Indian J. Pl. Genet. Resources 12(3): 341-347, 1999

CHARACTERIZATION OF MANGO GERMPLASM IN NORTH KARNATAKA, INDIA: 2. CLUSTER ANALYSIS

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Numerical taxonomic approach of unweighted pair group method using arithmetic average (UPGMA) in one of SAHN (sequential, aglomerative, hierarchical and non-overlapping) techniques of clustering methods, has resulted in 11 clusters amongst 67 genotypes. The canonical roots analysis after standardization of the data matrix for 37 quantitative and 6 qualitative characters has resulted in 78.1 per cent of the variation depicted in first 3 vectors. The major contributors to the diversity were the fruit characters upto 49.0 per cent, followed by the yield components (18.4%), panicle characters (11.5%) leaf characters (8.5%), tree size and shoot characters (8.4%) and the phenological characters (4.2%). Clusters 2, 4, 3 and 10 were most homogenous, whereas cluster 9, 7 and 11 were highly heterogeneous. Cluster 7 (Neelum, Baramasi, Kalepad) and cluster 11 (Batlimavu and Cowasji patel)were the most divergent, followed by cluster 10 (Dophasla, nl.him-46, Neeluddin, Local-4, KO-11, Creeping) and cluster 11, while the cluster 3 (Dashehari, Pahutan, nl.him-32, nl.him-33, Local-1, csr.nl, Nekkare-2, Nekkare 1) and cluster 10 were the least divergent.

Key words: *Mangifera indica,* cluster analysis, canonical roots, intra and inter-cluster distances

The nature of heritable variability in clonally propagated fruit species must be understood for the success of the breeding strategy. But, because of the high costs and the required land involved in maintenance of the trees, it may be difficult to keep very many entries in the germplasm (Chan, 1992). However it is essential to maintain optimum variability as it is connected to breeding relationships among the individuals. Multivariate statistical analysis has been used effectively in quantifying the degree of divergence in the germplasm in many crop species (Rao, 1952; Sneath and Sokal, 1973). In the numerical taxonomic approaches, generally the similarity coefficients or average Euclidean distances are used in concurrence with the principal component analysis or canonical roots analysis, to arrive at more meaningful cluster formations. However such information is lacking in mango (*Mangifera indica* L.). The main objectives of the present study were therefore, to assess the degree of genetic divergence, its distribution pattern in relationship with geographic and ecological background, to identify the main contributing characters towards divergence and the most divergent parental groups that may likely lead to exploit the hybrid vigour for any chosen character.

MATERIAL AND METHODS

The data were collected from 67 genotypes for 2 successive years, during their 17-19 years of orchard life, at the College of Agriculture, Dharwad, Karnataka, India. All the characters as listed in part 1 were used here, except mean

fruit weight (*Frw*), ripe fruit firmness (*Fir*) and reducing sugars (*Rs*) which showed high correlations (0.99, 0.60 and 0.71) to fruit volume (*Frv*), juiciness (*Jui*) and total sugars (*Ts*) respectively. In addition, the ratings of certain qualitative characters of tree volume (*Tvq*, as : small-0, medium-1, large-2); fruit number per tree (*Frnq*, as : shy-0, average-1, good-2); irregularity index (*Irq*, as: low-0, moderate-1, high-2, very high-3); fruit volume (*Frvq*, as: small-0, medium-1, big-2); fruit major shape index (*Shp1*, as :round-0, oval-1, oblong-2) and fruit minor shape index (*Shp2*, as: flat-0, cylindrical-1), were also utilized in the data set. The clustering method adopted was the numerical taxonomic approach as explained by Sneath and Sokal (1973). The standardized data (where $\mu = 0$ and $\sigma = 1$) were utilized to calculate average similarity coefficient (SG) between each pair of the 67 genotypes as given by Gower (1971).The cluster analysis was done by UPGMA (unweighted pair group method using arithmetic average) technique of the SAHN (sequential, aglomerative, hierarchic and non-overlapping) clustering methods and the taxonomic structure was presented in a dendrogram. The clusters were identified from the dendrogram at SG equivalent to 0.7. Both the intra and intercluster distance coefficients were computed and the cluster means for all the variables were subjected to ANOVA (analysis of variance) for group comparisons. The canonical roots analysis was carried out with the standardized data set to arrive at Eigen values and vectors.

