

## Estimation of Genetic Divergence in Apple (*Malus x domestica* Borkh.)

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Genetic diversity was assessed in twenty-five apple genotypes on the basis of twenty characters. These genotypes were grouped into four clusters on the basis of relative magnitude of  $D^2$  values using Tocher's method. Cluster I was the largest with twenty genotypes followed by cluster II consisting of three genotypes. The inter-cluster D value was maximum between cluster III and IV (55.46) followed by cluster I and IV (46.59). The maximum intra-cluster distance was in cluster II (19.10). Crossing between the genotypes belonging to cluster III and IV as well as cluster I and IV is expected to give maximum heterosis.

**Key Words: Apple, Diversity, Mahalanobis**

Genetic diversity is the result of evolution, including domestication and plant breeding. The process of natural evolution resulted in a build up of genetic diversity in natural population (Hintum, 1995). In order to understand the usable variability, grouping or classification of genetic stocks based on suitable scale is quite imperative. The choice of genetically divergent parents for hybridization under transgressive breeding programme is dependent upon categorization of breeding materials on the basis of appropriate criteria (Sharma, 1998). The information about the extent of genetic divergence is critical for the improvement of any crop in order to have high heterotic response and desirable segregants (George, 1976; Valsalakumari *et al.*, 1985). Though clonally propagated, significant variation is observed among apple cultivars and the estimation of genetic divergence in this fruit crop has not been done so far in detail. Apple being an important temperate fruit crop, high yielding, disease resistant and delicious apple varieties with good keeping quality are needed to be developed for the benefit of the apple cultivators.

### Materials and Methods

The present investigation was carried out during 1999 using Randomized Block Design with three replications on twenty-five apple genotypes planted at a spacing of 5m x 3.5 m. The genotypes are listed in Table 1. The experimental site was located at 1250 meters above mean sea level and situated at 31° N latitude and 77° E longitude with an average annual rainfall of about 1200 mm. Three plants for each genotype were taken into consideration for recording observations on twenty characters. Ten fruits were taken randomly from each tree for recording data on mean fruit weight, length

and breadth. The genetic divergence among the entries were estimated by Mahalanobis  $D^2$  statistic as suggested by Rao (1952), Chaudhary and Singh (1975) and George (1976). All the genotypes were grouped into clusters according to Tocher's method as described by Rao (1952).

### Results and Discussion

The assessment of genetic divergence among the genotypes showed the presence of appreciable amount of divergence. The genotypes were grouped into four clusters (Table 1). It was found that the early cultivars like Scab Resistant, Stark Red Rome, Paragon and Sweet Semi Red, mid cultivars Red Baron, Hardeman and Top Red, and late cultivars Skyline Supreme, Maayan and McIntosh were grouped in cluster I. The earliest cultivar, Early McIntosh and very late cultivar, Aziza fell into cluster III and II, respectively. Similar trend of clustering pattern was reported by Dwivedi and Mitra (1995) in litchi.

The average intra-cluster distance (Table 1) was maximum (19.10) in cluster II followed by cluster I (16.76). Highest inter-cluster distance was obtained between cluster III and IV (55.46) followed by cluster I and IV (46.59). Crossing between the genotypes Tropical Beauty and Early McIntosh falling in the most distant clusters IV and III, respectively, should result in maximum hybrid vigour and eventually desirable segregants leading to the development of useful genetic stocks. Cultivars Sweet Semi Red, Maayan, Red Baron, Spur Type Red Delicious, Skyline Supreme and Top Red from cluster I can be crossed with Tropical Beauty (cluster IV), as the earlier cultivars exhibited higher mean values for the yield contributing characters

**Table 1. Clustering pattern of 25 genotypes and their average intra- and inter-cluster distance**

Clusters	Genotypes	I	II	III	IV
I	McIntosh, Spur Type Red Delicious, Emperor, Top Red, Morspur, Red Royal, Skyline Supreme, Hardeman, Stoyanova Krasavista, Mollie's Delicious, Nemared Delicious, Maayan, Red Baron, Idared, Paragon, Stark Summer Gold, Alkane, Sweet Semi Red, Scab Resistant, Stark Red Rome	16.76	33.34	27.29	46.59
II	Cox's Orange Pippin, Parlin's Beauty, Aziza		19.10	43.58	29.78
III	Early McIntosh			0.00	55.46
IV	Tropical Beauty				0.00

and are likely to show desirable transgressive segregants.

