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Analysis of genetic divergence in basil (*Ocimum* spp.)

Mayuri Sahu, A K Geda, Anjali Shrivastava & Prabha Nirmodh

Department of Plant Breeding and Genetics
Indira Gandhi Agricultural University
Raipur-492 006, Chattisgargh, India.

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Abstract

Analysis of 21 basil (*Ocimum* spp.) genotypes grown at Raipur (Chhattisgarh) revealed that a maximum of five genotypes were accommodated in clusters I and II followed by four genotypes in clusters III and V, and three genotypes in cluster IV. The intra-cluster distance between members of cluster IV was maximum followed by clusters I, II, III and V, suggesting that the genotypes in cluster IV were relatively more diverse.

Keywords: basil, cluster analysis, genetic divergence, *Ocimum* spp.

Basil (*Ocimum* spp.) has long been recognized as a diverse and rich source of cyto-taxonomical, genetical and chemical variability in different geographical races (Pushpangadan *et al*. 1979). However, not much effort has been made for its genetic improvement. Hence, the present study was undertaken to classify and understand the nature and magnitude of genetic diversity present in 21 indigenous basil genotypes available at Indira Gandhi Agricultural University, Raipur (Chhattisgarh).

The material for the present investigation included 21 genotypes/accessions of *Ocimum* spp. collected from different sources. These were grown in a complete randomized block design with three replications at Raipur, during the wet season of 2004. Appropriate management and cultural practices were undertaken. Each genotype was grown in plots of 3 rows of 2 m length at spacing of 45 cm between row and 30 cm between plants in a row. A uniform rate of fertilizer dose of NPK @ 60, 40, 40 kg ha^{-1} with farmyard manure @ 10 t ha^{-1} was applied. Observations were recorded in five randomly selected plants of each accession. The data were subjected to the Mahalanobis D^2 analysis (1936) to measure the genetic divergence.

The genotypes were grouped into a number of clusters. The criteria was that any two genotypes on an average showing lower D^2 value were grouped in the same cluster, while those showing high D^2 values were grouped into different clusters. Based on the relative magnitude of D^2 values, the 21 genotypes were grouped into five clusters (Table 1). A maximum of five genotypes were accommodated in clusters I and II followed by four genotypes each in clusters III and V, and three genotypes in cluster IV. The intra-cluster distance between members of cluster IV was maximum followed by clusters I, II, III and V, suggesting that genotypes in cluster IV were relatively more diverse. The minimum intra-cluster distance exhibited by cluster V indicated limited genetic diversity among the constituents genotypes (Table 2).

Table 1. Clustering pattern of 21 genotypes of basil

Cluster	No. of genotypes included	Genotype	Place of origin/adaptation
I	5	OCL-1	Neemuch (Madhya Pradesh)
		OCL-3, OCL-10	Akola, Pune (Maharashtra)
		OCL-11, OCL-12	Raipur (Chhattishgarh)
II	5	*O. sanctum*-1	RRL-Jammu (Jammu & Kashmir)
		O. kilimandscharicum-1	RRL-Jammu (Jammu & Kashmir)
		RRL-Og-14	RRL-Jammu (Jammu & Kashmir)
		O. kilimandscharicum-2	RRL-Jammu (Jammu & Kashmir)
		O. sanctum-2	Mandi (Himachal Pradesh)
III	4	OCL-4	Rajgarh (Madhya Pradesh)
		CIM-Shayam,	CIMAP (Uattar Pradesh)
		O. basilicum, RRL-OC-12	RRL-Jammu (Jammu & Kashmir)
IV	3	OCL-5	Raipur (Chhattishgarh)
		OCL-6	Palampur (Himachal Pradesh)
		OCL-8	Rewa (Madhya Pradesh)
V	4	OCL-2	Raipur (Chhattishgarh)
		OCL-9	Rajnandgaon (Chhattishgarh)
		OCL- 7	Jaipur (Rajasthan)
		RRL-OC-11	RRL-Jammu (Jammu & Kashmir)