RESULTS AND DISCUSSION

The canonical roots analysis of 37 quantitative and 6 qualitative characters of all the 67 genotypes revealed that the first three vectors could explain up to 78.1 per cent of the total variation (Table 1). The major contributors to the genetic diversity were minor fruit-width (4.3%), fruit yield (4.2%), major fruit -width (4.2%), ripe fruit weight (4.1%), fruit volume (4.1%), fruit number per tree (4.0%), pulp weight (3.9%), physiological loss of weight (3.8%), bearing panicles (3.5%), fruit length (3.5%), fruit volume per tree-frvq (3.4%), total sugars (3.3%), leaf length (3.2%), stone weight (3.2%), leaf area (3.2%), fruit retention (3.1%) and tree volume (3.0%), accounting for 62.0 per cent of the total divergence. The external fruit characters (fruit volume, fruit retention, major fruit-width, minor fruit-width, physiological loss of weight, ripe fruit weight, ripe fruit skin colour, Frvq, major shape index and minor shape index) have contributed upto 29.6 per cent, whereas the internal fruit characters (pulp weight, stone weight, total soluble solids, total sugars, titratable acidity, ascorbic acid content, pulp fibreness, juiciness of pulp content and pulp colour) have contributed upto 19.4 per cent and together contributing upto 49.0 per cent of the total variation. Thus fruit characters were the most important for explaining the genetic variability in mango. These results have also confirmed the earlier report by Suman *et al.* (1985) that the fruit size and shape factor was accounted for 58.3 per cent of total variation among the 84 cultivars studied. In the present study other sets of characters, that have contributed considerably were the fruit yield components (panicles per tree, bearing panicles, initial fruit set, fruit retention, fruit yield, irregularity index, fruit no. per tree and irregularity index) upto 18.4 per cent, followed by the panicle characters (length of panicle, thickness of primary rachis, total flowers per panicle, rachii per panicle and colour of primary rachis) with 11.5 per cent, leaf characters (leaf length, maximum leaf width, and leaf area) with 8.5 per cent, tree size and shoot characters (tree volume, bearing shoot length, proximal shoot length, leaves per shoot and qualitative characters of tree volume) with 8.4 per cent and the phenological characters (period of panicle emergence and duration of flowering) with only 4.2 per cent, towards the total variation. The pattern of istribution of the 67 entries in

Table 1. Canonical roots and vectors of 43 characters from 67 mango genotypes

Character		Vector 1	Vector 2	Vector 3	Contribution towards diversity (%)
Tree volume	m^3	0.16l	0.34	0.12	3.0
Bearing Shoot length	cm	–0.06	0.03	0.17	1.0
Proximal shoot length	cm	–0.06	–0.09	0.12	1.2
Leaves/shoot	No.	0.05	0.01	–0.01	0.4
Leaf length	cm	0.14	0.34	0.35	3.2
Max. leaf width	cm	0.09	0.06	0.48	2.1
Leaf area	cm^2	0.13	0.19	0.47	3.2
Period of panicle emergence	rating	0.07	0.30	–0.08	2.2
Panicles/tree	No.	–0.03	0.21	–0.27	2.0
Bearing panicles	No.	–0.04	0.59	–0.16	3.5
Length of panicles	cm	0.07	0.13	0.28	1.5
Thickness of primary rachis	mm	–0.06	0.13	0.37	2.0
Rachii/panicle	No.	0.05	0.32	0.22	2.5
Colour of primary rachis	rating	–0.03	–0.06	0.15	0.9
Total flowers	No.	0.22	0.14	0.14	2.4
Hermaphrodite flowers	No.	0.04	0.35	0.16	2.3
Flowering duration	days	–0.10	–0.29	0.10	2.0
Initial fruit set	No.	0.02	0.09	0.13	0.8
Fruit retention	No.	–0.14	0.41	0.08	3.1
Fruit yield	No.	–0.15	0.58	–0.16	4.2
Irregularity index	Per cent	0.01	–0.08	0.08	0.6
Tree volume		0.14	0.29	0.22	2.8
Fruit no. per tree		–0.16	0.55	–0.11	4.0
Irregularity index per tree	–0.01	0.01	–0.06	0.2	
Fruit volume	cm^3	0.59	–0.04	–0.02	4.1
Fruit length	cm	0.51	–0.03	0.04	3.5
Major fr. width	cm	0.55	–0.08	–0.07	4.2
Major fr. width	cm	0.55	–0.11	–0.08	4.3
Physiological loss of weight	g	0.51	–0.08	–0.07	3.8
Ripe fr. weight	g	0.59	–0.04	–0.03	4.1
Pulp weight	g	0.59	–0.02	–0.02	3.9
Stone weight	g	0.46	–0.04	–0.02	3.2
Total soluble slides	"brix	0.02	–0.16	–0.03	1.0
Total sugars	g	0.55	–0.11	–0.05	3.3
Titrable acidity	g	0.40	0.00	–0.02	2.1
Ascorpic acid content	mg	0.23	0.05	–0.19	2.3
Pulp fibre content	rating	–0.14	–0.02	0.08	1.3
Juiciness of the pulp	rating	–0.03	0.17	0.14	1.3
Ripe fruit skin colour	rating	0.07	–0.03	–0.05	0.8
Pulp colour	rating	–0.04	–0.08	0.10	1.0
Fr. no. per tree		0.53	–0.01	0.00	3.4
Fruit major shape index		0.04	0.03	0.10	0.7
Fruit minor shape index		–0.03	–0.06	–0.05	0.7
Eigen Root		19.00	10.29	4.28	-
% Var. Explained		44.22	23.93	9.95	-
Cum. Perc. Var.		-	68.15	78.10	100.0

