Short Communication

Genetic divergence of mandarin genotypes in Nagaland

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Abstract

Genetic divergence of 50 mandarin genotypes for general plant features and physico-chemical parameters in Nagaland was estimated using Mahanalobis D^2 analysis. The genotypes were grouped into five clusters. The clusters I was the largest with 34 genotypes followed by cluster II with 12 genotypes, cluster IV with 2 genotypes while cluster III and V included 1 genotype each. Clustering pattern indicated no association between geographical distribution of genotypes and genetic divergence. The inter-cluster distances were higher than the average intra-cluster distances exhibiting wide genetic diversity among the genotypes of different groups than those of the same cluster. The intra-cluster distance was highest in cluster IV, while inter-cluster distance was maximum between I and IV followed by I and V, showing wide diversity between the groups. Leaf length, stamen length, fruit weight, equatorial diameter, polar diameter and juice percent showed maximum contribution towards total divergence among the genotypes.

Key words: Mandarin, genetic divergence, cluster, genotype

The North Eastern Himalayan region is one of the richest sources of diversity among the major centres of mandarin orange (*Citrus reticulata* Blanco) cultivation in the country. The crop is distributed over nine North Eastern states comprising Darjeeling district of West Bengal, Sikkim, Tripura, Nagaland, Mizoram, Manipur, Arunachal Pradesh, Meghalaya and Assam states and contributes substantially to the region's small farm economy [1]. Ecotypes of mandarin like Naga mandarin is a major fruit crop cultivated in the state of Nagaland.

The state is rich in mandarin germplasm and it is cultivated commercially in different districts from time immemorial. However, very little is known about mandarin orange cultivars of Nagaland and its quality characteristics. The vast genetic resources and biodiversity has neither been focused nor has any effort been exerted in conservation of germplasm. As a consequence in due course of time many exotic types or landraces have been eroded in nature. The importance of genetic diversity for improvement of citrus has been emphasized earlier [2, 3]. Genetic diversity of selected genotypes need not always be based on geographical diversity [3]. Since the published work on this aspect of mandarin is scanty, the present investigation was undertaken to classify the genotypes into different groups, depict the nature and magnitude of genetic divergence and characters contributing genetic diversity with respect to some plant morphological and physico-chemical traits.

Fifty distinct genotypes were selected based on grower's choice and preliminary observation from 16 different locations distributed in six districts *viz.*, Mokokchung (6 locations), Wokha (6 locations), Mon, Phek, Kohima and Zunheboto (each one location) at an altitude varying from 560.80 to 1874.22 m (above mean sea level). General features and morphological characters of each selected genotypes were assessed during the month of February to March in 2009 and 2010 and fruit physical and chemical characters were evaluated during ripening and optimum harvesting season from November to December in 2009 and 2010.

The parameters for study were chosen following International Plant Genetic Resource Institute (IPGRI) descriptors of *Citrus* [4]. Genetic divergence was studied following Mahalanobis's [5] generalized distance (D^2) extended by Rao [6]. Clustering of genotypes was done according to Tocher's Method [6]. Average inter cluster distance was calculated by following formula as suggested by Singh and Chaudhury [7] using statistical software SPAR-1.

Fifty genotypes of orange were grouped into five clusters based on D^2 values for all the possible pairs (Table 1). The distribution pattern indicate that the maximum number of 34 genotypes were included in cluster I followed by 12 genotypes in cluster II and 2 genotypes in cluster IV. Minimum of only one genotype was in cluster III and V respectively. The genotypes distributed randomly among the different clusters irrespective of their geographical origin. The intra and inter cluster distance represent the index of genetic diversity among the cluster as given in Table 2. The inter-cluster distances were higher than the average intra-cluster distances, which indicated wide genetic diversity among the genotypes of different groups than those of same cluster. The highest inter cluster distance was observed between I and IV followed by cluster I and V, cluster III and IV, cluster III and V, cluster I and II and lowest between cluster II and V (Table 2). The highest intra-cluster distance was observed for cluster IV and lowest for cluster III and V. The highest values for inter-cluster distance between I and IV indicated that the genotype belonging to cluster I was far away from those of cluster IV. The minimum inter-cluster divergence between II and V showed that the genotype of these cluster were generally close. Cluster mean values for morphological characters and fruit characters are presented in Tables 3 and 4, respectively. With regards to morphological characters of genotypes, cluster I has highest mean value for stamen and leaf length, cluster III has highest mean for plant height and calyx diameter, while cluster IV had highest mean for canopy diameter, stamen length, style length, leaf width and age of plant. With regard to fruit characters cluster V is most important, as genotypes of this cluster has highest mean for fruit weight, equatorial diameter, polar diameter, pulp weight, peel thickness, number of segments, juice weight and medium acidity. Apart from this, cluster I has highest mean for juice percent, cluster II for number of seed and cluster III for TSS, lowest acidity and medium

