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## Genetic diversity of Mandarins from Northeast India along with three other wild species using morphological markers

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### Abstract

Mandarins are highly preferred fruit crop in India where maximum genetic diversity is seen in Northeast part of the country. The present investigation was conducted during the year 2018-21 by collecting mandarin genotypes from different parts of Northeast India (Arunachal Pradesh, Assam, Meghalaya, Manipur, Mizoram, Nagaland, Tripura and Sikkim) along with three wild species to evaluate the genetic diversity using morphological markers. On the basis of mean performance genotypes showed better results in the desirable traits chosen such as maximum fruit weight in G31, G6, G34, G23, G4, G40, G9 while minimum seeds per fruit in G16, G38, G1, G29, G38. Maximum number of genotypes were found in cluster 2 and least number of genotypes are found in cluster 5, cluster 9 and cluster 10 by cluster analysis. From the cluster mean analysis of different parameters of genotypes cluster 4 was found to be promising with maximum number of seeds, titratable acidity, shelf life but minimum of yield, number of fruits, pH, vitamin C, total sugar, fruit length and fruit weight while cluster 10 provides maximum yield number of fruits, vitamin C, total sugar, TSS and minimum seed weight and titratable acidity. The highest (2766.74) inter-cluster distance was recorded between cluster 4 and cluster 10 and least (24.48) inter-cluster distance was recorded between cluster 8 and cluster 5. Genetic diversity revealed that characters like number of fruits and vitamin C (mg/100g) imparted maximum percent with respect to genetic divergence (11%). From these results obtained it can be concluded that mandarin found in North East India are morphologically diverse and could be utilized for future crop improvement.

**Keywords:** Diversity, genotypes, mandarin and morphological

### Introduction

*Citrus* is the most important fruit crops of the family Rutaceae grown commercially throughout the country and known to world over for their characteristics flavour, attractive evergreen foliage and flowers as well as the extraordinary fragrance which added aesthetic value of *Citrus* trees (Swingle and Reece, 1967) [28]. The *Citrus* genus belongs to the subfamily *Aurantioideae* of the family Rutaceae. It is considered as third most important fruit crops after mango and banana in India which belongs to the subtribe *Citrinae* under tribe *Citreaea*. Among the entire *Citrus* genus, Mandarins are phenotypically heterogeneous group, consisting of several species together with various interspecific and intergeneric hybrids and mutants. It is fully fledged throughout the tropical and subtropical regions of the world. However, the finest fruit quality is observed under subtropical conditions. Among the different *Citrus* fruits in India, mandarin is placed at first position with respect to area and production followed by sweet oranges and limes. North-Eastern Region of India is a treasure house of *Citrus* germplasms because of the existence of 23 species, 1 subspecies and 68 varieties (Sharma *et al.*, 2004) [23].

Khasi mandarin is the most popular and widely cultivated variety of North Eastern States. After satisfactory performance for few years mandarin orchards start to decline in production. This decline of productivity is caused by various factors like plantation on unsuitable land, lack of irrigation, lack of quality planting materials, improper nutrition and incidence of insect-pest and diseases. *Citrus* decline results in loss of vigour and general health and decreased fruit production by showing symptoms like defoliation of young shoots and dying back of twigs from the tip. This in due course leads to decline of productivity to a greater extent (Yadav *et al.*, 2003) [30]. Khasi Mandarins are grown in all the states of North East India. Maximum area of mandarin cultivation is from Arunachal Pradesh (32.73 thousand hectare) with a production and productivity as 69.74 thousand metric tons and 2.13 MT/ha respectively. Following this Mizoram (16.37 thousand hectare) bags second in area and 44.02 thousand metric tons and

2.69 MT/ha production and productivity respectively. Other states include Assam (14.69 thousand hectare area, 203.72 thousand metric tons production, 13.63 MT/ha productivity); Sikkim (13.08 thousand hectare area, 18.99 thousand metric tons production, 1.45 MT/ha productivity); Meghalaya (9.28 thousand hectare area, 45.24 thousand metric tons production, 4.88 MT/ha productivity); Nagaland (6.52 thousand hectare area, 47.33 thousand metric tons production, 7.26 MT/ha productivity); Tripura (5.62 thousand hectare area, 25.33 thousand metric tons production, 4.51 MT/ha productivity) and Manipur (4.46 thousand hectare area, 39.89 thousand metric tons production, 8.94 MT/ha productivity). However maximum productivity of Mandarin cultivation in North East is seen at Assam (13.63 MT/Ha) followed by Manipur (8.94 MT/Ha) (Anon., 2018) [3]. Considering the importance of Mandarins in this area and their close knit with the wild species the following investigation was carried out in the year 2018-2021 to evaluate 42 genotypes including 39 mandarins and 3 wild species using morphological markers.

### Materials and Method

The experimental material for the present study comprised of selected mandarin genotypes in which collection and survey was achieved from all the North-East states of Arunachal Pradesh, Meghalaya, Manipur, Mizoram, Tripura, Sikkim and Assam as wide variability specifically exists all through these particular locations. Kinnow mandarin, *Citrus indica*, Hill mandarin and cleopatra mandarin were also added in the genotypes for comparison with the mandarins (Table 1). The morphological characters will be studied by following IPGRI citrus descriptor (Anon, 1999) [4]. The sampling of fruit, leaves and seed were done in the month of December to February for two consecutive bearing years. The plant samples from each genotypes included tree leaves, fruit and seeds along with the plant characteristics recording with the passport data of the location. The samples collected were further evaluated from the Department of fruit science of College of Horticulture and Forestry, Central Agricultural University, Pasighat. The data evaluated were statistically analysed with SPSS software.

