randomly collected and observations on Fruit weight (g), Fruit diameter (cm), Fruit length (cm), Fruit rind thickness (cm), Number of segments per fruit, diameter of fruit axis (cm), Juice content (ml), Fruit yield per tree (kg), average number of seeds per fruit, Average weight of 10 seeds (g), Total soluble solids (<sup>0</sup>Brix), Titratable acidity % (AOAC, 1985), Reducing sugar % (Somogyi, 1952), Non reducing sugar %, Total sugar % (Hodge and Hofreiter, 1962), Ascorbic acid (mg/100g) (Jagota and Dani, 1982).

The genotypic and phenotypic coefficients of variation were calculated (Burton and De Vane, 1953). Heritability and genetic advance were calculated as suggested by Allard (1960) and genetic gain was estimated using the method suggested by Johanson

*et al.* (1955). Genotypic and phenotypic correlations were calculated as per the procedures given by Al-Jibouri *et al.* (1958). The direct and indirect paths were obtained according to the method of given by Dewey and Lu (1959).

**Table 2: Analysis of Variance for Physical characters of 40 Genotypes**

Characters	Sources of variations		
	Mean of square		
	Replication	Treatment	Error
	Degree of freedom		
	2	39	78
Fruit Weight (g)	618.012	483151.542 **	483151.542
Fruit Diameter (cm)	0.129	8.568 **	0.215
Fruit Length (cm)	1.458	14.156 **	1.108
No. of Segments/ Fruit	0.025	5.887 **	1.222
Fruit Juice (ml)	14.400	73174.345 **	117.289
Fruit Rind Thickness (cm)	0.006	0.464 **	0.019
Fruit Axis (cm)	0.001	0.639 **	0.016
Seeds/ Fruit	0.108	2766.409 **	7.843
Average Weight of 10 Seeds (g)	0.010	1.327 **	0.015
Yield (Kg/ tree)	36.719	70086.164 **	32.114
TSS (°Brix)	0.207	2.823 **	0.225
Vitamin C (mg/100 g)	11.997	195.046 **	4.984
Acidity (%)	0.002	0.101 **	0.001
Reducing Sugar (%)	0.013	4.048 **	0.026
Non-reducing Sugar (%)	0.057	1.469 **	0.034
Total Sugars (%)	0.032	0.032 **	0.080

\*, \*\* Significant at 5% and 1% respectively.

### 3. RESULTS AND DISCUSSION

The present investigations were carried out on 40 diverse genotypes of pummelo after surveying 1500 trees to study their mean performance, genetic variability, correlation, path and genetic divergence for different morphological and quality traits of fruit. The extent of variation recorded for different traits are discussed in the light of available literature.

### 4. VARIABILITY IN PHYSICO-CHEMICAL CHARACTERS

#### Variability in physical characters

The fruit weight varied significantly and ranges from 343.07 g in T<sub>33</sub> to 2403.23 g in T<sub>36</sub> with the mean value of 1332.04 g. The variation was more or less similar as studied by Mitra *et al.* (2011) and Rahman *et al.* (2003) While highest fruit weight (2515 g).

In respect of fruit diameter, significant variations were seen among the fruit of different genotypes. The observed values ranged from 10.03 cm in T<sub>33</sub> to 18.17 cm in T<sub>36</sub>. Fruit diameter observed by Rahman *et al.* (2003) ranged from 9.54 cm to 18.94, which is in agreement with the present investigation. The fruit length varied from 11.03 cm in T<sub>33</sub> to 21.40 cm in T<sub>4</sub> and the average fruit length was 16.07 cm. In contrast Hazarika *et al.* (2013) obtained more narrow range of fruit length (7.52-13.75 cm).

As regard to the fruit juice content, it varied from 706 ml to 109.33 ml with the mean value of 348.60 ml. But Bharali and Saikia (2004) found highest volume of juice (208.50 ml).