Table 2. Mean intra- (diagonal and bold) and inter-cluster D^2 values of 21 genotypes of basil

Cluster	I	II	III	IV	V
I	**2.492**				
II	3.859	**2.396**			
III	3.582	3.247	**2.203**		
IV	5.461	4.249	4.021	**2.779**	
V	3.238	4.350	3.601	4.386	**2.046**

The relative divergence of each cluster from the other cluster (inter-cluster distance) indicated greater divergence between cluster I and IV (D^2=5.461) followed by cluster IV and V (D^2=4.386), cluster II and V (D^2=4.350) and cluster II and IV (D^2=4.249). The selection of diversed genotypes from these clusters would produce a broad spectrum of variability for oil yield, which may enable further selection and improvement of yield components. The hybrids developed from the selected genotypes within the limits of compatibility of these clusters, may produce high magnitude of heterosis or desirable trangressive segregants, which would be rewarding in a breeding programme. Due emphasis in breeding programme should be given to genotypes OCL-3 and OCL-11 of cluster I; OCL-5 and OCL-8 of cluster IV; RRL-OC-11 and OCL-7 of cluster V. Crosses among parents having genetic divergence are likely to yield desirable combinations therefore, a crossing programme should be initiated between genotypes belonging to different clusters. Particular genotypes may be selected from selected clusters for consideration as parent in crossing schemes. There was a wide range of variation in cluster mean values for most of the traits except number of inflorescence plant^{-1} (Table 3). The maximum and minimum mean value for characters were, days to 50% flowering: 51.44 (IV) and 84.80 (II); days to maturity: 124.54 (V) and 178.67 (II); plant height: 66.32 (I) and 97.18 (IV); number of primary branches plant^{-1}: 6.11 (IV) and 13.42 (V); number of secondary branches plant^{-1}: 3.20 (II) and 9.58 (III); length of inflorescences: 8.39 (IV) and 16.46 (I); plant spread: 64.52 (II) and 80.74 (V); dry plant biomass: 155.23 (I) and 293.11 (IV); fresh plant biomass: 328.17 (I) and 814.67 (IV); acid value of oil: 1.85 (III) and 5.16 (I); ester value of oil: 17.11 (IV) and 46.32 (V) and

Table 3. Cluster means for various quantitative characters of basil

Cluster	No. of genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches plant $^{-1}$	No. of secondary branches plant $^{-1}$	No. of inflorescences branch $^{-1}$	Length of inflorescences (cm)	Plant spread (cm)	Dry plant biomass (g)	Fresh plant biomass (g)	Acid value of oil	Ester value of oil	Oil content (%)
I	5	62.00	129.27	66.32	13.07	8.00	3.87	16.46	69.20	155.23	328.17	5.16	29.32	0.46
II	5	84.80	178.67	77.49	9.67	3.20	4.13	11.59	64.52	224.57	607.70	4.10	18.81	0.61
III	4	75.92	155.17	77.17	11.33	9.58	3.58	14.91	69.84	260.67	749.53	1.85	20.41	0.38
IV	3	51.44	129.89	97.18	6.11	5.00	2.56	8.39	73.91	293.11	814.67	4.87	17.11	0.55
V	4	52.08	124.50	70.72	13.42	5.75	3.33	13.20	80.74	187.81	635.38	1.93	46.32	0.55

essential oil per cent: 0.38 (III) and 0.61 (II), respectively. This indicated that while planning hybridization programmes, genotypes like OCL-3 and OCL-11 from cluster I (for characters such as dwarfness, length of inflorescence and acid value of oil); OCL-5 and OCL-8 of cluster IV (for tallness, earliness, dry and fresh plant biomass); RRl-OC-11 and OCL-7 of cluster V (for primary branches plant-1 and ester value of oil) and genotypes *O. kilimandscharicum*-1 and *O. kilimandscharicum*-2 of cluster II (for oil %, number of inflorescence plant^{-1}, least number secondary branches plant^{-1}, least plant spread); are expected to give promising and desirable recombinants in segregating generations as they possess desirable features as seen from their cluster means.

References

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