**Table 1:** Selected genotypes and wild species

Genotypes	Place	State
G1	<i>Citrus indica</i> , Sibut (Pagla Nadi)	Arunachal Pradesh
G2	Adi Pasi	Arunachal Pradesh
G3	Wokha, Nagaland	Nagaland
G4	Doribokre, Nokrek, West Garo Hills	Meghalaya
G5	Mandel Noket, Nokrek, West Garo hills	Meghalaya
G6	Jampui Hills	Tripura
G7	Duragre, West Garo hills	Meghalaya
G8	Along	Arunachal Pradesh
G9	Geyzing, West Sikkim	Sikkim
G10	Jengging	Arunachal Pradesh
G11	Mardoloi, Near Nongpoh, Near East Khasi Hills	Meghalaya
G12	Mokokchung	Nagaland
G13	Darechikgre, West Garo hills, Nokrek	Meghalaya
G14	Rengging	Arunachal Pradesh
G15	Ukhrul, Kamjong region	Manipur
G16	Moreh Komla, Chandel District	Manipur
G17	Serchhip	Mizoram
G18	Singtam, East Sikkim	Sikkim
G19	Lhathao, Junapathar, Namsai	Arunachal Pradesh
G20	Jeru village, Upper Siang	Arunachal Pradesh
G21	Nagpur mandarin, Basar	Arunachal Pradesh
G22	Zero point, Near Dambuk	Arunachal Pradesh
G23	Sonapur	Assam
G24	Chani Village, Yazali	Arunachal Pradesh
G25	Miglung, Pasighat	Arunachal Pradesh
G26	Mebo	Arunachal Pradesh
G27	Roing	Arunachal Pradesh
G28	Tamenglong	Manipur
G29	Sikkim Mandarin, Basar	Arunachal Pradesh
G30	Yagrunge Village	Arunachal Pradesh
G31	Kinnow Mandarin, Basar	Arunachal Pradesh
G32	Khasi Mandarin, Basar	Arunachal Pradesh
G33	Sissen Village	Arunachal Pradesh
G34	Dambuk	Arunachal Pradesh
G35	Karko	Arunachal Pradesh
G36	Nagpur mandarin, Biswanath Charali	Assam
G37	Bodak village	Arunachal Pradesh
G38	Boleng, Siang	Arunachal Pradesh
G39	Balek	Arunachal Pradesh
G40	Taki Lalung	Arunachal Pradesh
G41	Hill Mandarin, CHF, Pasighat	Arunachal Pradesh
G42	Cleopatra Mandarin, CHF, Pasighat	Arunachal Pradesh

## Results and Discussion

### Analysis of Variance of Morphological Characterization of tree, leaf, fruit and seed

The variance analysis in the investigation showed significant differences among 42 genotypes for studied traits and a diverse range of variability was observed in Tree Height (m), Canopy width –EW(m), Canopy width- NS (m), tree girth (cm), leaf lamina length (mm), leaf lamina width (mm), leaf lamina length and width ratio, fruit weight (g), fruit length (mm), fruit width (mm), fruit length to width ratio, peel weight, fruit weight without peel, number of seeds per fruit, juice content (ml), number of oil glands, number of segments, seed weight (g), seed width (mm), seed length (mm), peel thickness or rind thickness. This findings had also agreed with which was reported by Goldenberg *et al.* (2014)<sup>[13]</sup> which was reported for mandarin fruit quality traits. Variations in fruit size depends on growth conditions, inflorescence type, number of seeds per fruit and growth regulators used in the plants as reported by Rajae *et al.* (2019)<sup>[20]</sup>.

### Qualitative Characterization of tree, leaf, fruit and seed

Consumer demands and expectation in the market for the *Citrus* fruits are increasing alarmingly. All the qualitative characters of tree, leaf, fruit and seed showed wide degree of variations among the genotypes. The age of all the genotypes tree ranges from 10 year to 21 year. These come under young (10-16) and moderate (20-27) age group (Aregay *et al.*, 2021)<sup>[5]</sup> and can be comparable. Ellipsoid tree shape was seen all the genotypes except spheroid tree shape (G2, G3, G4, G5, G7, G13, G21, G29, G31, and G4) and obloid tree shape were seen in G1 and G16. Similar kind of observation was recorded by Khan *et al.* (2008)<sup>[15]</sup>. Dense (G5, G6, G7, G8, G9, G10, G11, G12, G19 and G20) and medium (G2, G3, G4, G13, G14, G15, G16, G17, G18, G21, G22, G23, G24, G25, G26, G27, G28, G29, G30, G31, G32, G33, G34, G35, G36, G37, G38, G39, G40, G41 and G42) branching density were recorded in maximum genotypes except G1 which is sparse branching in nature. Khan *et al.* (2008)<sup>[15]</sup> reported spreading growth habit in Kinnow Mandarins. All the genotypes have low spine density except G1 (high) and G41 (medium). Maximum tree growth habit was erect whereas drooping was found in G1 and upright in G41. Spreading growth habit of tree was seen in G18, G21, G27, G29, G36 and G42. Kinley and Chinawat (2011)<sup>[16]</sup> reported sparse branch density in mandarin. Maximum genotypes are recorded average leaf aroma except genotypes G41 (weak) and G42 (strong). During study of all the 42 genotypes all the genotypes were seen as evergreen vegetative leaf cycle. The observations on leaf division were seen as simple among all the selected genotypes. Similar kind of observation was reported by Singh *et al.* (2010)<sup>[26]</sup>.

