# Studies on Genetic Divergence in Basil (Ocimum basilicum L.) Germplasm

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(Received: 21 August 2010; Revised: 13 September 2010; Accepted: 11 November 2010)

The genetic diversity studies was conducted on 30 genotypes of basil comprising 20 exotic introductions and 10 indigenous collections representing from different phyto-geographical regions. The experiments were laid down during *kharif* season of 2004 and 2005 at National Bureau of Plant Genetic Resources (NBPGR), Experimental Station, Issapur, New Delhi. The genetic divergence for sixteen characters using Mahalanobis D<sup>2</sup> statistical analysis revealed the presence of considerable genetic diversity in the germplasm. These germplasm lines were grouped into seven clusters with variable number of genotypes. The intra-cluster distance ranged from 2.078 to 3.051. The maximum intra-cluster distance was observed in cluster VI and minimum in cluster I. The grouping of genotypes (intra- or inter-) were not consistent over the environments exemplify variations due to phytogeographical regions.

Key Words: Basil, Genetic Divergence, Germplasm

### Introduction

The genus Ocimum belongs to family Lamiaceae and 160 species are known to occur world wide. It is widely distributed and extensively grown throughout India (Pushpangadan and Bradu, 1995; Verma et. al., 1998, Pandey and Chowdhary, 2002). Ocimum basilicum L., commonly known as basil, is one of the important medicinal and aromatic herb. Assessment of genetic diversity in germplasm collection can facilitate classification and identification of diverse genotypes with maximum utilization for specific traits. Superior genotypes can be used as parents for development of improved cultivar for specific traits like essential oil yield and quality and other traits of breeding importance. This requires a well established statistical tool to quantify the degree of genetic diversity among the available genotypes. Grouping of the genotypes based on the character association through multivariate analysis had been suggested by Mahalanobis (1936); Rao (1952) and Anderson (1957). The most simple and convenient method for assessment of the genetic diversity and grouping of genotypes is D<sup>2</sup> analysis. Genetically diverse parents are expected to produce physiologically and morphologically more efficient genotypes. Present study was therefore, aimed to estimate the quantum of genetic diversity for various agro-morphological and photo-chemical characters in germplasm collection of basil.

#### **Materials and Methods**

The experimental material of thirty accessions of Ocimum comprised 20 exotic introductions (USA-10, USSR-07, Poland 01, Hungary-01 and Germany-01) and 10 indigenous collections were collected by taking into consideration their place of origin (Madhya Pradesh-6, Gujarat-2, Andhra Pradesh-1 and Uttar Pradesh-1) to represent the maximum variability. The experimental material was grown in nursery and transplanted in a Randomized Block Design (RBD) with three replications during Kharif 2004 and 2005 at National Bureau of Plant Genetic Resources (NBPGR), Experimental Farm, Issapur, New Delhi. The NBPGR Experimental Farm (latitude 28°36′N, longitude 76°50′E) has semi-arid climate with average annual rainfall of 400 mm. The soil of the experimental field was sandy loam (pH 8.0). Three rows of each accession having 10 plants per row were transplanted with row to row and plant to plant spacing of 45 and 30 cm, respectively. Observations were recorded on five randomly selected plants in each genotype for sixteen characters viz., number of primary branches/plant, lamina length (cm), lamina width (cm), leaf-stem ratio, days to flower initiation, number of spikes/plant, spike length (cm), number of flower-whorls/ spike, plant height (cm), fresh herbage yield/plant (g), dry herbage yield/plant (g), days to seed maturity, seed yield/plant(g), 1000-seed weight(g), essential oil content (%) and essential oil yield/plant (ml). Genetic divergence

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was estimated by utilizing Mahalanobis D<sup>2</sup> statistics as described by Rao (1952) and genotypes were grouped into different clusters.

### **Results and Discussion**

Analysis of variance revealed significant differences among 30 genotypes for all the 16 characters studied. The  $D^2$  values determining the genetic distances among the genotypes were computed and thirty genotypes were grouped into seven clusters. Clustering pattern of these genotypes, their cluster mean values and intraand inter-cluster distances are depicted in Tables 1 to 5 respectively.

During *Kharif* 2004, it was observed that Cluster III has the maximum number of genotypes (9) followed by Cluster II (8), Cluster IV (5), Cluster I (4), Cluster VII (2), Cluster V (1) and Cluster VI (1). The maximum and minimum was recorded in intra cluster distance Cluster I (2.729) and Cluster VI (0.001) respectively. The maximum inter Cluster (D<sup>2</sup>) value was observed between Cluster VI and Cluster V (10.685) followed by Cluster I and Cluster VI (9.275) and minimum inter cluster distance was observed between cluster I and cluster II (3.216). The cluster mean values when examined across the clusters