Among the studied genotypes the fruit rind thickness of T<sub>40</sub> was found to be thinnest (1.10 cm) while T<sub>2</sub> showed thickest rind (3.13 cm) and most of the genotypes, it was less than 2 cm with an average fruit rind thickness was 1.77 cm. So, fruit rind of most genotypes are lesser than the cultivar 'Chandler' (Chen and Wu, 1994) grown in china. In addition Shen *et al.* (1999) found cultivar shatianyou 2 has the thinnest rind thickness (1.14 cm), which is in agreement with the present work.

The number of segments per fruit varied from 12.67 to 18. This finding is in conformity with the finding of Webber and Batchelor (1948).

The number of seeds per fruit significantly differed among the genotypes and ranged from 17.67 in T<sub>32</sub> to 129.67 in T<sub>18</sub> and there was no seedless fruit under the studied genotypes. In this regard, Roy *et al.* (2014) also found 50-164 numbers of seed per fruit. Fruit yield per plant of different pummelo genotypes ranged from 67.67 Kg/tree in T<sub>11</sub> to 630.20 Kg/tree in T<sub>36</sub> with the average yield of 311.82 Kg/tree. This is in conformity with the studies of Samarasinghe (2005) and Mitra *et al.* (2011).

### Variability in chemical characters of fruit

Total soluble solids (TSS) of different genotypes varied from 8.47 °Brix in T<sub>8</sub> to 12.90 °Brix in T<sub>27</sub>. The results are in consonance with the results obtained by Suthanukool *et al.* (2008) and Mitra *et al.* (2011).

Different selected genotypes showed significant variation for ascorbic acid content and varied from 20.82 mg/ 100g in T<sub>34</sub> to 53.98 mg/ 100g in T<sub>25</sub>, with the mean value of 35.75 mg/ 100g. The variation in ascorbic acid of fruit is more or less similar to the earlier findings (Hazarika *et al.*, 2013 and Roy *et al.*, 2014).

In titratable acidity the minimum acidity was recorded in T<sub>11</sub> (0.37 %) whereas maximum titratable acidity was observed in T<sub>30</sub> (1.27 %). In this regard, Mitra *et al.* (2011) finding is in agreement with present studied.

The observed values on reducing sugar content of fruit vary significantly among genotypes. T<sub>1</sub> was recorded highest (6.81 %) where as lowest was recorded in T<sub>7</sub> (1.99 %). While non reducing sugar varied from 1.35 % in T<sub>16</sub> to 4.34 % in T<sub>13</sub>. The similar finding was observed by Hazarika *et al.* (2013). The observed data on total sugar content of fruit revealed significantly variation among genotypes and varied from 4.60 % in T<sub>32</sub> to 9.45 % in T<sub>1</sub>. Similar result was reported by Mitra *et al.* (2011) and Roy *et al.* (2014).

The sugar/acid ratio was found highest in genotype T<sub>18</sub> (20.38 %) and lowest in T<sub>29</sub> (5.96 %). The result was consonance with the finding of Bharali and Saikia (2004) and Hazarika *et al.* (2013)

### Coefficients of variation Physical characters

Amongst the physical characters, the PCV were recorded high in fruit yield (49.04 %), fruit weight (30.36 %) and seed/fruit (38.54 %); moderate for rind thickness (23.13 %) (Table 3). Whereas, GCV were recorded high for the trait fruit yield (49.01 %), fruit weight (30.01 %) and seed/fruit (38.38 %); moderate in rind thickness (21.80 %) The present investigation is in agreement with the findings of Roy *et al.* (2014).