Mandarin genotypes observed wide variety of leaf lamina shapes as it was observed as elliptic in most of the genotypes except ovate lamina (G5, G6, G8, G16, G17, G18, G19 and G20), orbicular lamina (G1, G41 and G42) and obovate (G36). Whereas, leaf lamina margin shape was entire for all the genotypes except G1 (dentate), G41 (crenate) and G42 (sinuate). These distinguished characters will be because of the wild nature they exhibit while others were the cultivable genotypes chosen from farmers' field. Similarly in leaf lamina attachment it was brevipedicelate in all the genotypes except sessile in G1, G16, G41 and G42. In the fruit characters ellipsoid fruit shape was recorded in G1 while obloid fruit shape in maximum genotypes and spheroid fruit shape in G5,

G6, G20, G25, G26, G41, G42. Shape of fruit bases were also shown wide variability like concave fruit base (G4, G7, G8, G9, G11, G12, G13, G14, G16, G18, G19, G21, G22, G23, G24, G25, G26, G27, G28, G31, G32, G33, G34, G35, G37, G38 and G39), convex fruit base (G1, G6, G10, G17, G40, G41 and G42), truncate fruit base (G2, G3, G20 and G30), collared with neck (G15, G29 and G36) fruit bases. Maximum number of genotypes showed depressed fruit apex followed by truncate shaped fruit apex. Fruit surface texture was mostly smooth in all the genotypes except G1 which is rough and bumpy. Rind colour of maximum genotypes of the present study was observed as light orange while fruit aroma is average in most of the genotypes. These were similar to the finding of Khan *et al.* (2008)<sup>[14]</sup>. North East India has various climatic conditions at different states and altitudes at which the fruit is grown. Various colours at the time of maturity can be because of differences in the diurnal temperature at these locations as cold temperature treatment proved to increase the rind colour development in the study of Barry and van Wyk (2006)<sup>[6]</sup>.

Based on the observations recorded, mid season fruiting season was mostly observed followed by late and early. Under the influence of subtropical climate a large proportion of the axillary buds grow in the extremities of shoots. These differences might be because of the differences in the growing conditions (Cruse *et al.*, 1982)<sup>[7]</sup>. Pulp consistencies of all the genotypes are found to be fleshy. Albedo colour is white in all the genotypes except yellow (G1) and orange (G16). Adherence of albedo to pulp is weak as mandarins are easily peelable fruit. However it is strong in case of G1, G41 and medium in case of G31 and G42. This is because as G1 (*Citrus indica*), G41 (Hill mandarin) and G42 (Cleopatra Mandarin- *Citrus reshni* Hort. Ex Tan.) being the wild species chosen among the genotypes. Adherence of segment walls was weak and non uniform segments were observed in maximum genotypes. Seed shape was observed as clavate, cuneiform, fusiform and spheroid in the maximum genotypes. Most of the seed colour is cream in nature. Seed surface is smooth in all the genotypes except wrinkled in G2, G11, G16, G27 and G42. The advantages of these morphological characters will save time and cost as well as the provision of many horticultural traits can be accessed from these. The distinguishable phenotypic characters of genotypes can be used for easy identification, description and classification (Dorji and Yapwattanaphun, 2016)<sup>[9]</sup>.

### Mean performance of tree, leaf, fruit and seeds characteristics

Statistical analysis of various quantitative traits of tree, leaves, fruit and seed from the present investigation showed significant variations. Highest tree height was recorded in G18 (7.82 m) and lowest in G1 (3.04 m). Also, the highest canopy width EW and canopy width NS highest value was recorded in G28 as 5.94 m and 6.01 m respectively. G18 (89.79 cm) recorded highest tree girth followed by G2 (88.97 cm) and G17 (87.56 cm) respectively whereas lowest tree girth was recorded in G1 (24.75 cm). Shigure (2013)<sup>[24]</sup> also reported that the average height of mandarin tree ranged from 4.57 m to 4.83 m while stock girth from 51.5 cm to 56.3 cm. This vigorous growth might be because of rains and high humid conditions favouring vegetative growth. The leaf lamina length was ranging from 59.15 mm to 94.69 mm of which the highest length was recorded in G15 (94.69 mm) followed by G6 (90.40 mm) and lowest length was seen in

G37 (59.15 mm). Leaf lamina width recorded highest in G32 (58.90 mm) followed by G7 (50.80 mm) and lowest in leaf lamina width was recorded in G19 (22.31 mm). The ratio of leaf lamina length and width ranges from G6 (2.87) to G32 (1.13). The highest ratio was recorded in G6 (2.87) followed by G19 (2.73) and G5 (2.56) respectively. The variation in the leaf width was due to the environmental factors or the interaction of environment with the genotype. Similar kind of observation was reported by Estellana and Odtojan (1992)<sup>[11]</sup>. While the observation of fruits in the genotypes chosen, fruit weight ranges from 237.73 g (G31) to 24.46 g (G1). The highest value recorded in fruit width was 237.73 g (G31) followed by 205.06 g (G6) and 178.81 g (G34) respectively whereas fruit length was recorded maximum in G31 (63.33 mm) followed by G27 (61.88 mm) whereas the lowest value was seen in G1 (25.96 mm). Fruit width was ranging from 30.82 mm to 74.03 mm with highest in G6 (74.03 mm) followed by G7 (72.42 mm) and lowest in G42 (30.82 mm). This was similar to the findings of De *et al.* (2004)<sup>[8]</sup>. The highest ratio of fruit length to width is a dependent parameter of fruit length and width. When the fruit length increases, ratio increases whereas when fruit width decreases ratio increases. It is seen maximum in G42 (1.01) and G5 (0.99). Under study the lowest peel weight was observed in G42 (6.86 g). The highest peel weight was recorded in G23 (105.30 g) followed by G34 (101.60 g). Maximum fruit weight without peel was seen in G31 (140.35 g) whereas minimum fruit weight without peel was seen in G1 (13.42 g). Number of segments ranges from 13 to 7.50. The highest number of segments was found in G13 (13) and G15 (13). Lowest number of segment was found in G12 (7.50). Juice content was maximum in G24 (116 ml) and minimum in G16 (9.75 ml). Maximum number of oil glands were seen in G42 (245.83) and minimum in G16 (41.33). Maximum peel

