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Genetic Divergence in Sunnhemp [*Crotalaria juncea* (L.)]

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ABSTRACT

Background: Sunnhemp is a very important green manuring crop. The crop is utilized for various purposes like reducing soil erosion, improving soil properties and recycling plant nutrients. The knowledge regarding the crop is still not exploited, due to lack of research in this crop. So, the present study was conducted to know the extent of genetic diversity present in the crop. From the divergence analysis, it may be concluded that the genotypes belonging to different clusters separated by high estimated statistical distance may be used in the hybridization programme for developing high green biomass yielding sunnhemp varieties.

Methods: A field experiment was conducted at the research farm of Department of Genetics and Plant Breeding, Navsari Agricultural University, Navsari, Gujarat with thirty sunnhemp genotypes to know the extent of genetic diversity by D^2 analysis in a randomized block design during late *Kharif* 2017.

Result: The analysis was conducted for D^2 analysis and was concluded from D^2 analysis that, the characters *viz*., days to 50% flowering, fresh weight of root nodules per plant, fresh weight of plant, root nodules per plant, leaf length, root length, dry weight of root nodules per plant, C: N ratio, internodes per plant, plant height and stem diameter contributed towards the genetic divergence. Traits like primary branches per plant and leaf area didn't contribute towards genetic divergence. The thirty genotypes were grouped into seven clusters following Tocher's method (Rao, 1952). The cluster III was largest having eleven genotypes. Cluster IV and cluster II was second largest which contained seven and five genotypes respectively. Cluster I and cluster V contained three and two genotypes respectively, cluster VI and VII had only one genotype. The intra cluster distance was more in cluster III and the inter cluster distance was maximum between cluster V and cluster VII.

Key words: Cluster distance, Cluster mean, Genetic diveregence, Grouping, Sunnhemp.

INTRODUCTION

(*Crotalaria juncea* L.) (2n=16) is an important crop known for its high quality fibre. The native of the crop is India. It is utilised for crop rotation as well as fodder. The crop is traditionally used for making ropes, strings, twines, floor mat, fishing nets, hand-made paper, *etc*. in cottage industry. Apart from these industrial values, the crop being a legume is advantageous to grow on poor fallow or freshly reclaimed soil where its major role would be soil builder or renovator as well as deterrent to nematode.

Diversification of the selected parents is very essential for successful completion of any breeding programme. The desirable recombinants can only be obtained when we select the diversified parents based on the knowledge of genetic diversity. In view of this, the investigation was under taken to elicit the information with the objective to know the genetic divergence existing in the Crotolaria germplasm.

MATERIALS AND METHODS

Thirty genotypes of sunnhemp collected from various locations throughout the country was used for this study. The thirty genotypes were planted at the research farm of Department of Genetics and Plant Breeding, N. M. College of Agriculture, Navsari Agricultural University, Navsari during late *kharif* 2017. The experiment was laid using randomized block design with three replications. There was a single row of 3 m length for each genotype in each replication grown at a spacing of 30 cm between rows and 10 cm between plants within the row was maintained for the crop. In order to avoid the damage and border effects the experiment was surrounded by two guard rows. All the recommended package of practices was followed for the crop. Data was collected from five randomly selected plants tagged from each accession. The data was collected on characters *viz*., days to 50% flowering, plant height, internodes per plant, primary branches per plant, stem diameter, leaf area, leaf length, root length, fresh weight of plant, C:N ratio, root nodules per plant, fresh weight of root nodules per plant and dry weight of root nodules per plant (g).

The mean data was subjected to statistical analysis Mahalanobis D^2 (1928) statistics was utilized for genetic divergence. The test of significance of the correlated

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variables were done following Rao (1948) using 'V' statistic which in turn utilizes Wilk's criterion. According to Rao (1952) the different genotypes were grouped into different clusters and the relative contribution of different characters towards total divergence was calculated following Singh and Choudhury (1985).

RESULTS AND DISCUSSION

The data was collected on characters *viz*., days to 50% flowering, plant height, internodes per plant, primary branches per plant, stem diameter, leaf area, leaf length, root length, fresh weight of plant, C:N ratio, root nodules per plant, fresh weight of root nodules per plant and dry weight of root nodules per plant (g) and subjected to multivariate analysis using wilk's criterion for thirty genotypes of sunnhemp. The analysis of variance showed that the genotypes under study differed significantly among themselves for all the thirteen characters indicating the presence of diversity among the genotypes. Thirty genotypes of sunnhemp were grouped into seven clusters. The composition of cluster is given in Table 1. Cluster III was largest having eleven genotypes. Cluster IV and cluster II was second largest which contained seven and five genotypes respectively. Cluster VI and VII consisted of only one genotype. The genotypes belonging to different clusters indicate far relatedness while genotypes belonging to same cluster indicate more closely relatedness. Cluster consisting of only one genotype provide the information that the genetic constitution of the genotype belonging to the cluster is totally different from the all genotypes present in the study. According to Win *et al*. (2011), due to different genetic constitution of various genotypes the intra and inter cluster distances are arising.