**Table 3: Variability in Physico-chemical characters of selected 40 Genotypes**

Sl no.	Characters	General Mean	Range	Variance			ECV (%)	PCV (%)	GCV (%)
				Environmental	Phenotypic	Genotypic			
1	Fruit Weight (g)	1332.04	343.07 - 2403.23	3746.50	163548.19	159801.69	4.60	30.36	30.01
2	Fruit Diameter (cm)	14.97	10.03 -18.17	0.21	3.00	2.78	3.10	11.57	11.15
3	Fruit Length (cm)	16.07	11.03 - 21.40	1.11	5.46	4.35	6.55	14.53	12.97
4	No. of Segments/ Fruit	15.22	12.67 - 18.00	1.22	2.78	1.56	7.26	10.94	8.19
5	Fruit Juice (ml)	348.60	109.33 - 706.00	117.29	24469.64	24352.35	3.11	44.87	44.77
6	Fruit Rind Thickness (cm)	1.77	1.10 - 3.13	0.02	0.17	0.15	7.71	23.13	21.80
7	Fruit Axis (cm)	1.72	0.40 - 2.83	0.02	0.22	0.21	7.37	27.46	26.45
8	Seeds/ Fruit	79.02	17.67 - 129.67	7.84	927.37	919.52	3.54	38.54	38.38
9	Average Weight of 10 Seed, (g)	4.25	3.00 - 5.57	0.02	0.45	0.44	2.90	15.81	15.54
10	Yield (Kg/tree)	311.82	67.67 - 630.20	32.11	23383.46	23351.35	1.82	49.04	49.01
11	TSS (°Brix)	10.20	8.47 - 12.90	0.23	1.09	0.87	4.65	10.24	9.12
12	Vitamin C (mg/100 g)	35.75	20.82 - 53.98	4.98	68.34	63.35	6.25	23.12	22.26
13	Acidity (%)	0.62	0.37 - 1.27	0.00	0.03	0.03	5.20	29.96	29.50
14	Reducing Sugar (%)	4.43	1.99 - 6.81	0.03	1.37	1.34	3.63	26.40	26.15
15	Non-reducing Sugar (%)	2.91	1.35 - 4.34	0.03	0.51	0.48	6.37	24.58	23.74
16	Total Sugars (%)	7.34	4.60 - 9.45	0.08	1.23	1.15	3.86	15.10	14.59

### Fruit quality characters

Quality characters like vitamin C and acidity showed moderate values for PCV and GCV, whereas only TSS and total sugar showed low value of PCV and GCV (Table 3). The PCV and GCV for fruit quality characters were recorded highest in acidity 29.96 % and 29.50 % respectively. TSS showed lowest both in GCV (9.12 %) and PCV (10.24 %). The present observation is in conformity the work of Roy *et al.* (2014) who observed moderate PCV and GCV for vitamin C and acidity; and low PCV and GCV for TSS and total sugar which is in agreement with the present investigation.

### Heritability, genetic advance and genetic gain

The genotypic coefficient of variation does not offer full scope to estimate the variations that are heritable and therefore, estimation of heritability becomes necessary. Burton and De Vane (1953) had suggested that genetic coefficient of variation along with heritability estimates would give a reliable indication of expected amount of improvement through selection. The most important function of heritability in the genetic study of quantitative characters is its predictive role to indicate the reliability of the phenotypic value as a guide to breeding value (Dabholkar, 1992; Falconer and Mackay, 1996). The GCV, along with heritability estimates, provides reliable estimates of the amount of GA to be expected through phenotypic selection (Burton, 1952).

High heritability more than 80 % was found in characters such as fruit yield per plant, fruit diameter, fruit juice, rind thickness, seed weight, number of seeds per fruit, acidity, total sugar, ascorbic acid and sugar/acid ratio (Table 4). Maximum (99.9 %) heritability was observed in fruit yield. In this regard, Roy *et al.* (2014) found comparable result with high heritability (>60) in number of fruits per plant, fruit yield per plant, seed weight, number of seeds per fruit, total sugar and ascorbic acid, except in the maximum heritability (97.30) in number of fruits per plant.