thickness was seen in G39 (5.54 mm) followed by G37 (5.08 mm). The least peel thickness was recorded in G16 (1.86 mm). Seedlessness is one of the prime objective in breeding of *Citrus* (Liu and Deng, 2007)<sup>[17]</sup> but there is only low chance of selecting seedless *Citrus* varieties from existing seeded types (Fathima, 2004)<sup>[12]</sup>. However less number of seeds can be used by breeders for improvement works. In the present investigation, maximum number of seeds per fruit was seen in G42 (26.50) followed by G6 (23.50) and G24 (18.50). The least number of seeds were recorded in G16 (0.83) followed by G1 (5.67) and G29 (6.00) and G38 (6.00) respectively. Minimum seed weight was recorded in G42 (0.08 g) followed by G16 (0.14 g). The maximum seed weight was recorded in G1 (1.44 g) followed by G16 (0.14 g), G26 (1.06 g), G30 (1.05 g). Similar kind of variation in the number of seeds was observed by Altaf and Khan (2008)<sup>[2]</sup>. Maximum seed width was recorded in G41 (7.93 mm). Least seed width is recorded in (2.63 mm) followed by G14 (4.07 mm) and G42 (4.22 mm) respectively. Maximum seed length was recorded in G36 (12.37 mm) and minimum seed length in G16 (5.11 mm). Shirgure (2014)<sup>[25]</sup> reported maximum average fruit weight of mandarin to be 121.5 g which is relatable to the present investigation. However, Singh and Singh (2004)<sup>[27]</sup> reported maximum peel weight and thickness in Kinnow mandarin as compared to mandarins which is disagreeing with the present finding. Variations in the present study may not be only because of environmental factors as variations are shown irrespective of the collection taken from the nearby locations. This was against the previous assumptions of all the ecotypes obtained from different locations as a single variety or altogether called as “local mandarins”. This was in agreement with the findings of Dorji (2011)<sup>[10]</sup>.

**Table 2:** Mean performances of genotypes for morphological characters of tree and leaf

Genotypes	Tree Height (m)	Canopy width (EW) m	Canopy width (NS) m	Tree girth (cm)	leaf lamina length (mm)	leaf lamina width	Ratio (L/ W)
G1	3.04	2.08	2.88	24.75	70.62	47.30	1.50
G2	7.04	5.26	5.70	88.97	77.23	31.30	2.47
G3	6.68	5.56	5.74	72.68	70.25	29.13	2.41
G4	5.52	3.65	3.49	69.68	75.98	33.77	2.27
G5	5.70	3.13	3.55	80.05	81.00	32.91	2.56
G6	6.05	3.38	3.68	65.67	90.40	32.10	2.87
G7	6.02	4.65	5.00	74.97	88.54	50.80	1.75
G8	4.45	3.59	3.87	60.24	87.73	38.15	2.30
G9	6.63	2.98	3.11	40.67	86.40	34.82	2.48
G10	3.83	4.15	4.36	76.97	77.65	37.93	2.05
G11	6.44	3.99	4.05	75.55	75.63	35.81	2.14
G12	5.60	2.99	3.06	76.58	82.01	38.36	2.15
G13	6.72	5.01	4.94	71.06	83.21	45.65	1.84
G14	5.98	3.72	3.92	70.85	81.00	37.69	2.15
G15	6.67	5.02	4.99	67.00	94.69	37.53	2.53
G16	4.89	4.48	4.79	47.67	82.00	32.93	2.49
G17	7.36	4.16	4.29	87.56	85.55	40.77	2.10
G18	7.82	4.65	4.63	89.79	87.94	35.64	2.49
G19	6.73	5.35	5.72	66.37	60.73	22.31	2.73
G20	7.03	5.05	5.09	57.28	77.26	41.71	1.86
G21	5.73	3.15	3.30	76.60	71.51	39.16	1.84
G22	6.01	3.84	4.00	55.49	69.33	29.57	2.35
G23	4.50	5.35	5.48	59.38	76.80	37.38	2.06
G24	7.00	3.34	3.72	72.34	73.94	32.69	2.26
G25	6.05	3.94	4.29	51.37	75.80	33.16	2.29
G26	5.70	2.85	3.02	54.94	67.86	35.34	1.96
G27	6.89	3.55	3.72	58.37	88.75	41.76	2.13
G28	4.85	5.94	6.01	65.37	65.30	32.16	2.16

G29	5.75	4.91	4.99	69.68	80.19	41.40	1.94
G30	5.98	5.70	5.88	70.02	74.46	33.91	2.21
G31	7.02	4.59	4.77	70.34	82.45	41.94	1.97
G32	5.92	2.17	2.31	79.77	66.26	58.90	1.13
G33	4.85	2.68	2.91	78.68	79.44	32.90	2.42
G34	5.60	3.17	3.46	49.18	66.60	34.40	1.94
G35	5.55	2.57	2.82	75.30	72.65	33.16	2.21
G36	6.15	3.20	3.45	53.17	68.99	35.90	1.94
G37	6.32	3.99	4.25	61.27	59.15	29.15	2.03
G38	4.16	3.68	3.88	57.00	76.34	39.65	1.93
G39	5.79	3.48	3.70	68.56	80.34	41.30	1.95
G40	4.70	2.58	2.72	77.62	71.88	35.65	2.02
G41	5.70	4.22	4.41	32.15	82.80	43.17	1.92
G42	5.96	3.45	3.56	29.47	74.62	33.16	2.25
Mean	5.86	3.93	4.13	65.01	77.17	36.96	2.14
C.V.	1.59	0.64	1.46	0.13	1.84	9.44	11.05
S.E.	0.07	0.02	0.04	0.06	1.01	2.47	0.17
C.D. 5%	0.19	0.05	0.12	0.18	2.87	7.05	0.48