11 clusters is depicted in Table 2 and were clearly dentified from the dendrogram (Fig. 1). A maximum of 12 genotypes were recorded in cluster 8 followed by cluster 5 with 10 genotypes, cluster 3 and cluster 6 with 8 genotypes each, cluster 1 and cluster 10 with 6 genotypes each, cluster 2 with 5 genotypes, cluster 4 with 4 genotypes, cluster 7 and cluster 9 with 3 genotypes

Table 2. Cluster compositions based on SAHN multivariate technique involving 67 mango genotypes

Cluster	Frequency	Accessions
1	6	Alphonso, Pairi, Neelgoa, Swarna Jehangir, Neeleshan, Local-3
2	5	Chandramaru, Fernandin, Chausa, Lal Pairi, Neelam × Himayuddin 3/7
3	8	Dashehari, Pahutan, Neelam × Himyuddin-32, Neemal × Himdyuddin-33, Local-1, Suvernrekha × Neelam, Nekkare-1, Nekkare-2
4	4	Suvernrekha, Olour, Ratna, Bappekshi
5	10	Lucknow Safeda, Neelam × Pamchadarakalasa-77, Rataul, Neelam × Alampur Baneshan 137, Neelam × Himayuddin-63, Neelam × Panchadarakalasa-4, Neelam × Alampur Baneshan-92, Neelam × Alampur Baneshan-94, Mallika, Suvernrekha × Khader
6	8	Kari Isbad, Langra, Nazuk Pasand, Neelam × Panchadarakalasa-4, Pulihora, Kurukkanko-27, Rumani
7	3	Neelam, Beramasi, Kalepade
8	12	Baneshan, Cherukurasam, Alampur Baneshan, Dilpasand, Himayuddin, Bombay Green, Sardar, Au Rumani, Fazli, Vellaikolamban, Local-2, Totapari
9	3	Peddarasam, Mulgoa, Jehangir
10	6	Dophasala, Neelam × Himayuddin-46, Neeluddin, Local-4, ko-11, creeping
11	2	Batlimavu, Cowasji Patel