**Table 4: Heritability and Genetic Gain for 16 characters of Selected Genotypes**

Sl. No.	Characters	Heritability (Broad Sense) (%)	Genetic Advance 5%	Genetic Gain (%)	Expected Mean next Generation
1	Fruit Weight (g)	97.7	814.00	61.11	2146.04
2	Fruit Diameter (cm)	92.8	3.31	22.13	18.28
3	Fruit Length (cm)	79.7	3.84	23.86	19.91
4	No. of Segments/ Fruit	56.0	1.92	12.63	17.15
5	Fruit Juice (ml)	99.5	320.70	92.00	669.30
6	Fruit Rind Thickness (cm)	88.9	0.75	42.35	2.51
7	Fruit Axis (cm)	92.8	0.90	52.48	2.63
8	Seeds/ Fruit	99.2	62.20	78.72	141.22
9	Average Weight of 10 Seeds (g)	96.6	1.34	31.47	5.59
10	Yield (Kg/tree)	99.9	314.58	100.89	626.39
11	TSS (°Brix)	79.4	1.71	16.74	11.91
12	Vitamin C (mg/100 g)	92.7	15.79	44.16	51.54
13	Acidity (%)	97.0	0.37	59.86	0.99
14	Reducing Sugars (%)	98.1	2.36	53.36	6.79
15	Non-reducing Sugar (%)	93.3	1.38	47.23	4.29
16	Total Sugar (%)	93.5	2.13	29.07	9.48

GCV associated with high heritability indicated that selection would be effective for the improvement of these characters but for a character with low heritability, selection may be comparatively difficult due to masking effect of the environment on the genotypic effects.

The values for genetic gain (as percentage of mean) ranged from 12.63 % to 100.89 %. The high (>50 %) genetic gain was observed for characters like fruit yield, fruit weight, fruit juice content, seed per fruit, average weight of 10 seed, acidity, reducing sugar and sugar/acid ratio. Consonance result was report was Roy *et al.* (2014) on pummelo, in which the genetic advance (as percentage of mean) was higher (>30) in the number of fruits per plant, fruit yield per plant and number of seeds per fruit.

### Correlation

The correlation coefficients among different characters were worked out at phenotypic and genotypic levels. In the present study, the genotypic correlation coefficients were higher in magnitude than phenotypic correlation coefficients for most of the traits, this means that there is a strong association between any two characters, but the phenotypic values are lessened by the significant interaction of environment.

The phenotypic and genotypic correlation coefficients among different characters showed that yield per plant had positive and significant association with fruit weight, fruit diameter, fruit length, fruit juice content and vitamin C (Table 5). Related results were obtained by Alam *et al.* (2016) who observed positive and significant correlations between fruit yield per plant and plant height, fruit weight, fruit diameter and number of flower bud per cluster.

**Table 5: Phenotypic Correlation Coefficient for different pairs of Physicochemical Characters**

Character	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	1.000	0.676 **	0.543 **	0.136	0.643 **	-0.023	0.190 *	0.309 **	0.190 *	-0.131	0.008	0.035	0.325 **	-0.212 *	0.454 **
2		1.000	0.649 **	0.130	0.589 **	0.225 *	0.318 **	0.278 **	0.211 *	-0.251 **	-0.003	-0.022	0.161	-0.033	0.478 **
3			1.000	-0.058	0.492 **	0.287 **	0.168	0.082	-0.001	-0.238 **	-0.007	0.009	0.031	-0.105	0.441 **
4				1.000	-0.018	0.192 *	0.005	-0.151	0.092	0.059	-0.131	-0.008	0.260 **	-0.138	-0.040
5					1.000	-0.133	-0.069	0.142	0.007	0.069	0.097	0.070	0.135	-0.093	0.645 **
6						1.000	0.153	0.162	0.133	-0.420 **	-0.171	0.001	0.066	0.131	-0.265 **
7							1.000	0.516 **	0.061	-0.178	-0.121	-0.043	0.070	0.213 *	-0.034
8								1.000	0.293 **	-0.015	-0.018	-0.128	0.098	0.176	0.149
9									1.000	-0.026	-0.118	0.191 *	0.210 *	-0.125	-0.003
10										1.000	0.432 **	0.195 *	0.314 **	-0.182 *	0.152
11											1.000	0.183 *	0.162	-0.062	0.216 *
12												1.000	0.077	-0.073	-0.068
13													1.000	-0.393 **	0.130
14														1.000	-0.278 **
15															1.000

A positive and highly significant association was expressed by fruit weight with fruit diameter, fruit length, fruit juice content, seeds per fruit, reducing sugar and fruit yield per plant. In Alam *et al.* (2016) observed that fruit weight showed significant positive correlation with fruit length and breath, which is in conformity with the present investigation.