**Table 3:** Mean performance of 42 genotypes for morphological character of fruit

Genotypes	Fruit Weight (g)	Fruit length (mm)	Fruit width (mm)	Fruit length to width ratio	Peel weight (g)	Fruit weight without peel
G1	24.46	25.96	35.07	0.74	11.04	13.42
G2	62.96	41.62	50.72	0.82	13.48	49.48
G3	123.24	58.83	65.70	0.90	47.53	75.71
G4	170.66	44.62	58.81	0.76	52.75	117.91
G5	142.17	46.76	47.50	0.99	55.29	86.88
G6	205.06	55.33	74.03	0.75	65.32	139.74
G7	158.14	57.32	72.42	0.79	37.19	120.95
G8	116.63	48.43	67.50	0.72	46.86	69.77
G9	166.02	40.12	49.98	0.81	57.85	108.18
G10	41.54	37.74	42.59	0.89	12.76	28.78
G11	109.29	52.96	62.16	0.85	48.78	60.51
G12	160.60	58.73	70.99	0.83	47.80	112.80
G13	138.19	56.26	68.74	0.82	44.12	94.08
G14	119.08	52.47	63.53	0.83	62.85	56.23
G15	91.36	54.28	63.08	0.72	31.67	59.69
G16	35.38	33.68	46.78	0.73	8.40	26.99
G17	118.99	56.67	66.10	0.86	34.20	84.79
G18	84.55	47.62	56.22	0.85	22.38	62.17
G19	85.78	47.07	56.43	0.84	29.04	56.75
G20	135.69	54.62	68.44	0.80	44.02	91.67
G21	124.43	61.25	66.70	0.92	62.81	61.62
G22	121.19	53.35	63.68	0.84	44.81	76.37
G23	178.30	48.35	49.75	0.97	105.30	72.99
G24	124.26	47.67	62.32	0.77	49.46	74.80
G25	123.55	59.37	62.19	0.96	62.90	60.65
G26	132.25	56.19	63.25	0.89	63.50	68.75
G27	153.53	61.88	70.14	0.88	79.36	74.18
G28	119.16	48.88	66.17	0.75	39.77	79.40
G29	115.15	51.17	66.83	0.77	37.65	77.50
G30	132.85	58.33	67.40	0.87	60.04	72.81
G31	237.73	63.33	65.86	0.94	97.38	140.35
G32	94.77	49.16	56.54	0.87	27.48	67.29
G33	121.84	50.81	63.06	0.82	55.79	66.05
G34	178.81	59.12	71.77	0.83	101.60	77.22
G35	108.05	57.00	63.37	0.90	25.52	82.53
G36	76.33	44.51	55.22	0.81	28.16	48.17
G37	131.59	51.37	53.66	0.96	58.75	72.85
G38	118.85	55.73	56.99	0.98	50.32	68.53
G39	149.90	47.16	48.48	0.97	80.94	68.97
G40	170.93	43.68	44.65	0.98	76.47	94.47
G41	90.74	48.86	55.43	0.89	25.44	65.31
G42	47.24	29.94	30.82	1.01	6.86	40.39
Mean	122.41	50.43	59.31	0.85	47.94	74.47
C.V.	11.08	6.96	6.73	8.91	23.50	13.29
S.E.	5.54	1.43	1.63	0.03	4.60	4.04
C.D. 5%	15.44	4.00	4.54	0.09	12.82	11.26

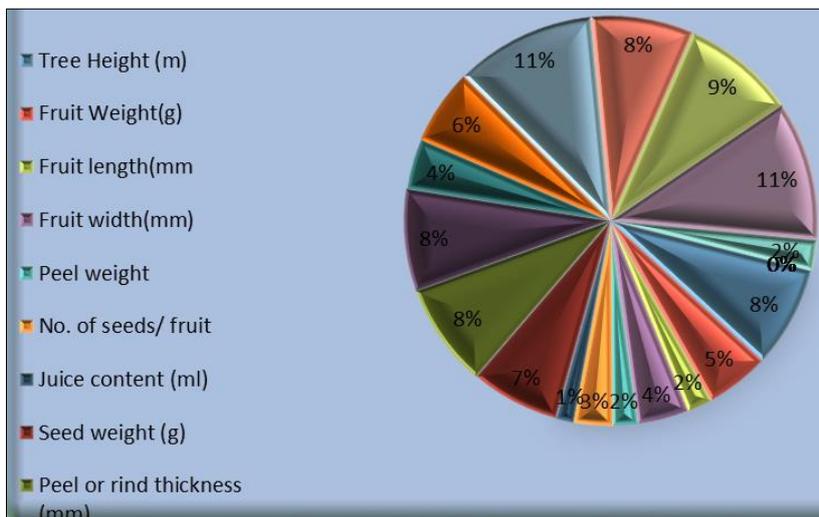
**Table 4:** Mean performance of 42 genotypes for morphological characters of fruit and seed