Table 1. Distribution of 50 mandarin genotypes in 5 clusters

Cluster	Genotypes	Locations
I	Selection no. 9, 10, 11, 12, 13, 14, 15, 16, 20, 21 and 22	Mokokchung (3 locations)
	Selection no. 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33 34, 35, 36, 37, 38, 39 and 40	Wokha (6 locations)
	Selection no. 41and 42	Kohima
	Selection no. 44, 45 and 46	Mon
II	Selection no. 2, 3, 5, 6, 7, 8, 18 and 19	Mokokchung (3 locations)
	Selection no. 47 and 48	Phek
	Selection no. 49 and 50	Zunheboto
III	Selection no. 43	Kohima
IV	Selection no. 1 and 17	Mokokchung (2 locations)
V	Selection no. 4	Mokokchung

Table 2. Average intra (bold) and inter cluster distances of 50 genotypes

Cluster	I	II	III	IV	V
I	**17.310**				
II	41.186	**13.109**			
III	26.996	31.344	**0.000**		
IV	52.052	25.595	44.967	**23.890**	
V	47.876	24.635	44.929	30.489	**0.000**

peel thickness while cluster IV has highest mean for acidity, and lowest mean for peel thickness.

Per cent character contribution towards genetic divergence among the mandarin orange genotypes for morphological character was high from leaf length, stamen length, plant height, number of stamen and calyx diameter and for fruit physico-chemical characters high from equatorial diameter, polar diameter, juice per cent and fruit weight showing

Table 3. Cluster mean value for morphological characters

Cluster	Canopy diameter (m)	Plant height (m)	Calyx diameter (mm)	Stamen length (mm)	No. of stamen	Style length (mm)	Leaf length (mm)	Leaf width (mm)	Age of plant (yrs)
I	1.40	3.58	4.36	7.44	18.73	6.36	77.27	37.98	12.85
II	1.74	3.44	4.33	7.44	18.37	6.51	77.15	37.21	14.21
III	1.62	4.02	4.52	6.99	18.33	5.91	73.70	32.08	15.00
IV	2.66	3.61	4.13	7.59	17.55	6.71	76.47	39.37	17.63
V	2.27	2.10	4.24	7.30	17.89	6.38	74.35	36.37	11.00
Percent contribution towards total divergence	5.34	6.85	6.57	7.07	6.40	6.25	7.24	6.16	4.00

Table 4. Cluster mean value for fruit characters

Cluster	Fruit weight (g)	Equatorial diameter (cm)	Polar diameter (cm)	Pulp weight/ fruit (g)	Peel thick- ness	No.of seg- ment	No.of seed/ fruit	Juice weight (g)	Juice %	TSS (°Brix)	Acidity (%)
I	143.04	6.81	6.23	99.17	2.75	10.25	16.10	64.82	65.81	10.60	0.52
II	134.34	6.84	6.28	96.09	2.79	10.49	16.64	61.56	63.97	10.50	0.51
III	82.33	5.72	5.19	51.67	2.26	10.00	14.66	29.30	56.64	12.93	0.40
IV	101.46	5.53	4.68	78.75	2.21	10.21	14.55	53.41	64.35	10.50	0.74
V	243.56	8.23	7.97	189.33	3.41	10.55	15.22	107.58	56.96	11.53	0.50
Percent contribution towards total divergence	5.00	5.96	5.72	1.94	1.97	3.29	4.27	4.22	4.57	3.76	3.41

possibility of selection of these characters (Table 3 & 4).

Morphological characters of citrus genotypes is particularly important because inheritance of agronomic traits of citrus is reported to be controlled by multiple genes which can be assessed only through morphological assessment [8]. The bud sport mutations, introduction and trials of materials in location different from its original habitat and lack of reproductive barriers both within species and genus might have continually added to its variation and heterogeneity [2]. These factors attributed towards grouping of genotypes from different geographical regions of Nagaland in same cluster indicating no relation between geographical distribution and genetic divergence. Further, the results indicate that the genotypes for highest mean stamen number, leaf length, medium stamen length and calyx diameter, and highest juice percent from cluster I, genotypes for highest stamen length, style length, leaf width, acidity, lowest peel thickness and seed number, medium juice per cent from cluster IV and high fruit

weight, diameter (equatorial and polar), pulp weight, number of segments, juice weight and medium TSS from cluster V could be selected as parents for hybridization programme. Selection of parents for crosses should be made between genotypes belonging to the distant cluster for high heterotic response [3]. In the present investigation, the breeding of genotypes from highly divergent cluster (between cluster I and IV; I and V; III and IV; III and V) and few genotypes from less divergent clusters (I and II; II and III) are expected to produce potential types of medium to large fruit size and higher weight with lower peel thickness, seed number and high juice, TSS content and TSS:acid ratio through hybridization and raising potential hybrids. The elite hybrids after selection can be propagated further clonally [4] or through nucellar polyembroynic seedlings to maintain true-to-parental type [9].

Acknowledgement

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