#### Path coefficient

The path coefficient analysis data revealed that fruit juice content (1.5667) had maximum positive direct effect on yield per plant followed by, fruit diameter (1.4618), vitamin C (0.9307) and number of fruit segment (0.7044) (Table 6 & 7). In this regard Alam *et al.* (2016) observed number of flowers per cluster, fruit length, number of segment per fruit and number of seeds per fruit had positive direct effect on the fruit yield per plant.

**Table 6: Genotypic Correlation Coefficient for different pairs of Physico-chemical Characters**

Character	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	1.000	0.707 **	0.606 **	0.168 *	0.652 **	-0.029	0.199 *	0.314 **	0.200 *	-0.143	0.002	0.041	0.339 **	-0.217 *	0.460**
2		1.000	0.730 **	0.123	0.612 **	0.219 *	0.340 **	0.285 **	0.217 *	-0.282 **	-0.017	-0.025	0.165	-0.043	0.497**
3			1.000	-0.044	0.549 **	0.311 **	0.197 *	0.087	0.004	-0.325 **	-0.003	0.017	0.043	-0.098	0.494**
4				1.000	-0.030	0.238 **	-0.036	-0.194 *	0.110	0.104	-0.204 *	-0.018	0.364 **	-0.155	-0.049
5					1.000	-0.141	-0.073	0.141	0.007	0.077	0.099	0.070	0.137	-0.097	0.647**
6						1.000	0.156	0.166	0.135	-0.460 **	-0.201 *	0.012	0.066	0.157	-0.280**
7							1.000	0.534 **	0.060	-0.184 *	-0.127	-0.051	0.083	0.250 **	-0.038
8								1.000	0.301 **	-0.016	-0.017	-0.129	0.101	0.183 *	0.149

9									<b>1.000</b>	-0.023	-0.117	0.196*	0.212**	-0.132	-0.003
18										<b>1.000</b>	0.483**	0.218*	0.365**	-0.215*	0.173
19											<b>1.000</b>	0.195*	0.170	-0.069	0.225**
20												<b>1.000</b>	0.074	-0.071	-0.070
21													<b>1.000</b>	-0.417**	0.132
22														<b>1.000</b>	-0.287**
23															<b>1.000</b>

\*, \*\* Significant at 5% and 1% respectively.

**1:**Fruit Weight (g), **2:**Fruit Diameter (cm), **3:**Fruit Length (cm), **4:** No. of Segments/ Fruit, **5:**Fruit Juice (ml), **6:** Fruit Rind Thickness (cm), **7:**Fruit Axis (cm), **8:**Seeds/ Fruit, **9:**Average Weight of 10 Seeds (g), **10:** TSS ( $^{\circ}$ Brix), **11:**Vitamin C (mg/100 g), **12:**Acidity (%), **13:**Reducing Sugar (%), **14:**Non-reducing Sugar (%), **15:** Yield

**Table 7: Phenotypic Path Coefficient Analysis showing Direct and Indirect effect of physicochemical characters on Yield**