Genotypes	No of seeds/fruit	Juice content (ml)	No. of oil glands	No of segments	Seed weight (g)	Seed width (mm)	Seed length (mm)	Peel or rind thickness (mm)
G1	5.67	35.43	98.67	8.33	1.44	6.19	8.94	2.77
G2	13.17	41.00	103.33	10.33	0.42	5.61	8.50	3.56
G3	11.33	44.60	150.67	11.33	0.66	5.77	8.52	4.59
G4	13.50	36.33	96.00	8.67	0.74	6.10	7.68	4.51
G5	11.50	64.75	142.50	11.00	0.58	6.19	8.76	4.57
G6	23.50	46.50	95.33	10.50	0.68	5.85	9.30	4.66
G7	12.33	60.75	132.17	11.50	0.64	6.06	10.34	4.87
G8	14.00	55.17	128.83	11.83	0.77	5.88	11.09	2.90
G9	12.33	48.83	146.33	11.17	0.79	5.51	9.58	4.79
G10	14.50	58.57	110.83	9.50	0.74	5.46	9.46	2.94
G11	15.83	49.07	109.50	10.17	0.70	5.60	10.46	3.17
G12	9.67	45.83	146.83	7.50	0.72	5.60	7.74	4.39
G13	11.67	64.65	164.83	13.00	0.67	4.87	8.98	4.50
G14	12.50	35.35	121.67	11.67	0.75	4.07	7.76	4.46
G15	12.00	32.33	121.17	13.00	0.34	6.08	9.71	4.63
G16	0.83	9.75	41.33	8.50	0.14	2.63	5.11	1.86
G17	9.83	50.77	111.83	8.83	0.68	5.06	8.67	3.43
G18	11.83	47.45	111.17	9.00	0.26	4.90	11.10	3.06
G19	14.50	56.66	107.50	12.50	0.76	6.13	9.70	3.86
G20	13.33	62.19	106.50	12.00	0.57	5.07	8.72	4.84
G21	14.67	57.01	150.17	9.83	0.87	5.70	10.63	4.05
G22	14.67	62.84	116.33	11.83	0.84	5.49	8.76	4.82
G23	15.17	56.56	122.83	9.33	0.88	5.31	8.74	2.87
G24	18.50	116.00	112.17	10.50	0.96	5.61	7.55	4.64
G25	13.83	54.14	114.33	12.33	0.55	5.32	8.73	4.85
G26	13.83	56.48	113.33	11.33	1.06	5.63	8.69	3.67
G27	12.50	65.49	123.67	10.83	1.03	5.63	8.80	3.69
G28	11.50	64.72	156.17	11.83	0.65	4.53	10.14	3.71
G29	6.00	38.25	148.33	11.50	0.90	5.36	12.13	3.35
G30	14.50	64.15	116.00	11.50	1.05	5.45	8.70	3.91
G31	12.33	66.57	179.17	11.67	0.69	4.96	7.56	4.75
G32	10.67	26.97	159.67	9.67	0.83	5.52	11.34	3.64
G33	17.17	65.62	106.17	11.50	0.58	5.65	8.33	4.37
G34	11.83	75.73	139.00	10.50	0.61	5.05	8.66	4.16
G35	14.83	37.58	165.67	8.50	1.01	5.10	10.86	2.57
G36	14.83	44.84	171.00	10.17	0.64	4.80	12.37	3.26
G37	9.83	45.76	164.83	12.00	1.03	5.82	9.59	5.08
G38	6.00	34.08	135.33	12.67	1.03	5.46	8.48	1.95
G39	14.67	66.67	172.00	12.83	1.05	4.93	7.67	5.54
G40	12.83	70.17	149.50	12.50	0.76	4.64	8.74	4.15
G41	13.50	47.22	165.33	10.00	0.39	7.93	10.13	2.70
G42	26.50	37.52	245.83	11.67	0.08	4.22	9.45	2.45
Mean	12.95	52.39	132.71	10.83	0.73	5.40	9.19	3.87
C.V.	11.10	7.97	6.45	7.87	13.63	10.25	9.09	6.86
S.E.	0.59	1.70	3.50	0.35	0.04	0.23	0.34	0.11
C.D. 5%	1.64	4.75	9.75	0.97	0.11	0.63	0.95	0.30

**Mahanalobis generalized distance**

The genetic diversity analysis among 42 genotypes of mandarin was measured by employing D<sup>2</sup> Statistics (Mahanalobis, 1936) [18]. Out of these 17 characters were studied. Number of fruits and Vitamin C (mg/100g) imparted maximum percent with respect to genetic divergence (11%). This is followed by pH (9%), peel or rind thickness (8.2%), TSS (8%), shelf life under ambient temperature (8%), tree

