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Genetic divergence in lemongrass [*Cymbopogon flexuosus* Steud (Wats)]

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Abstract

Genetic divergence analysis among forty three clones of lemongrass, *Cymbopogon flexuosus* [Steud {Wats}] was carried out through study of tiller number, plant height, leaf length, leaf width, leaf sheeth, leaf sheeth, leaf blade, leaf yield, oil content and oil yield in research farm of field station Pant Nagar of Central Institute of Medicinal and Aromatic Plants, Lucknow. All the clones were grouped in nine clusters. AH-10-19 did not cluster with any clone and formed a separate cluster. Intracluster distance was highest for cluster I which included largest number of clones. Cluster IX has shown largest intercluster distance with cluster VII followed by cluster VI, cluster II, cluster IV and III. With an aim to get maximum chance of transgressive segregants, developing of polycross among AH-10-19 and one clone from each cluster, V, VII, VI and I was suggested.

Key words : Lemongrass, *Cymbopogon flexuosus*, genetic divergence, citral

Introduction

Lemongrass is native to India and has spread in some parts of China, WestIndies and Central and South America. It is a cross pollinated grass and is being cultivated through clones for fresh leaves which gives essential oil on steam/hydro distillation. It's oil is a rich source of citral {nerol + gereniol}. Some of the chemotypes are reported to be rich in gereniol, methyl euginol, and α bisabolol [1-3]. These chemicals are of high value for the production of ionones and β ionones for the synthesis of many aromatic compounds and vitamin 'A'.

India had been producing essential oil to the tune of 1700 tons (1963-64) but current level of production has come down to 200 tons. One of the major constraints of reduced production was limited genetic knowledge and non availability of superior cultivars for wide adaptation. In the process of genetic improvement a number of clones which constitute the basis of future breeding programme were developed. For effective use of these clones as superior genotypes to be polycrossed with the expectation of getting potential transgressive segregants, knowledge of genetic divergence among clones is desired. Mahalanobis D^2 statistics which is a powerful tool in discerning genetic divergence among groups based on actual expression of multiple characters was applied to estimate the nature and magnitude of genetic diversity among clones.

Materials and methods

Forty clones developed from a polycross of selected clones from Kodaikanal, Orissa and Lucknow with three released cultivars of lemongrass - *Pragati* and *Praman* (selection from OD-19 in north Indian plain conditions) and *Kavery* (selection from OD-19 in Southern plateau region) were evaluated during 1997-98 in the research farm of Field Station Pant Nagar, U. S. Nagar of Central Institute of Medicinal and Aromatic Plants, Lucknow. Ten slips (vegetative propagules) from each clone were space planted during July, 1997 at a distance of 60 × 60 cm in three replications in complete randomized block design.

Uniform cultural practices viz., hoeing, weeding, irrigation and fertilizer application (@160 N:80 P: 60 K/ha/year) were followed to grow the crop. Observations were recorded on number of tillers per plant (hill), plant height (cm), length of sheeth (cm), width of lamina (cm), leaf blade : leaf sheeth (length), leaf yield (g) and percent oil content (v/w) in fresh herb during October 1997, March, 1998 and July, 1998 on three randomly selected hills from each replication in each treatment. Oil content estimations were done in clavenger type apparatus from pooled samples of each clone in each replication. Oil yield per plant (hill) was calculated from herb yield and percent oil content. The analysis of genetic divergence using Mahalanobis D^2 was carried out. On the basis of magnitude of D^2 values clones were grouped into clusters by Tocher's method [2].

Results and discussion

The test of significance for multiple measurements using 'V' statistics (1665.75) which utilized Wilk's criterion confirmed significant differences among the cultivars and suggested the adequacy of continuing of D^2 analysis.

D^2 values computed for all possible 903 pairs ranged from 1.369 (between AH-7 and AH-15) to 924.429 (between AH-1 and AH-1019). All the genotypes were grouped in nine clusters (Table 1). Cluster I containing sixteen genotypes was the biggest cluster. *Pragati* and *Praman* (selected from OD-19 in North Indian plain conditions) developed in CIMAP, Lucknow, reflecting similarity with the biggest group, occupied their positions in the cluster I. Cluster II accommodated eight genotypes including *Cavery* (selected from OD-19 in Southern Plateau conditions). Cluster III and cluster IV, each included four genotypes. Cluster V and cluster VI each had only three clones. AH-1 and AH-40 and AH-5 and AH-16 formed separate clusters showing considerable amount of diversity.