Character	1	2	3	4	5	6	7	8	9	10	11	12	13	14
<b>1</b>	<b>0.1803</b>	-0.1219	-0.0979	-0.0244	-0.1160	0.0042	-0.0342	-0.0558	-0.0343	0.0236	-0.0015	-0.0064	-0.0585	0.0382
<b>2</b>	0.2246	<b>0.3323</b>	0.2155	0.0433	0.1958	0.0749	0.1057	0.0924	0.0702	-0.0836	-0.0009	-0.0073	0.0535	-0.0111
<b>3</b>	0.0735	0.0878	<b>0.1353</b>	-0.0078	0.0666	0.0389	0.0227	0.0111	0.0000	-0.0322	-0.0010	0.0012	0.0042	-0.0142
<b>4</b>	0.0063	0.0061	-0.0027	<b>0.0465</b>	-0.0009	0.0089	0.0002	-0.0070	0.0043	0.0028	-0.0061	-0.0004	0.0121	-0.0064
<b>5</b>	0.2368	0.2169	0.1810	-0.0068	<b>0.3681</b>	-0.0490	-0.0253	0.0522	0.0025	0.0254	0.0357	0.0256	0.0498	-0.0342
<b>6</b>	0.0053	-0.0513	-0.0654	-0.0437	0.0303	<b>-0.2274</b>	-0.0349	-0.0369	-0.0303	0.0956	0.0389	-0.0002	-0.0151	-0.0299
<b>7</b>	0.0212	-0.0355	-0.0187	-0.0006	0.0077	-0.0171	<b>-0.1117</b>	-0.0576	-0.0068	0.0199	0.0135	0.0048	-0.0078	-0.0238
<b>8</b>	0.0023	0.0021	0.0006	-0.0011	0.0011	0.0012	0.0038	<b>0.0074</b>	0.0022	-0.0001	-0.0001	-0.0010	0.0007	0.0013
<b>9</b>	0.0051	0.0056	0.0000	0.0024	0.0002	0.0035	0.0016	0.0078	<b>0.0265</b>	-0.0007	-0.0031	0.0051	0.0056	-0.0033
<b>10</b>	0.0190	0.0364	0.0345	-0.0086	-0.0100	0.0609	0.0258	0.0022	0.0038	<b>-0.1449</b>	-0.0626	-0.0283	-0.0455	0.0264
<b>11</b>	0.0006	-0.0002	-0.0005	-0.0092	0.0069	-0.0121	-0.0085	-0.0012	-0.0084	0.0306	<b>0.0707</b>	0.0130	0.0115	-0.0044
<b>12</b>	0.0024	0.0015	-0.0006	0.0005	-0.0047	-0.0001	0.0029	0.0086	-0.0128	-0.0131	-0.0123	<b>-0.0671</b>	-0.0052	0.0049
<b>13</b>	0.0305	0.0151	0.0029	0.0244	0.0127	0.0062	0.0066	0.0092	0.0197	0.0294	0.0152	0.0072	<b>0.0938</b>	-0.0369
<b>14</b>	0.0454	0.0072	0.0225	0.0296	0.0199	-0.0282	-0.0457	-0.0377	0.0269	0.0391	0.0132	0.0157	0.0843	<b>-0.2144</b>
<b>Yield</b>	0.4542	0.4778	0.4407	-0.0400	0.6449	-0.2649	-0.0340	0.1489	-0.0031	0.1523	0.2163	-0.0684	0.1305	-0.2783
Partial R <sup>2</sup>	0.0819	0.1587	0.0596	-0.0019	0.2374	0.0602	0.0038	0.0011	-0.0001	-0.0221	0.0153	0.0046	0.0122	0.0597

Beside this, negative direct effect of TSS (-2.2752), fruit length (-1.4534), fruit weight (-0.8402), non-reducing sugar (-0.8218) and number of seeds per fruit (-0.7657) was observed on fruit yield per plant (Table 6 & 7). The present investigations is in agreement with the work of Ferdowsi (2013) who observed direct negative effect of fruit weight and number of the seeds per fruit on fruit per plant.

### Genetic divergence

Genetic divergence in the 40 genotypes of pummelo used in the present study was worked-out to identify the potential genotypes to be involved in the selection or for further hybridization programmed. On the basis of performance of various physico-chemical traits, 40 genotypes of pummelo were grouped into 7 clusters (Table 8) and which was very useful in selection process. In this regard, Shrestha *et al.* (2012) demonstrated the role of morphological and chemical characters in development of cluster group to distinguishing 5 landraces of *Citrus aurantifolia* and used in genotype selection for breeding programs. Susandarini *et al.* (2013) also suggested that the clustering of pummelo through morphological characters will be helpful in further analysis.