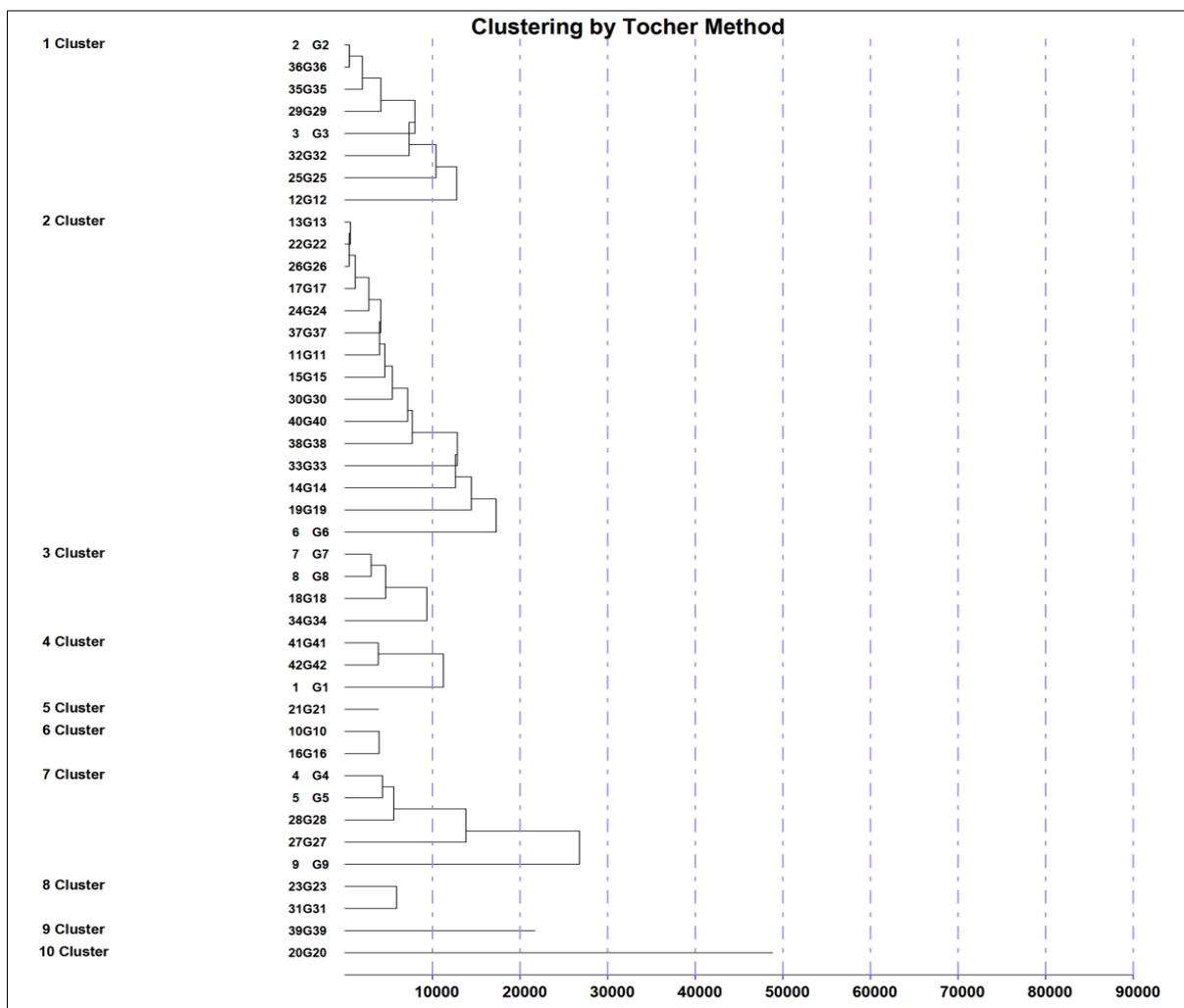
height (8%), seed weight (7%), total sugar (6%), fruit weight (5%), titratable acidity (4%), fruit width (4%), number of seeds per fruit (3%), yield (2.41%), fruit length (2%), peel weight (2%) and juice content (1.39%). Genetic diversity is usually associated with geographical diversity. The diversity can be not directly related with the geographical distribution. This shows that geographical and genetic distribution does not follow the same way as reported by Akanda *et al.* (1999) [1].



**Fig 1:** Percentage contributions towards genetic divergence

As per Toucher’s method (Rao, 1952) [21] 42 genotypes were clustered into ten clusters based on the D<sup>2</sup> values obtained. For all the variables D<sup>2</sup> statistics is the amount of square for each Y values was determined for all combinations in the genotypes. Maximum number of genotypes is found in cluster 2 and least number of genotypes are found in cluster 5, cluster 9 and cluster 10. The cluster 2 consist of 15 genotypes which are G13, G22, G26, G17, G24, G37, G11, G15, G30, G40, G38, G33, G14, G19, G6 followed by Cluster 1 with 8

genotypes (G2, G2, G36, G35, G29, G3, G32, G25 and G12), Cluster 7 with 5 genotypes (G16, G4, G5, G28, G27, G9), Cluster 3 with 4 genotypes (G7, G8, G18, G34), cluster 4 with 3 genotypes (G41, G42, G1), Cluster 8 (G23, G31) and Cluster6 (G10, G16) with 2 genotypes each. Cluster 5, Cluster 9 and 10 have 1 genotype. Uddin and Mitra (1994) [29] and Rahman and Munsur (2009) [19] found similar kind of observation in their investigation.



**Fig 2:** Dendrogram based on 42 genotypes using hierarchical cluster analysis for seventeen characters (Tocher’s Method)

### Average inter and Intra cluster distance

Higher inter and intra cluster distances indicate the presence of genetic variability between and within the clusters respectively while minimum inter and intra cluster distance indicate their closeness between the two clusters and within

that particular cluster. The intra-cluster distance was found maximum in cluster 7 (21.03) followed by cluster 4 (12.53). The highest (2766.74) inter-cluster distance was recorded between cluster 4 and cluster 10 and least (24.48) inter-cluster distance was recorded between cluster 8 and cluster 5.

**Table 5:** Average inter and intra cluster distance ( $D^2$ ) for 42 genotypes

Cluster	1	2	3	4	5	6	7	8	9	10
1	10.07	144.20	28.76	159.42	25.57	116.48	711.29	24.69	1137.02	1635.28
2		10.42	59.77	577.93	261.63	26.10	233.04	174.39	490.86	833.84
3			9.06	289.97	82.02	55.76	494.32	43.22	855.48	1296.21
4				12.53	72.13	498.48	1505.13	166.27	2105.85	2766.74
5					0.00	227.79	958.37	24.48	1446.60	2007.90
6						3.91	305.72	177.20	588.92	945.36
7							21.03	760.96	61.15	205.64
8								5.91	1196.61	1718.04
9									0.00	48.82
10										0.00