The average cluster means (Table 2) showed that for the traits stem girth (72.33 cm), plant height (6.87 m), leaf area (264.77 cm<sup>2</sup>), tree volume (132.73 m<sup>3</sup>), days to full bloom (22.00 days), days between date of petal fall and date of commencement of June drop (89.67 days), fruit set 20 days after full bloom (41.73%) fruit set 40 days after full bloom (26.54%), final fruit before harvesting (24.67%), yield per plant (25.00 kg), mean fruit weight (188.33 g), mean fruit length (6.10 cm), mean fruit breadth (7.92 cm) and fruit yield per unit shoot length (1783.33g), cluster IV had the highest values. Cluster III was superior in respect of days to full bloom (22.00 days) and number of flowers per unit shoot length (24.42). Cluster II showed the maximum value for the traits like mean tree spread (6.02 m), total duration of flowering (18.20 days), days after full bloom (131.33 days) and number of fruits per unit shoot length (8.23). The character, days between date of commencement of June drop and date of harvesting possessed highest value (40.15 days) in cluster I. Thus,

by involving the genotypes of outstanding mean performance from these clusters as potential parents in crosses, hybrids with high yield and quality can be developed.

The most important trait contributing maximum genetic divergence was yield per plant (22.00%, 1618) followed by mean fruit length (21.33 %, 1687) as per cent contribution and rank total, respectively. The minimum contribution towards genetic divergence was made by tree volume (0.00%, 4847) followed by stem girth (0.00%, 4605) and plant height (0.00%, 4425). The characters contributing maximum divergence can be given more emphasis for the purpose of fixing priority of parents in hybridization programme. It is suggested to effect crosses between cultivars selected from most distant clusters with high mean performance to get desirable transgressive segregants.

**References**

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**Table 2. Cluster means for the characters among 25 genotypes and their contribution towards divergence**

Traits	Clusters				Per cent contribution	Rank Total
	I	II	III	IV		
Stem girth (cm)	45.22	55.89	31.67	72.33	0.00	4605
Plant height (m)	5.39	4.61	3.40	6.87	0.00	4425
Mean tree spread (m)	4.32	6.02	2.60	5.78	0.00	3976
Leaf area (cm <sup>2</sup> )	176.65	194.36	138.73	264.77	0.00	3617
Tree volume (m <sup>3</sup> )	58.33	80.45	13.93	132.73	0.00	4847
Days to full bloom	20.15	19.67	22.00	22.00	0.33	3909
Total duration of flowering	13.88	18.20	14.67	15.30	0.33	3073
Days after full bloom	121.33	131.33	101.00	126.67	20.33	1959
Days between petal fall and commencement of June drop	76.97	88.78	77.33	89.67	10.00	2305
Days between commencement of June drop and harvesting	40.15	37.78	19.33	32.33	0.67	3137
No. of flowers/unit shoot length	10.93	22.12	24.42	15.72	1.33	2819
No. of fruits/unit shoot length	5.86	8.23	5.67	7.67	3.67	2924
Fruit set 20 days after full bloom (%)	24.38	35.14	28.15	41.73	0.00	3581
Fruit set 40 days after full bloom (%)	15.65	22.18	22.33	26.54	1.33	2732
Final fruit before harvesting (%)	13.25	17.12	20.65	24.67	0.00	4141
Yield per plant (kg)	4.71	18.56	4.33	25.00	20.00	1618
Mean fruit weight (g)	113.85	99.22	107.00	188.33	14.33	2014
Mean fruit length (cm)	5.65	4.66	5.18	6.10	21.33	1687
Mean fruit breadth (cm)	6.75	5.21	6.61	7.92	1.00	2837
Fruit yield/unit shoot length (g)	764.43	1002.67	1068.67	1783.33	3.33	2794

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