**Table 8: Genotypic Path Coefficient Analysis showing Direct and Indirect effect of physico-chemical characters on Yield**

Character	1	2	3	4	5	6	7	8	9	10	11	12	13	14
<b>1</b>	<b>0.8402</b>	-0.5937	-0.5089	-0.1409	-0.5477	0.0245	-0.1679	-0.2640	-0.1684	0.1199	-0.0013	-0.0341	-0.2846	0.1826
<b>2</b>	1.0329	<b>1.4618</b>	1.0679	0.1804	0.8948	0.3201	0.4977	0.4161	0.3176	-0.4123	-0.0243	-0.0362	0.2407	-0.0626

3	-0.8803	-1.0618	<b>-1.4534</b>	0.0646	-0.7985	-0.4528	-0.2868	-0.1259	-0.0061	0.4720	0.0036	-0.0244	-0.0619	0.1419
4	0.1181	0.0869	-0.0313	<b>0.7044</b>	-0.0211	0.1673	-0.0257	-0.1370	0.0778	0.0730	-0.1440	-0.0129	0.2565	-0.1095
5	1.0213	0.9590	0.8607	-0.0469	<b>1.5667</b>	-0.2215	-0.1149	0.2217	0.0107	0.1214	0.1554	0.1103	0.2153	-0.1524
6	0.0039	-0.0294	-0.0418	-0.0319	0.0190	<b>-0.1342</b>	-0.0209	-0.0223	-0.0181	0.0617	0.0270	-0.0014	-0.0089	-0.0210
7	0.0834	0.1421	0.0824	-0.0152	-0.0306	0.0649	<b>0.4174</b>	0.2230	0.0249	-0.0769	-0.0530	-0.0212	0.0345	0.1042
8	-0.2406	-0.2180	-0.0663	0.1489	-0.1084	-0.1275	-0.4091	<b>-0.7657</b>	-0.2303	0.0119	0.0131	0.0990	-0.0775	-0.1403
9	0.0225	0.0244	0.0005	0.0124	0.0008	0.0152	0.0067	0.0338	<b>0.1125</b>	-0.0026	-0.0132	0.0220	0.0238	-0.0148
10	0.3246	0.6418	0.7389	-0.2358	-0.1764	1.0457	0.4194	0.0355	0.0536	<b>-2.2752</b>	-1.1001	-0.4959	-0.8311	0.4892
11	0.0014	-0.0155	-0.0023	-0.1903	0.0923	-0.1870	-0.1182	-0.0159	-0.1093	0.4500	<b>0.9307</b>	0.1811	0.1582	-0.0639
12	0.0179	-0.0109	0.0074	-0.0081	0.0311	0.0047	-0.0224	-0.0571	0.0864	0.0963	0.0860	<b>0.4418</b>	0.0329	-0.0316
13	-0.0108	-0.0052	-0.0014	-0.0116	-0.0044	-0.0021	-0.0026	-0.0032	-0.0067	-0.0116	-0.0054	-0.0024	<b>-0.0318</b>	0.0132
14	0.1786	0.0352	0.0802	0.1277	0.0800	-0.1288	-0.2052	-0.1506	0.1083	0.1767	0.0564	0.0588	0.3425	<b>-0.8218</b>
<b>Yield</b>	0.4605	0.4966	0.4945	-0.0498	0.6470	-0.2801	-0.0377	0.1499	-0.0036	0.1732	0.2250	-0.0704	0.1323	-0.2868
Partial R <sup>2</sup>	-0.3870	0.7260	-0.7187	-0.0351	1.0136	0.0376	-0.0158	-0.1148	-0.0004	-0.3940	0.2094	-0.0311	-0.0042	0.2357

1:Fruit Weight (g), 2:Fruit Diameter (cm), 3:Fruit Length (cm), 4: No. of Segments/ Fruit, 5:Fruit Juice (ml), 6: Fruit Rind Thickness (cm), 7:Fruit Axis (cm), 8:Seeds/ Fruit, 9:Average Weight of 10 Seeds (g), 10:TSS (°Brix), 11:Vitamin C (mg/100 g), 12.:Acidity (%), 13:Reducing Sugar (%), 14:Non-reducing Sugar (%), with dependent variable i.e. yield