Table 1. Clustering pattern of 30 genotypes of basil in Kharif 2004

Cluster	Genotypes (no.)	Germplasm accession (s)
I	4	EC 388893, EC 388891, EC 387837, EC 388896
		EC 388890, EC 388895, EC 387838, EC 388788
II	8	EC 338794,
		EC 338782, EC 338772, EC 338773
		IC 326735, IC 336833, IC 344638, EC 174527,
III	9	IC 201233, IC 211313, IC 326732, EC 388889,
		IC 338959
13.7	_	IC 110267, IC 333332, EC 312264, EC 112548,
IV	5	EC 388887
V	1	EC 338775
VI	1	EC 338785
VII	2	IC 326711, EC 338776

Table 2. Clustering pattern of 30 genotypes of basil in Kharif 2005

Cluster	Genotypes (no.)	Germplasm accession (s)
I	2	EC 387837, IC 326732
II	3	EC 338785, EC 388891, IC 326711
III	4	IC 110267, EC 388890, EC 388788, EC 338773
IV	5	EC 388895, EC 388893, EC 387838, IC 326735, EC 112548
V	4	EC 338794, IC 333332, EC 338782, EC 388887
VI	2	EC 338775, EC 338776
VII	10	IC 336833, EC 312264, EC 338772, IC 344638, EC 174527, IC 201233, EC 388896, IC 211313, EC 388889, IC 338959

Table 3. Cluster mean values of 16 characters of 30 genotypes of basil

	Cluster I	ter I	Clust	ter II	Clust	er III	Clust	er IV	Clusi	ter V	Clust	er VI	Cluste	ır VII
Character (s)	2004	2005	2004	2005	2004	2005	2004	2005	2004	2005	2004	2005	2004	2005
Number of primary branches per plant	12.47	11.20	13.40	11.00	12.24		12.11	1	11.93	1	12.00	12.90	12.07	11.17
Lamina length (cm)	4.73	4.09	5.00	4.93	5.05		5.28		4.62		6.18	4.34	5.37	4.72
Lamina width (cm)	2.86	2.43	2.93	2.70	2.96	2.56	3.03	2.59	3.01	2.63	3.79	3.72	3.26	2.58
Leaf-stem ratio	1.33	1.06	1.04	1.05	0.80		0.76		1.73		1.21	1.46	1.25	0.87
Days to flower Initiation	61.75	64.00	61.53	70.78	64.68		65.64		74.00		62.27	62.50	72.90	63.67
Number of spikes per plant	61.90	76.47	63.33	72.33	59.96		60.47		93.93		52.20	63.80	54.30	79.52
Spike length (cm)	16.03	14.23	16.68	20.87	15.36		13.01		20.19		27.73	23.95	20.82	17.34
Number of flower-whorls per spike	13.00	12.23	12.80	14.13	12.10		11.68		12.20		16.80	13.03	12.00	12.91
Plant height (cm)	55.50	44.62	56.18	65.92	52.33		51.99		57.49		83.27	57.08	64.55	50.82
Fresh herbage yield per plant (g)	279.92	263.67	351.50	254.78	303.89		357.94		306.67		375.00	261.50	244.17	231.90
Dry herbage yield per plant (g)	58.49	55.56	72.79	52.94	64.11		76.14		63.58		79.48	55.06	51.35	48.99
Days to seed maturity	160.08	159.67	156.54	166.78	157.52		163.27		156.67		162.33	157.50	161.50	158.57
Seed yield per plant (g)	29.90	11.11	27.21	36.50	13.88		24.82		11.92		48.55	11.54	14.47	14.95
1000-seed weight (g)	1.45	1.28	1.44	1.69	1.30		1.46		1.21		1.66	1.45	1.68	1.32
Essential oil content (%)	0.22	0.28	0.19	0.20	0.17		0.21		0.19		0.13	0.18	0.18	0.17
Essential oil yield per plant (ml)	0.63	0.75	89.0	0.50	0.51		0.75		0.57		0.50	0.46	4.0	0.40

Table 4. Intra- and inter-cluster divergence  $D^2$  values among seven clusters in *Kharif* 2004

Cluster	I	II	III	IV	V	VI	VII
I	2.729						
II	3.216	2.271					
III	3.619	3.360	2.534				
IV	4.151	3.341	3.808	2.716			
V	5.745	6.099	5.606	6.816	0.004		
VI	9.275	8.431	9.162	9.065	10.685	0.001	
VII	5.168	6.128	4.822	6.238	6.596	8.122	2.486

Table 5. Intra- and inter-cluster divergence  $D^2$  values among seven clusters in *Kharif* 2005

