The Pharma Innovation Journal 2022; 11(4): 1888-1893

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(4): 1888-1893

www.thepharmajournal.com
Received: 03-02-2022
Accepted: 09-03-2022

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Study of genetic diversity in finger millet (*Eleusine coracana* (L.) Geartn.) Genotypes

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Abstract
Multivariate analysis is a crucial statistical tool which enables us to easily assess critical polygenic characters which are of great importance in a plant breeding programme. The present experiment was conducted during *Kharif* 2020 and 2021, with 50 germplasm accessions of finger millet at C.S.A. University of Agriculture & Technology, Kanpur in a randomized block design. The present investigation was carried out to assess the extent of genetic diversity analysis to identify the superior genotypes for yield and protein content. The observations for fifteen characters were recorded as well as multivariate technique; cluster analysis was applied. The fifty genotypes were grouped into eight distinct clusters on the basis of Euclidean distance. Cluster IV included maximum number of genotypes (fifteen) followed by Cluster I with nine genotypes; Cluster III with seven genotypes; Cluster VIII with five genotypes, Cluster VII with two genotypes and Cluster II, Cluster V, Cluster VI with four genotypes each, indicating wide diversity. The maximum inter-cluster distances for grain yield were recorded between Cluster IV and VIII followed by Cluster III and VIII, Cluster I and VII, Cluster II and VII and Cluster V and IV indicating the presence of wide diversity between these clusters therefore the use of genotypes from these clusters would serve as potential parents for hybridization. Plant height contributed the most towards genetic divergence in fifty genotypes of finger millet, indicating the presence of wide variability for this trait among the studied genotypes. Cluster III had highest maximum cluster means for most of the desirable characters *viz*., harvest index, 1000grain weight, protein content and grain yield per plant. Considering the high inter-cluster distances, cluster means and mean performance of genotypes, crossing of entry of clusters III with entries of cluster VI and VII would be fruitful for obtaining transgressive segregants for developing high yielding, high protein containing and better quality finger millet varieties.

Keywords: Finger millet, diversity, cluster analysis

Introduction
Millets is a collective term used for some members of graminae family, having coarse nature of grains. Finger millet (*Eleusine coracana* (L.) Geartn.), commonly known as Ragi/nutritious millet is nutritionally superior over other cereals. The word ragi is derived from Sanskrit word "Rajika" meaning red. The cultivated Eleusine coracana is an allotetraploid (2n = 4x = 36, AABB), evolved from *E. indica* (AA) and *E. floccifolia* or *E. tristachya* (BB) which has a genome size of 1,593Mb. It is a self-pollinated annual herbaceous plant that belongs to the family Poaceae, genus Eleusine. It is one of the important hardiest subsistence food crop largely grown in the arid and semi-arid areas of Africa and Asia. Being rich in protein and calcium, it serves as an important food source for rural population residing in developing tropical countries where calcium deficiency and anemia are chronic. It consists of almost all nutrients like protein (9.2 per cent), carbohydrates (76.32 per cent), methionine, and fat (1. per cent). It is also rich in minerals (2.70 per cent) such as calcium (452 mg/1000g), iron (3.90 mg/100g) and ash (3.90 per cent) which are core ingredients of a normal human diet (Pandey and Kumar, 2005) [16]. Calorific value of Ragi is 29 and per 100gms of it provides 345 calories of energy. Thus it shares a pivotal status in food habits of rural folk across the entire country and is colloquially referred to as "poor man's food". It is effective against measles, pleurisy, pneumonia and small pox. It is also recognized for numerous health beneficial effects *viz*; anti-diabetic, anti-tumerogenic, atherosclerogenic effects, anti-oxidant and antimicrobial properties. The dietary fibre, minerals, phenolics and vitamins concentrated in the outer layer of the seed coat offer high nutritional and health benefits (Chandra *et al*., 2016) [3].

Apart from its nutritional attributes, finger millet has excellent environmental sustainability credentials. It has long shelf life traits and is valuable in areas where farmers suffer huge losses due to dearth of post-harvest management (Kumar *et al*., 2016) [11].

Looking at the multiple utilities of this particular crop, enhancing its productivity needs to be the center of attention in forthcoming crop improvement programmes. One of the means to boost its production and productivity is by identification and development of the improved genotypes with wider adaptability over environments factoring the knowledge of variability, inheritance, direction and magnitude of association between various traits. The progress in breeding for yield and yield contributing characters of any crop is genetically controlled, environmentally influenced and determined by the magnitude and nature of its genetic variability (Wright, 1921 and Fisher, 1936) [22, 7].