Average intra cluster distance ranged between 0.00 and 3.56 (Table 2). The intra cluster distance indicates the closeness of the genotypes falling in the same cluster. The clusters exhibiting an intra cluster distance of 0.00 reveal to be monogenotypic and less heterogeneous. While the high intra cluster D^2 values indicate more genetic divergence between genotypes belonging to the same cluster and therefore more heterogeneous. Cluster III pertained highest intra cluster distance (3.56) followed by cluster IV (3.28) and cluster V (3.06). Success of the hybridization followed by selection depends largely on the choice of parents showing high genetic diversity for traits of interest (Murthy and Arunachalam, 1966). Therefore, such intra cluster heterogeneity among the constituents' genotypes obtained in the present experiment might serve as guideline to choose parents for the recombination breeding programme.

Average inter cluster distance ranged between 4.03 and 9.66. The maximum inter-cluster distance (D= 9.66) was found between clusters V and VII carrying two and one genotypes followed by the clusters between II and VII (D= 9.26) and II and IV (D= 8.43). The minimum inter-cluster distance (D= 4.03) was found between clusters II and V. It indicated that these cluster pairs were most divergent or in other words, the genotypic constituent of these cluster pairs comprised the genes from most distantly related parents in respect of the characters studied. The genotypes belonging to different clusters separated by high estimated statistical distance can be utilized in the hybridization programme for crop improvement as well as for studying the inheritance pattern of different characters in sunnhemp. Considering the individual genotype, those belonging to the cluster III (NVS-18, NVS-19, NVS-9, NVS-10, NVS-23, NVS-17, NVS-22, NVS-21, NVS-16, NVS-8, NVS-14), cluster IV (NVS-2, NVS-4, NVS-6, NVS-5, NVS-7, NVS-1, NVS-3), cluster II (NVS-28, NVS- 29, NVS-27, NVS-30, NVS-25), cluster I (NVS-11, NVS-12, NVS-13) and cluster V (NVS-24, NVS-26) were found most divergent from those which belonged to cluster VI (NVS-15) and cluster VII (NVS-20). The above results further reveal that considering individual character the genotypes were more divergent than that considering a constellation of characters.

Since improvement in green biomass and other related characters is the basic objective in the breeding programme

Table 1: Composition of sunnhemp genotypes into seven different clusters by Mahalanobis's D^2 statistic.

Cluster no.	No. of genotypes	Genotypes included
III	11	NVS-18, NVS-19, NVS-9, NVS-10, NVS-23, NVS-17, NVS-22, NVS-21, NVS-16, NVS-8, NVS-14
IV	7	NVS-2, NVS-4, NVS-6, NVS-5, NVS-7, NVS-1, NVS-3
II	5	NVS-28, NVS- 29, NVS-27, NVS-30, NVS-25
I	3	NVS-11, NVS-12, NVS-13
V	2	NVS-24, NVS-26
VI	1	NVS-15
VII	1	NVS-20

Table 2: Average inter and intra cluster (D^2) values for thirty genotypes of sunnhemp.

Cluster no.	I	II	III	IV	V	VI	VII
I	1.68	5.77	4.91	6.97	5.18	4.79	6.98
II		3.00	5.90	8.43	4.03	7.16	9.26
III			3.56	5.46	6.20	4.39	5.06
IV				3.28	7.68	4.81	6.91
V					3.06	6.33	9.66
VI						0.00	5.70
VII							0.00

Table 3: Cluster means for thirteen characters in sunnhemp.

Characters / Clusters	Days to 50% flowering	Plant height (cm)	Internodes per plant	Primary branches per plant	Stem diameter (cm)	Leaf length (cm)	Leaf area (cm^2)	Root length (cm)	C:N ratio	Root nodules per plant	Fresh weight of root nodules per plant (g)	Dry weight of root nodules per plant (g)	Fresh weight of plant (g)
I	66.00	**166.67**	37.89	4.22	**2.80**	**10.78**	**7.67**	**36.44**	**30.58**	12.00	2.88	**1.27**	83.44
II	**81.13**	155.53	37.87	3.47	2.67	8.60	7.13	30.93	24.21	12.27	**3.19**	1.26	66.47
III	64.52	154.58	35.58	3.79	2.42	9.18	6.82	32.27	24.67	10.85	2.84	1.15	59.67
IV	63.90	155.33	35.10	3.62	2.40	10.57	5.95	32.86	23.65	**6.86**	**1.87**	**0.78**	66.52
V	80.50	157.67	40.50	4.17	2.28	**8.50**	7.00	**30.50**	24.02	11.83	2.70	1.16	82.83
VI	63.00	**149.00**	**40.67**	**3.00**	**2.03**	10.67	**5.33**	30.67	25.13	10.00	2.85	1.09	**85.67**
VII	**50.00**	155.67	**34.67**	**4.33**	2.50	9.67	7.00	31.00	**23.03**	**13.00**	3.11	1.20	**50.33**