Cluster	I	II	III	IV	V	VI	VII
I	2.078						
II	6.862	3.051					
III	4.813	5.194	2.968				
IV	5.976	4.730	3.823	2.597			
V	4.797	4.874	3.932	4.268	2.509		
VI	7.051	6.409	5.735	5.844	6.636	2.644	
VII	4.998	5.181	4.074	2.594	4.034	5.548	2.414

revealed that Cluster I had highest mean value for essential oil content (0.22%) and lowest for lamina width (2.86 cm) like-wise Cluster II had highest cluster mean value for number of primary branches/plant (13.40) and lowest for days to flower initiation (61.53 days) and days to seed maturity (156.54 days). No highest or lowest values were recorded in cluster III. Days to seed maturity (163.27 days) and essential oil yield/plant (0.75 ml) had highest leaf-stem ratio (0.76), spike length (13.01 cm), number of flower-whorls/spike (11.68) and plant height (51.99 cm) had lowest cluster mean values in cluster IV. In Cluster V leaf-stem ratio (1.73), days to flower initiation (74.00 days) and number of spikes/plant (93.93) had high cluster means and number of primary branches/plant (11.93), lamina length (4.62 cm), seed yield/plant (11.92 g) and 1000-seed weight (1.21 g) had low cluster mean values. Cluster VI had highest cluster mean for lamina length (6.18 cm), lamina width (3.79 cm), spike length (27.73 cm), number of flower-whorls/spike (16.80), plant height (83.27 cm), fresh herbage yield/plant (375.00 g), dry herbage yield/plant (79.48 g), seed yield/plant (48.55 g) and lowest value for number of spikes/plant (52.20) and essential oil content (0.13 %). Cluster VII showed highest cluster mean value for 1000-seed weight (1.68 g) and fresh herbage yield/plant (244.17 g) whereas dry herbage yield/plant (51.35 g) and essential oil yield/plant (0.44 ml) had lowest cluster mean values.

In *Kharif* 2005, it was observed that out of seven clusters, Cluster VII had highest number of genotypes

(10) followed by Cluster IV (5), Cluster III (4), Cluster V (4), Cluster II (3) and Cluster I (2) and Cluster VI (2) genotypes. Minimum and maximum intra-cluster distance was observed in cluster I (2.078) and Cluster II (3.051) respectively. The maximum inter-cluster value (D<sup>2</sup>) was obtained between clusters I and VI (7.051) while minimum inter cluster value (D<sup>2</sup>) was recorded between Clusters IV and VII (2.594). The highest mean value for essential oil content (0.28 %), essential oil yield/plant (0.75 ml) and lowest mean value for lamina length (4.09 cm), lamina width (2.43 cm), plant height (44.62 cm), seed yield/plant (11.11 g) and 1000-seed weight (1.28 g) were recoded in cluster I. The highest cluster mean values for days to flower initiation (70.78 days), number of flower-whorls/spike (14.13), plant height (65.92 cm), days to seed maturity (166.78 days), seed yield/plant (36.50 g) and 1000-seed weight (1.69 g) were recorded in Cluster II. Cluster III was characterized by maximum cluster mean value for fresh herbage yield/plant (308.67 g) and dry herbage yield/plant (63.85 g) and minimum for days to flower initiation (61.67 days). Maximum cluster mean value for lamina length (5.29 cm) and minimum cluster mean value for primary branches/plant (10.71), days to seed maturity (156.07 days) and essential oil content (0.17 %) were observed in Cluster IV. The highest cluster mean value in Cluster V was recoded for number of spikes/plant (80.97) and minimum cluster mean value for leaf-stem ratio (0.85), spike length (13.24 cm) and number of flowerwhorls/spike (11.72). Cluster VI recoded high cluster mean for primary branches/plant (12.90), lamina width (3.72 cm), leaf-stem ratio (1.46), spike length (23.95 cm) where as minimum cluster mean value was recorded for number of spikes/plant (63.80). The lowest cluster mean values for fresh herbage yield/plant (231.90 g), dry herbage yield/plant (48.99 g), essential oil content (0.17 %) and essential oil yield/plant (0.40 ml) were observed in Cluster VII. The genetic divergence studied in Ocimum species by earlier workers demonstrated a clear relationship between clustering pattern and geographical distribution (Vieira et al., 2001; Ahmad and Khalid, 2002; Vieira et al., 2003; Sharma, 2005).

Genetic diversity is an important component for a plant breeding programme. The hybrids derived from genotypes of diverse origin generally display greater heterosis then those between closely related genotypes. In addition to facilitate the selection of divergent parent for hybridization, genetic divergence analyses measures the degree of diversification and determine the relative proportion of each component character to the total divergence. The genotypes grouped together within a cluster are less divergent than the ones which are placed in different clusters. The clusters which are separated by the greatest distance show the maximum divergence. The genotypes which were grouped in a cluster were not consistent over the environments in all the seven clusters exemplifying great variations due to environments. Higher genetic variability is likely to be created when the crosses are made between selected parents from distant clusters than within cluster.

## Acknowledgements

The authors are highly grateful to the Director, National Bureau of Plant Genetic Resources (NBPGR), New Delhi, for providing permission and required facilities for executing the experiments. The authors are also thankful to Head, Plant Exploration and Germplasm Collection and Head, Germplasm Evaluation Division, NBPGR, New Delhi, for their generous help and critical suggestions from time to time.

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