In India, finger millet is grown over an area of 1.19 million hectares with an annual production of 1.20 million tonnes and average productivity of 1.66 tonnes ha^{-1}. Enhancement of economic yield is the prime objective in all plant breeding programmes. But yield has low heritability and direct selection for yield is not sufficiently effective. Therefore, knowledge of association among the yield attributing characters is useful to breeders for the improvement as it significantly affect the methods of selection (Mishra *et al*., 1980) [13]. Genetic improvement through conventional breeding approaches depends mainly on the availability of the diverse germplasm and the amount of genetic variability present in the population (Arun *et al*., 2008) [1]. A method suggested by Mahalanobis (1936) [12] known as "Mahalanobis D^2 statistics" is a powerful tool for quantifying the divergence between two populations. Therefore, the present study was undertaken to assess the nature and magnitude of genetic divergence for yield and its component in finger millet and also to identify divergent parents from distantly related clusters for suitable hybridization through genetic divergence analysis.

Material and Methods

The present investigation was carried out during *Kharif* 2020 and 2021 at C.S. Azad University of Agriculture & Technology, Kanpur using Complete Randomized Block Design (Federer, 1956) [6] with a spacing 30cm between rows and 10cm between plants, respectively. The material for present investigation comprised of a total of fifty finger millet genotypes including five varietal checks. The checks *viz*: VL-379, VL-380, VL-376, VL-352 and VL-324 were collected from Vivekananda Parvatiya Krishi Anusandhan Sansthan (Almora) Uttarakhand and 45 germplasm were collected from Indian Institute of Millets Research, Hyderabad, Telangana. Observations were recorded by random selection of 3 plants in each treatment on 15 characters *viz*; days to 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, number of fingers per ear, finger length (cm), finger width (cm), earhead width (cm), earhead length (cm), earhead weight (g), straw yield per plant (g), harvest index (%), 1000 grain weight (g), protein content (%) and grain yield per plant (g). The mean data of these three plants were utilized for the statistical analysis. The cluster analysis for quantitative data was performed using Standardized Euclidean Square Distance method and fifty genotypes of ragi millet were grouped into clusters based on 15 quantitative characters using Tocher's method. Inter and intracluster distance and cluster means were calculated for individual characters based on the performances of various genotypes in each cluster. Multivariate analysis using Mahalanobis D^2 statistic was used for assessing of the genetic divergence between genotypes. Grain protein content was estimated by using NIRS DS2500/DS2500F instrument.

Result and Discussion

The diversity of fifty ragi genotypes was studied based on 15 quantitative characters using Mahalanobis D^2 statistics. It carried out the quantitative assessment of genetic divergence for yield and its contributing characters among the fifty finger millet genotypes presented in Table 1 to 4. The genotypes were grouped into eight different clusters according to closeness of genotypes in respect of their D^2values in Table 1. Average intra and inter cluster distances were calculated and presented in Table 2. Intra cluster distance showed divergence among the genotype within a cluster while inter cluster distance expressed relation divergence between the clusters. The study also reveals the percentage of contribution of these characters towards total divergence, clustering pattern and intra-cluster and inter-cluster distance. The dendrogram and cluster diagram were prepared through the Tocher's method and Mahalanobis euclidean distance method, respectively. The detailed descriptions of different clusters are given here as under:

Table 1: Grouping of fifty genotypes of finger millet into eight clusters on the basis of D^2 analysis

Clusters	Genotypes	Number of genotypes per cluster
I	IC0476421, IC0475129,IC0346263, IC0475632, IC0478790, IC0475978,IC0283454, IC0476115, IC0475457	9
II	IC0478776, IC0346264, IC0474089, IC0478720	4
III	IC0475525, IC0475654, IC0476242, VL-376, IC0478760, VL-324, IC0283451,	7
IV	IC0474806, IC0476076, IC0476315, VL-379, IC0475798, IC0476006,IC0475678, IC0476418, IC0476359, IC0283409, IC0298482, IC0476610, IC0475697, IC0049949, VL-380	15
V	IC0476092, IC0347251, IC0347254, IC0347252	4
VI	IC0476577, IC0474840, IC0298448, IC0476818	4
VII	IC0474887, VL-352	2
VIII	IC0321513, IC0476303, IC0475334, IC0474862, IC0475053	5

Table 2: Intra and inter cluster distance (D^2) among eight clusters for fifty genotypes in finger millet

Cluster	I	II	III	IV	V	VI	VII	VIII
I	472.29	999.29	1191.73	1476.25	3792.09	1614.27	2225.03	10317.41
II		494.93	1791.91	2395.83	3183.09	1640.08	1700.80	8830.86
III			586.52	1949.68	4569.35	1626.14	1625.21	11287.80
IV				611.74	7614.80	3861.69	4985.25	16759.47

V					806.84	1421.70	2311.28	2619.16
VI						513.50	1136.01	5738.83
VII							219.38	6034.78
VIII								908.50

Table 3: Cluster mean among eight clusters for fifteen characters of fifty genotypes in finger millet

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of productive tillers per plant	Number of fingers per ear	Finger length (cm)	Finger width (cm)	Earhead Width (cm)
I	76.000	123.074	76.993	2.741	6.074	7.078	1.030	1.211
II	75.167	123.583	80.783	3.750	5.167	7.550	0.958	1.142
III	75.048	122.095	74.924	3.190	7.524	8.862	1.000	1.348
IV	71.911	115.489	67.560	3.378	6.911	6.329	0.931	1.280
V	85.167	126.917	97.292	3.250	7.333	7.708	1.042	1.317
VI	80.333	125.833	87.025	3.333	7.833	8.192	0.850	1.383
VII	76.167	125.333	85.583	3.667	6.500	10.100	1.083	1.233
VIII	85.800	128.867	112.067	3.267	6.867	8.853	0.953	1.273