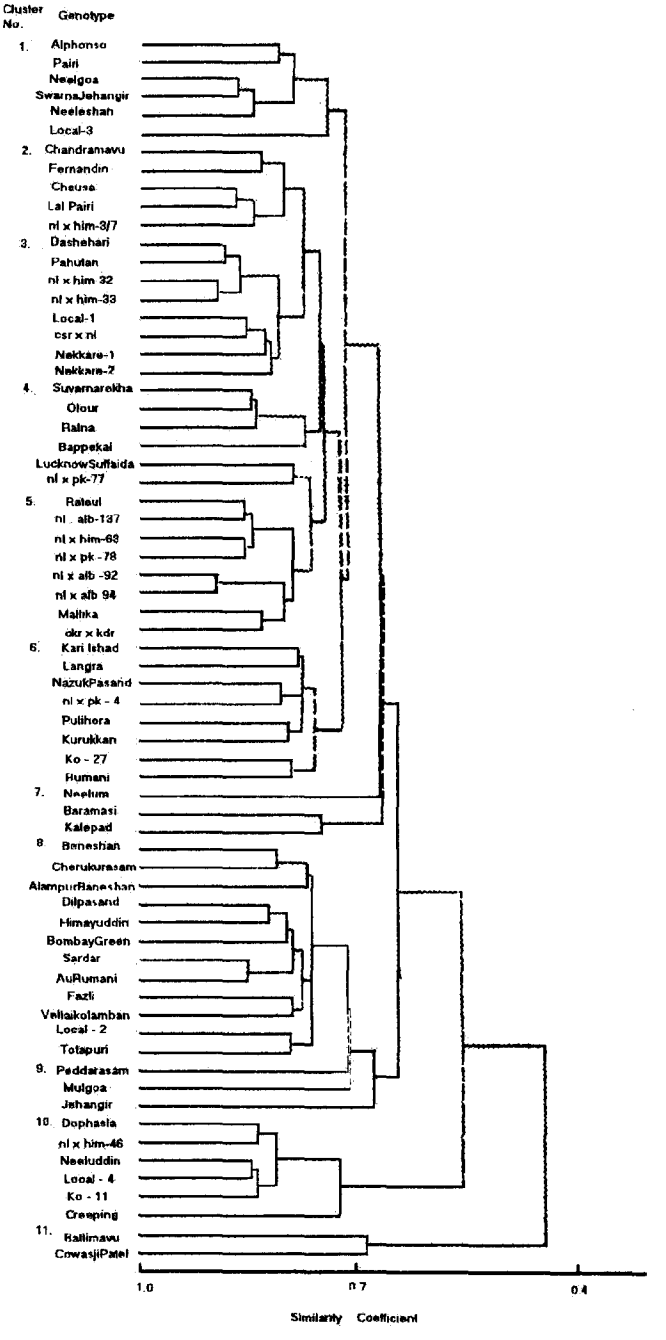

Fig. 1. Dendrogram showing heirarchical clustering of 67 mango genotypes based on similarity coefficient in 43 characters

each and cluster 11 with only 2 genotypes. The criterion used for clustering was that any two genotypes falling in the same cluster would show smaller genetic distance than those belonging to any other cluster. A perusal of the cluster

Table 3. Average intra(bold) and inter cluster distances

Cluster	1	2	3	4	5	6	7	8	9	10	11
1	**5.51**	7.60	8.38	8.06	6.35	8.60	7.79	7.64	9.25	9.28	11.26
2	-	**4.30**	6.34	5.81	5.96	5.89	5.49	6.73	8.28	6.76	11.53
3		-	**4.82**	5.92	6.31	6.53	8.15	8.38	10.27	5.35	14.57
4			-	**4.62**	6.37	5.97	8.84	6.33	7.99	5.70	11.98
5				-	**5.34**	6.81	7.66	7.05	8.72	6.96	12.37
6					-	**5.80**	9.04	7.31	8.46	6.30	12.05
7						-	**7.32**	9.81	11.02	8.85	14.72
8							-	**6.04**	8.34	8.14	9.75
9								-	**7.33**	9.82	9.71
10									-	**4.95**	14.11
11										-	**6.93**