Table 1. Clustering pattern of 43 genotypes on the basis of genetic divergence in lemongrass

Cluster number	Number of genotypes	Genotypes included
I	16	AH-7, AH-11, AH-12, AH-23, AH-14, AH-15, Pragti, AH13, AH-27, AH-29, AH-26, AH-28, AH-30, AH-34, AH-39 and Praman
II	8	AH-10-3, AH-4, AH-20, AH-21-5, AH-22-7, AH-24, Kavery, AH-33
III	4	AH-5-25, AH-5-41, AH-5-42, AH-5-43
IV	4	B-13-2, AH-6, AH-17, AH-36
VI	3	AH-5-18, BH-31, C-35
VII	3	B-3-8, C-3-9, B-2-10
VII	2	AH-1, AH-40
VIII	2	AH-5, AH-16
IX	1	AH-10-19

AH-10-19 did not cluster with any of the genotypes and formed a separate cluster. Clustering of clones derived from a common female of the polycross progeny together in one cluster (cluster III-AH-5-25, AH-5-41, AH-5-42-all selections from Half-sib family AH-5) have suggested the influence of the female parentage. Random distribution of some of the clones in most diverge groups were also observed. AH-10-3 derived from the half-sib family AH-10 did not cluster with its other half-sibs indicating the influence of genetic dissimilarities among the parents included in the polycross. The grouping of *Pragati* and *Praman* in cluster I with a large number of clones derived from the polycross of genetic material obtained from different pools suggested that the parentage of these varieties were very close to the present material.

Table 2. Average inter and intracluster D^2 values among nine clusters in lemongrass

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
Cluster I	*65.66*	109.08	134.43	200.61	134.81	161.61	231.63	93.04	324.60
Cluster II		*49.67*	77.78	191.68	284.47	77.52	92.48	147.26	619.48
Cluster III			*28.92*	375.72	217.62	179.52	87.67	262.13	606.59
Cluster IV				*29.61*	475.20	123.94	383.01	62.12	619.46
Cluster V					*38.50*	425.72	417.27	252.08	144.88
Cluster VI						*54.57*	140.07	136.94	750.50
Cluster VII							*52.72*	341.71	888.15
Cluster VIII								*34.92*	358.00
Cluster IX									*00.00*

Table 3. Cluster mean of nine characters in lemongrass

Cluster	Plant height (cm)	Tiller number	Length of sheeth (cm)	Leaf width (cm)	Leaf length (cm)	Blade sheath	Leaf yield (g)	Oil content (%)	Oil yield (g)
Cluster I	2.43±2.15	188.4±2.93	46.4±0.93	2.02±0.64	136.7±3.21	2.98±0.10	329.8±14.34	0.45±0.02	1.36±0.09
Cluster II	21.24±2.28	168.0±3.11	42.3±1.27	1.77±0.75	125.7±2.42	2.98±0.09	188.6±19.65	0.49±0.04	0.91±0.13
Cluster III	29.33±1.60	148.1±2.44	39.6±0.49	1.67±0.60	111.1±2.33	2.81±0.07	224.9±20.70	0.45±0.06	1.14±0.09
Cluster IV	19.41±1.72	208.6±1.42	51.7±2.18	1.86±0.24	156.9±2.44	3.05±0.17	226.2±11.31	0.44±0.07	0.82±0.10
Cluster V	42.00±3.06	182.6±2.55	42.6±2.50	2.08±0.80	139.9±3.01	3.30±0.23	411.6±10.32	0.48±0.08	2.45±0.35
Cluster VI	16.66±3.24	174.2±6.64	49.3±.2.88	1.98±1.13	124.8±5.15	2.51±0.15	105.7±9.92	0.55±0.05	0.57±0.05
Cluster VII	14.99±0.34	147.2±.5.37	36.0±0.0	1.63±0.33	109.6±7.00	2.94±0.30	133.5±1.75	0.71±0.12	0.91±0.11
Cluster VIII	27.00±1.0	203.8±4.5	50.3±0.67	2.05±1.5	153.3±5.00	3.05±0.14	297.1±21.17	0.29±0.07	1.20±0.29
Cluster IX	46.00±0.0	217.6±0.0	48.0±0.0	2.36±0.0	169.6±0.0	3.53±0.0	721.0±0.0	0.46±0.0	3.33±0.0

Intra-cluster value was minimum (0) where only one clone (AH-10-19) represented the cluster (IX). Highest value (65.65) was obtained in cluster I which included largest number of clones, followed by cluster VI, cluster VII, cluster II and cluster V (Table 2). Cluster IX has shown the highest intra-cluster distance with cluster VII (888.15) followed by cluster VI (750.50), II (619.48), IV (619.46) and III (606.59). Other than cluster IX, cluster V was divergent to cluster IV and cluster VII. Cluster II was closest to VI and cluster III.

While considering the genetic diversity for selection of clones to be included in polycross programme, cluster mean for oil yield and its major components should also be considered. Cluster IX consisting of AH-10-19 has established its separate identity exhibiting highest oil yield followed by cluster V and cluster I (Table 3). This cluster has further expressed highest mean values for number of tillers, plant height and leaf yield. Maximum oil content was observed in cluster VII followed by cluster VI and cluster V. Cluster I, which consisted major number of clones showed average performance as none of the characters occupied extreme positions. With an aim to create maximum possibility of getting transgressive segregants of practical utility, an emphasis should be given to include AH-10-19 and atleast one clone from each cluster V, VII, VI and I for developing a polycross. Breeding programme on similar lines were also suggested in lavender [1] to recover potential transgressive segregants for desired traits from crosses involving divergent parents.

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