### Cluster mean analysis

The accessions among the clusters obtained after separation by genetic divergence study can be used for wide spectrum of variations among the segregated populations (Seetharaman *et al.*, 1988) [22]. Crosses should be made between these distant clusters for high heterotic responses (Rahman and Munsur, 2009) [19]. Cluster means were obtained using Tocher's method for different characters. It is evident that mean value of tree height was recorded highest in cluster 10 (7.03) and least in cluster 6 (4.36). Mean value of fruit weight was found maximum in cluster 8 (208.01) and minimum in cluster 6 (38.46). Fruit length was found maximum in cluster 5 (61.25) and minimum in cluster 4 (34.92). Fruit width has maximum mean value in cluster 10 (68.44) followed by cluster 3 (66.98) while least mean was recorded in cluster 4 (40.44). Minimum peel weight is in cluster 6 (10.58) while maximum in cluster 8 (101.34). Cluster 4 with a value of 15.44 in number of seeds per fruit exhibits maximum value and cluster 6 with a value of 7.83 exhibit minimum value. Juice content was observed maximum in cluster 9 (66.8) and minimum in cluster 6 (33.52). Seed weight recorded maximum in cluster 9 (0.44) and least in cluster 10 (0.44). Cluster mean for peel or rind thickness found maximum in cluster 9 (5.51) and minimum in cluster 6 (2.47). Maximum TSS was found in cluster 10 (15.83) and minimum in cluster 4 (6.93). Genotypes of cluster 4 (3.32) exhibited maximum titratable acidity and genotypes of cluster 10 (0.62) exhibited minimum titratable acidity. Total sugar exhibited maximum mean value in cluster 10 (15.96) and minimum in cluster 4 (3.9). Vitamin C was found maximum in cluster 10 (32.77) and least in cluster 4 (21.6). Shelf life under ambient temperature was recorded maximum mean value in cluster 4 (18.67) and minimum value in cluster 6 (5.63). pH value was recorded highest in cluster 6 (4.74) and minimum in cluster 4 (2.27). No of fruits (1870.5) and yield per tree (255.24) were recorded highest mean value in cluster 10. Minimum value of number of fruits (229) and yield per tree (13.62) were recorded in cluster 4 in the present investigation. To choose a particular genotypes from these clusters to develop a particular trait in breeding programme as a parent source, cluster 4 was found to be promising with maximum number of seeds, Titratable acidity, shelf life but minimum of yield, number of fruits, pH, vitamin C, total sugar, fruit length and fruit weight. Cluster 10 provides maximum yield number of fruits, vitamin C, total sugar, TSS and minimum seed weight and titratable acidity. Cluster 6 was

found to be promising for minimum tree height, fruit weight, peel weight, number of seeds, juice content, peel or rind thickness shelf life and pH. Cluster 8 recorded having maximum fruit weight while cluster 5 for maximum fruit length respectively.

### Conclusion

The analysis of variance in the present investigation showed differences among 42 selected genotypes of mandarin including *Citrus indica*, Hill mandarin, Cleopatra mandarin, Khasi mandarin, Sikkim Mandarin, Nagpur Mandarin and Kinnow mandarin from North East India which indicates a scope of selection of suitable parent material for breeding in further crop improvement in Citrus. On the basis of mean performance the following mandarin genotypes showed better results in the desirable traits chosen such as maximum fruit weight (G31, G6, G34, G23, G4, G40, G9), number of fruits (G20, G39, G5). The minimum tree height was in G10, G38, G8 and least seeds per fruit in G16, G38, G1, G29, G38. Genotype G20 from Jeru village, Upper Siang, Arunachal Pradesh is considered as morphologically superior with most of preferable characters from present investigation. Genetic Diversity assessed by Mahanalobis  $D^2$  value, the 42 genotypes were clustered into ten clusters. Upon the genetic diversity analysis, maximum number of genotypes were found in cluster 2 and least number of genotypes are found in cluster 5, cluster 9 and cluster 10. The cluster 2 consist of 15 genotypes which are G13, G22, G26, G17, G24, G37, G11, G15, G30, G40, G38, G33, G14, G19, G6. From the cluster mean analysis of different parameters of the 42 genotypes, cluster 4 was found to be promising with maximum number of seeds, titratable acidity, shelf life but minimum of yield, number of fruits, pH, vitamin C, total sugar, fruit length and fruit weight. Cluster 10 provides maximum yield number of fruits, vitamin C, total sugar, TSS and minimum seed weight and titratable acidity. Cluster 6 was found to be promising for minimum tree height, fruit weight, peel weight, number of seeds, juice content, peel or rind thickness shelf life and pH. Cluster 8 is having maximum fruit weight while cluster 5 for maximum fruit length. Therefore, these particular characters from each cluster should be taken into consideration while attempting any crop improvement work in the mandarins. Average inter and intra cluster distances help in the choosing of diverse parents from the genotypes. The intra-cluster distance was found maximum in cluster 7 (21.03) followed by cluster 4

(12.53). The highest (2766.74) inter-cluster distance was recorded between cluster 4 and cluster 10 and least (24.48) inter-cluster distance was recorded between cluster 8 and cluster 5. It is therefore advisable to take far distant inter-cluster genotypes for breeding programme to increase variability. Genetic diversity revealed that characters like Number of fruits and vitamin C (mg/100g) imparted maximum percent with respect to genetic divergence (11%). This is followed by pH (9%), Peel or rind thickness (8.2%), TSS (8%), Shelf life under ambient temperature (8%), tree height (8%), seed weight (7%), Total sugar (6%), Fruit weight (5%), Titratable acidity (4%), Fruit width (4%), Number of seeds per fruit (3%), yield (2.41%), fruit length (2%), peel weight (2%) and juice content (1.39%). These can be considered as important parameters in selecting diverse parents for hybridization programme as well as for genetic diversity study in the mandarin.

Elite genotypes showing desirable yield and quality parameters can be involved in multiple crossing breeding programmes to recombine different productive component. In the current scenario of changing environment and climate more number of wild germplasms is needed to be identified and screened for both biotic and abiotic factor adaptations. Traits with direct effect on yield needed to be emphasized for further breeding programme.

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