compositions (Table 2) indicated that cluster 1 had accessions mostly from the peninsular India, but cluster 2 which is represented by the 4 peninsular cultivars, also had Chausa, a popular north Indian cultivar. Similarly, in cluster 3 only Dashehari was from the north Indian origin, whereas the rest of them belonged to the peninsular region. The clustering pattern of these accessions suggested that geographic diversity may not necessarily be related with genetic diversity. Therefore, the selection of parental lines for hybridization in mango should be based on genetic diversity rather than on the geographic diversity. Estimations of intra cluster distances indicated (Table 3) that the cluster 2 with 5 accessions (Chandramavu, Fernandin, Chausa, Lalpairi and Neelam × Himayuddin-3/7) had the least average distance (4.3), followed by cluster 4 4.62), cluster 3 (4.82) and cluster 10 (4.95) and suggested that the accessions falling within these clusters were more homogeneous than the accessions of other clusters, while the clusters 8, 6, 1 and 5 were moderately heterogeneous whereas cluster 9, with 3 accessions (Peddarasam, Mulgoa and Jehangir) recorded the maximum average intracluster distances (7.33), followed by cluster 7 (7.32) and cluster 11(6.93). Thus, the accessions falling within these clusters were highly heterogeneous. The average inter cluster distances revealed a maximum between cluster 7 and 11 (14.72) followed by cluster 3 and 11 (14.57), and cluster 10 and 11 (14.11). This indicated that cluster 11 (Batlimavu and Cowasji Patel) was highly divergent with cluster 3 (Dashehari, Pahutan, Neelam × Himayuddin-32, Neelam × Himayuddin-33, Local-1, Suvernrekha × Neelam, Nekkare-2 and Nekkare-1), cluster 7 (Neelum, Baramasi and Kalepad) and cluster 10 (Dophasla, Neelam × Himayuddin-46, Neeluddin, Local-4, Ko-11 and Creeping). The minimum average distance coefficient recorded between cluster 3 and 10 (5.35) indicated that the genotypes in these two clusters were relatively closer to each other. Similarly the lower intercluster distances were also recorded within the cluster pairs 2-4, 2-5, 3-4, 4-6 and 4-10 which indicated their closer relationships.Cluster means of the 37 quantitative characters are presented in Table 4 and the group differences for all these characters were significant by the statistical analysis. A perusal of these cluster means indicated that fruit yield (*Frn*) was maximum in cluster 7, minimum tree size (*Tv*) in cluster 4, maximum fruit size (Frv) in cluster 11, high Tss in cluster 9, attractive fruit skin colour (*Skc*) in cluster 4. Likewise, several other desirable attributes would be pin pointed from the cluster mean values. Hybridization between accessions falling in the most distant clusters (11 and 3 or 7) would be expected to result in a maximum hybrid vigour and eventually the desirable seggregates. Also the hybridization of cluster 11 with the cluster 10 should result in desirable combinations leading to the development of useful genetic stocks.