Note: Bold figures are minimum and maximum value.

for sunnhemp, so cluster means for fresh weight of plant and its major components need to be considered for selection of genotypes. The means for fresh weight of plant varied from 50.33 in cluster VII to 85.67 in cluster VI (Table 3). The means for fresh weight of root nodules per plant varied from 1.87 (cluster IV) to 3.19 (cluster II). The results clearly indicated appreciable difference among cluster means for most of the characters. As far as cluster means are concerned, greater range of mean values among the clusters was recorded for different traits. The cluster I revealed maximum values for plant height, stem diameter, leaf length, leaf area, root length, C:N ratio and dry weight of root nodules per plant comprising of NVS-11, NVS-12 and NVS-13. The cluster means for different character further indicate that cluster II comprising of NVS-28, NVS- 29, NVS-27, NVS-30 and NVS-25 showed second highest cluster mean for four different characters like stem diameter, leaf area, root nodules per plant and dry weight of root nodules per plant The cluster II had high mean value for days to 50% flowering and fresh weight of root nodules per plant. The cluster VI had high mean value for internodes per plant and fresh weight of plant. The cluster VII had high mean value for primary branches per plant and root nodules per plant. Cluster VII had minimum mean value for days to 50% flowering, internodes per plant, C:N ratio and fresh weight of plant. Cluster VI had minimum mean value for plant height, primary branches per plant, stem diameter and leaf area. Cluster V had minimum mean value for leaf length and root length. Cluster IV had minimum mean value for root nodules per plant, fresh weight of root nodules per plant and dry weight of root nodules per plant. The above results thus indicated that there was no cluster containing genotypes with all the desirable characters which could be directly selected and utilized. Interestingly, most of the minimum and maximum mean values were distributed in relatively distant clusters. Recombination breeding between genotypes of different clusters has been suggested by Sonawane and Patil (1991).

The analysis on contribution of various characters towards the expression of genetic divergence indicated that the characters *viz*., days to 50% flowering (31.26%), fresh weight of root nodules per plant (18.16%), fresh weight of plant (17.93%), root nodules per plant (17.70%), leaf length (7.36%), root length (2.99%), dry weight of root nodules per plant (2.53%), C:N ratio (1.15%), internodes per plant (0.46%), plant height (0.23%) and stem diameter (0.23%) contributed very much towards genetic divergence in the present material (Table 4). The traits like primary branches per plant and leaf area didn't contribute towards genetic divergence. Similar results were obtained by Navneet *et al*. (2017) for primary branches per plant, Pawar *et al*. (2013) for days to 50% flowering and Mishra and Singh (2012) for plant height.

Table 4: Contribution of thirteen characters towards total genetic divergence.

Characters	Number of times appearing First	% contribution towards divergence	Rank
Days to 50% flowering	136	31.26%	Ist
Plant height (cm)	1	0.23%	Xth
Internodes per plant	2	0.46%	IXth
Primary branches per plant	0	0.00%	0.00
Stem diameter (cm)	1	0.23%	Xth
Leaf length (cm)	32	7.36%	Vth
Leaf area (cm^2)	0	0.00%	0.00
Root length (cm)	13	2.99%	VIth
C:N ratio	5	1.15%	VIIIth
Root nodules per plant	77	17.70%	IV^{rth}
Fresh weight of root nodules per plant (g)	79	18.16%	IInd
Dry weight of root nodules per plant (g)	11	2.53%	VIIth
Fresh weight of plant	78	17.93%	IIIrd

CONCLUSION

The results showed that hybridization among genotypes of these cluster combinations is expected to enhanced variability. Apart from the high divergence, the performance of the genotypes and the characters with maximum contribution towards divergence should also be given due consideration which appears as desirable for inclusion for improvement in sunnhemp. Hence, apart from selecting genotypes for the clusters which have high inter-cluster distance for hybridization, selection of parents based on extent of genetic divergence in respect to a particular character of interest can also be thought. This is to mean that, if breeder's intention is to improve green biomass yield selection of parents which are highly divergent with respect to these characters can be selected.

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