table Fe content of fresh tissue was the physiologically active fraction and this correctly reflected the Fe status of the plant. The genotypic variation in absorption and utilisation of Fe among groundnut and blackgram cultivars was clearly understood here.

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GENETIC DIVERGENCE FOR YIELD AND ITS COMPONENTS IN COMMON MILLET (*Panicum miliaceum* L.)

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ABSTRACT

A set of eighty two different strains of common millet (*Panicum miliaceum*) collected from different places was used for estimation of genetic divergence. D^2 estimates based on 12 characters support that the differences in agroclimatic situations are not necessarily related to genetic divergence and thus the desirable diverse parents may not be selected for hybridization on the basis of climatic regions.

KEY WORDS: Genetic divergence, D^2 statistic, Millet.

Plant breeders have been appreciating the importance of genetic diversity since long. However, the main problem is to recognise and measure such diversity in order to use it in a breeding programme. Selection of

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parents based on individual attribute may not be as advantageous as that based on a number of important componenls collectively, particularly when the aim is to provide improvement in a complex quantitative trait such as seed yield. For measuring genetic diveristy, D^2 statistic has already been proved as a powerful tool. Therefore, the present study aims at determining the genetic divergence in common millet. (*Panicum miliaceum L.*).

MATERIALS AND METHODS

Genetic stock of 82 strains was grown in a randomised block design at Kanpur for two years (1982 and 1983). Data were recorded on plot basis in each of the three replications. D^2 estimates based on 12 characters were used in obtaining the clustering pattern and inter and intracluster distances. Clusters of related genotypes were prepared following Tocher's method (Rao, 1952) by pooled analysis of two years data.

RESULTS AND DISCUSSION

Clustering pattern of 82 genotypes furnished in Table 1 indicated that the cluster 1 retained maximum number of genotypes (51). It is thus evident that the genotypes falling in this group are not much genetically divergent. Cluster VII was the smallest group as it included two genotypes namely ICC-11 and ICC-59. Genotypes grouped in cluster II were also found genetically much divergent from those of cluster 1.

TABLE 2 ·Composition of clusters based on D^2-statistic in common millet.

Clusters	Total number	Genotypes
I	51	ICC 1, 1A, 2, 2A, 3, 5, 7, 8, 9, 10, 12, 15, 16, 17, 18, 31, 35, 37, 42, 44, 49, 52, 57, 78, 80, 84, 92, 96, 107, 108, 116, 118, 120, 121, 123, 124, 125, 127, 128, 129, 130, 132, 133, 134, 135, 137, 140, 145, 149, 150
II	10	ICC 4, 30, 47, 60, 71, 111, 113, 115, 122, 142
III	5	ICC 25, 43, 94, 109, 160
IV	6	ICC 6, 20, 40, 41, 54, 105
V	4	ICC 91, 97, 136, 148
VI	4	ICC 32, 75, 101, 130
VII	2	ICC 11, 59

If intra and intercluster distances are taken into consideration, the highest magnitude of genetic distance was observed between clusters III and VII (18.74). This clearly indicates that the strains included in these clusters are having broad spectrum of the genetic diversity (Table 3). Consequently it is suggested that these genetically different lines may be used in hybridiza-

Table 2. Intra cluster group means for 12 characters in common millet.

Characters / Cluster	Plant height	No. of tillers per plant	Length of main spike	No. of penicles per main spike	No. of nodal tillers per plant	Biological yield per plant	No. of seeds per main spike	1000 grains weight	Harvest Index	Days to flowering	Days to maturity	Grain yield per plant
I	66.13	1.82	21.94	7.70	4.55	10.43	360.27	6.70	43.37	38.56	61.66	4.50
II	66.62	1.69	22.30	8.00	4.70	10.20	327.00	7.20	46.30	33.70	59.60	4.50
III	70.74	2.04	23.20	7.80	5.40	13.00	371.00	5.60	43.60	42.00	70.00	5.00
IV	64.26	1.85	23.00	8.00	4.50	10.16	285.50	6.33	42.83	40.66	66.16	4.00
V	55.17	2.01	21.50	8.00	4.25	10.75	355.50	7.25	38.50	39.75	58.25	4.25
VI	58.08	1.81	22.75	8.50	5.00	9.00	326.75	8.00	46.00	32.75	64.00	4.25
VII	58.48	1.70	20.93	7.27	4.27	8.18	251.01	4.91	37.51	35.50	58.00	3.68

tion for obtaining the desirable recombinants in order to develop high yielding cultivars. Lowest intracluster value for cluster IV indicated that the varieties included in the group showed less variability as compared to the varieties

TABLE 3 Average intra-and intercluster distances

Cluster	I	II	III	IV	V	VI	VII
I	(5.44)	7.98	10.54	6.79	7.90	12.63	10.24
II		(4.69)	11.79	8.72	11.61	8.33	11.71
III			(4.72)	5.91	15.30	11.08	18.74
IV				(3.61)	11.37	10.54	14.35
IV					(5.61)	17.63	7.41
V						(4.96)	18.44
VI							(4.03)

(Average intracluster distances are given in parenthesis).

included in cluster V which showed maximum divergence within the group.

The comparison of cluster means for 12 characters under study marked considerable genetic differencess between the groups (Table 2). Cluster III was attributed as a group of highest mean value for almost all the characters except panicles number, 1000 grains weight and harvest index. On the other hand, cluster VII indicated minimum mean value in respect of all the characters except tillers number, nodal tillers and days to heading. Clusters I and IV neither exhibited the highest mean value nor the lowest one for any of the characters taken into study. Therefore, characters like biological yield, seed number, 1000 grain weight, harvest index and maturity period which contribute maximum to the total divergence should form the criteria for selection of parents for hybridization. The yield potential of parents may also be taken into consideration. The study indicates that the genotypes showing variation may be considered for selection to be involved in hybridization programme for improvement purposes, irrespective of geographical consideration.

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