**Table 9: Clustering Patterns for 16 Characters of 40 Genotypes**

Cluster	Number of genotype	Name of genotype	Source of genotype
I	7	T <sub>1</sub>	Boying
		T <sub>2</sub>	Boying
		T <sub>6</sub>	Roing
		T <sub>16</sub>	Takilalung
		T <sub>21</sub>	Napit
		T <sub>26</sub>	Mebo
		T <sub>27</sub>	Mebo
II	2	T <sub>14</sub>	5 mile
		T <sub>31</sub>	Sibo
III	6	T <sub>3</sub>	Oyan
		T <sub>5</sub>	Oyan
		T <sub>11</sub>	Tigra
		T <sub>12</sub>	Tigra
		T <sub>13</sub>	Rasam
		T <sub>15</sub>	5 mile
IV	7	T <sub>19</sub>	Takilalung
		T <sub>28</sub>	Motum
		T <sub>29</sub>	Motum
		T <sub>30</sub>	Sibo
		T <sub>34</sub>	Sibut
		T <sub>35</sub>	Sibut
		T <sub>39</sub>	Ledum
V	6	T <sub>7</sub>	Roing
		T <sub>8</sub>	Roing
		T <sub>9</sub>	Roing
		T <sub>10</sub>	Tigra
		T <sub>32</sub>	Sibut
		T <sub>33</sub>	Sibut
VI	5	T <sub>18</sub>	Takilalung
		T <sub>20</sub>	Napit
		T <sub>36</sub>	Ledum
		T <sub>37</sub>	Ledum
		T <sub>38</sub>	Ledum
VII	7	T <sub>4</sub>	Oyan



		T <sub>17</sub>	Takilalung
		T <sub>22</sub>	Sipi
		T <sub>23</sub>	Sipi
		T <sub>24</sub>	Mebo
		T <sub>25</sub>	Mebo
		T <sub>40</sub>	Ledum

Maximum numbers of genotypes were accommodated in cluster I, IV and VII (7) whereas other genotypes were under cluster-II, cluster-III, cluster-V and cluster-VI (2, 6, 6 and 5 respectively). The average intra cluster distance was highest in cluster VI (55.30) and lowest in cluster II (21.86). Inter cluster distance was maximum (130.75) was recorded between cluster II and VI; lowest (58.10) was observed between cluster I and IV. The inter cluster distance was found higher than intra cluster distance, confirming wide genetic diversity among the genotypes of different groups than those of same cluster. Furthermore, on the basis of cluster means for various characters studied, cluster VII was found superior for fruit yield per plant, TSS and ascorbic acid. Whereas cluster VI was found superior for fruit diameter, fruit length and fruit juice content. Number of seeds per fruit was recorded maximum in cluster II and minimum in cluster V. Fruit rind thickness as found highest in cluster I and lowest in cluster VII. Cluster III showed highest total sugar. Reducing sugar was found highest in cluster I. Cluster II showed maximum non reducing sugar. Sugar/acid ratio was found highest in cluster III and lowest cluster II.

The clustering patterns of genotypes also showed that the genotypes collected from the same geographical area did not necessarily belong to the same cluster. Similar result was reported by Susandarini *et al.* (2013) on pummelo, the grouping of accessions resulted from cluster analysis which represented considerable degree of variability did not show any correlation pattern to geographical location of the genotypes. Results of this study also suggested that physico-chemical characters provided a practical approach in distinguishing genotypes within pummelo and thus applicable for common people and breeders in selecting superior genotypes.

## 5. CONCLUSION

Based on the results obtained from the present investigation, it can be concluded that, selected pummelo genotypes exhibited noticeable variation in the morphological and biochemical characteristics. The genotype T<sub>36</sub> showed maximum yield (630.20 Kg/plant); T<sub>27</sub> highest TSS (12.90 °Brix); T<sub>40</sub> thinnest rind (1.10 cm); T<sub>32</sub> lowest seed (17.67) and T<sub>25</sub> highest vitamin C (53.98 mg/ 100g). Fruit yield per plant, fruit juice content, number of seeds/fruit, sugar and acidity had high heritability along with high genetic gain and also showed strong positive and significant correlations with most of the characters. Thus, selection may be possible for these characters for improving yield. Further, divergence studies indicated that cluster VII showed superior in most of the characters, so genotypes from this cluster can be utilised directly or cross with cluster VI and cluster II for getting the superior recombinants through breeding programmes.

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