Table 4. Cluster means of 37 characters in mango

Character		Cluster Number											Group Comparisons		
														CD	
Trait	Unit	1	2	3	4	5	6	7	8	9	10	11	SEd	5%	1%
Tree volume	m3	79.0	82.1	37.3	16.4	71.5	40.3	55.0	46.4	57.0	22.7	91.2	9.6	19.3	25.8
Primary sheet length	cm	9.7	9.7	11.7	9.2	11.1	9.5	11.3	11.1	10.0	10.0	10.2	0.9	1.9	2.4
Proximal shoot length	cm	6.9	8.1	11.4	7.2	9.6	7.8	8.7	7.9	6.3	7.3	8.3	1.2	2.4	3.2
Leaves per shoot	No.	13.7	13.1	13.0	12.9	12.6	12.4	12.1	11.7	11.6	11.5	9.7	0.8	1.7	2.3
Leaf length	cm	21.5	21.1	18.9	18.7	18.6	17.1	17.1	17.0	16.1	15.4	14.3	0.7	1.5	2.0
Max. leaf width	cm	5.2	5.1	4.7	4.6	4.7	4.2	3.6	5.1	4.2	4.2	6.0	0.3	0.7	0.9
Leaf area	cm^2	78.7	68.2	59.7	56.8	63.0	48.1	45.4	70.6	44.0	50.4	92.0	6.3	12.8	17.1
Period of panicle emergence	rating	4.5	4.2	3.2	3.5	3.9	3.7	3.8	3.5	3.3	2.5	3.2	0.3	0.7	0.9
Panicle per tree	No.	502.2	205.9	445.8	430.0	467.0	331.8	920.5	473.2	576.3	478.3	273.5	99.3	200.2	267.6
Bearing panicles	No.	305.1	90.1	150.0	141.0	195.9	122.8	322.5	146.3	142.0	113.1	126.7	23.9	48.2	64.4
Length of panicles	cm	29.2	26.1	3.3	24.2	29.0	22.8	26.6	30.3	24.4	26.9	23.6	2.0	4.1	5.4
Thickness of primary rachis	mm	5.3	5.7	5.5	6.0	6.1	5.7	4.6	5.9	5.7	5.8	5.4	0.4	0.9	1.1
Rachii per panicle	No.	44.7	37.7	37.6	37.5	42.9	30.3	38.5	42.1	39.2	34.9	33.8	1.9	3.8	5.1
Colour of primary rachis	rating	3.2	4.0	3.7	3.7	2.8	3.6	3.3	3.5	3.7	3.5	3.5	0.5	1.0	1.2
Total flowers	No.	1709	1111	1311	2171	1528	787	1631	1956	2134	1184	2065	190	383	512
Hermaphrodite flowers	No.	160.9	73.9	74.6	52.0	121.9	73.1	177.4	107.7	74.5	58.1	141.8	24.6	49.6	66.3
Flowering duration	days	29.7	32.2	34.6	37.0	35.5	34.2	31.0	35.5	35.6	50.9	32.6	2.8	5.7	7.6
Initial fr. set	No.	4.2	5.3	4.7	3.3	5.9	6.3	8.0	5.5	3.0	5.2	2.9	1.1	2.2	2.9
Fr. retention	No.	0.8	0.5	0.5	0.4	0.7	0.4	0.8	0.4	0.4	0.5	0.6	0.1	0.2	0.3
Fr. yield	No.	369.4	110.2	201.4	158.7	269.5	145.2	541.8	148.7	150.3	155.2	126.7	31.8	64.2	85.8
Irregularity index	percent	18.3	32.6	23.4	38.6	48.9	26.4	23.4	33.1	62.1	26.1	11.4	9.7	19.7	26.1
Fr. volume	cm^3	314.0	280.7	151.1	283.2	247.9	280.9	174.2	431.1	517.4	187.1	820.3	30.0	60.5	80.9
Fr. length	cm	10.2	10.6	8.4	11.1	10.2	9.6	8.9	12.4	12.7	9.0	14.9	0.6	1.2	1.6
Major fruit width	cm	7.9	7.8	6.2	8.0	7.2	8.0	6.5	8.8	9.6	6.6	11.1	0.3	0.6	1.2
Minor fr. width	cm	7.1	7.0	5.5	7.0	6.4	7.2	5.9	7.8	8.7	6.1	10.0	0.3	0.6	0.8
Physiological loss of wt	g	31.1	29.0	14.3	31.1	25.2	26.7	16.1	44.3	38.6	19.7	69.3	4.3	8.6	11.5
Ripe fr wt	g	283.4	258.8	136.3	259.4	228.4	262.2	166.0	388.7	478.9	172.3	745.3	26.9	54.2	72.4
Pulp wt	g	198.1	157.2	85.0	167.5	153.8	174.5	102.7	274.7	312.9	113.8	547.5	20.5	41.4	55.3
Stone weight	g	39.2	42.6	25.5	36.0	32.3	36.8	25.6	38.0	61.2	27.8	59.6	3.2	6.4	8.6
Total soluble solids	brix	14.8	16.9	17.4	17.9	17.7	17.4	15.8	17.8	20.0	17.0	13.7	1.5	3.0	3.9
Total sugars	g	22.3	21.0	11.9	22.4	21.1	26.1	13.3	36.3	48.7	14.5	55.5	3.4	6.8	9.1
Titrable acidity	g	0.4	0.3	0.2	0.3	0.3	0.5	0.3	0.4	0.6	0.3	1.9	0.1	0.2	0.3
Ascorbic acid content	,g	6.9	5.9	3.8	8.4	6.7	13.4	26.6	11.2	13.4	8.6	23.5	2.4	4.8	6.5
Pulp fibre content	rating	2.1	2.7	3.0	3.6	3.4	2.8	2.6	2.4	2.9	3.0	2.9	0.4	0.8	1.1
Juiciness of the pulp	rating	1.9	1.9	1.9	1.7	2.4	2.2	2.0	2.1	2.1	2.0	2.1	0.1	0.3	0.4
Ripe fr. skin colour	rating	4.6	4.8	3.9	5.3	3.4	4.8	4.0	4.4	4.0	3.6	4.6	0.5	1.0	1.3
Pulp colour	rating	2.3	2.4	2.6	2.2	2.3	2.3	2.1	2.1	2.3	2.3	2.6	0.2	0.3	0.4

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