Cluster	Earhead length (cm)	Earhead weight (g)	Straw yield per plant (g)	Harvest index (%)	1000 Grain weight (g)	Protein content (%)	Grain yield per plant (g)
I	7.211	7.507	26.519	35.663	2.515	6.778	14.911
II	7.717	4.942	43.575	25.258	1.942	7.250	14.792
III	9.067	11.519	36.033	37.824	3.433	7.667	21.662
IV	6.462	9.384	35.549	33.173	2.684	7.133	17.542
V	7.992	10.450	36.883	34.650	3.117	7.167	19.550
VI	8.367	12.033	37.608	36.525	3.058	7.417	21.383
VII	10.467	8.650	40.033	28.600	2.467	7.333	16.033
VIII	9.133	8.620	34.493	33.740	3.000	6.667	17.667

Table 4: Contribution of each character to the genetic divergence of finger millet

S. No.	Characters	Contribution % towards divergence
1.	Days to 50% flowering	0.00
2.	Days to maturity	0.49
3.	Plant height (cm)	66.69
4.	Number of productive tillers per plant	0.00
5.	Number of fingers per ear	0.00
6.	Finger length (cm)	8.90
7.	Finger width (cm)	0.49
8.	Earhead width (cm)	0.00
9.	Earhead length (cm)	4.90
10.	Earhead weight (g)	9.88
11.	Straw yield per plant (g)	8.57
12.	Harvest index (%)	0.08
13.	1000 Grain weight (g)	0.00
14.	Protein content (%)	0.00
15.	Grain yield per plant (g)	0.00

(a) Group constellation

Cluster IV included maximum number of genotypes (fifteen) followed by Cluster I with nine genotypes; Cluster III with seven genotypes; Cluster VIII with five genotypes, Cluster VII with two genotypes and Cluster II, Cluster V, Cluster VI with four genotypes each, indicating wide diversity from whole set as well as from each other. Moll *et al.* (1962) and Murthy (1966) [14, 15] used these methods in their studies as well. Kumar *et al.*, (2010) [9] grouped 140 genotypes in 10 clusters.

(b) Intra and inter-cluster distances

Intra and inter relation of clusters were judged based on the average D^2 values. The average D^2 values of intra and inter clusters distances are presented in Table 2. The Intra cluster average D^2 values ranged from 219.38 to 908.50. Among the clusters, Cluster VIII (908.50) had the maximum intra cluster distance followed by Cluster V (806.84), Cluster IV (611.74), Cluster III 586.52), Cluster VI (513.50), Cluster II (494.93), Cluster I (472.92) while the minimum was recorded in Cluster VII (219.38). High intra-cluster genetic distance in Cluster VIII was because of its heterogeneous composition. Collaborative results have also been given by Bedis *et al*., 2007 [2], Das *et al*., (2013) [4] and Wolie *et al*., (2013) [23].

The maximum inter cluster D^2 value was recorded between Cluster IV and VIII (16759.47), while the minimum D^2 value was found between Cluster I and II (999.29). Maximum inter-cluster genetic distance was observed between Cluster IV and VIII (16759.47) followed by Cluster III and VIII (11287.80), Cluster I and VII (10317.41), Cluster II and VII (8830.86) and Cluster V and IV (7614.80). Clusters with higher inter-cluster distances indicate that the genotypes included in those clusters had high genetic variation and hybridization between genotypes of these clusters may result heterotic hybrids because of convergence of diverse genes scattered in parents to progeny.

The minimum estimate for inter cluster distance was recorded between Cluster I and II (999.29) followed by Cluster VI and VII (1136.01), Cluster III and I (1191.73), and Cluster V and VI (1421.70). The clusters with least inter cluster distances indicate that genotypes present in these cluster pairs were genetically close to each other. The crosses between genotypes belonging to clusters separated by low inter cluster distance were likely to throw promising recombinants in the segregating generations. Similar results have also been obtained by Vidyadhar and Devi (2007), Kumar *et al*., (2010), Sahu *et al*., (2012), Harti *et al*., (2013) and Shinde *et al*., (2013) [21, 9, 18, 8, 19].

(c) Cluster means analysis for different characters

The cluster group means for fifteen characters across the eight clusters are mentioned in Table 3. Considerable differences between clusters were observed for most of the characters studied.

Cluster II, having 4 genotypes showed highest cluster mean

for number of productive tillers per plant and straw yield per plant. Cluster III, possessing 7 genotypes displayed highest cluster mean for harvest index, 1000grain weight, protein content and grain yield per plant. Cluster IV comprising of 15 genotypes showed least cluster mean for days to 50% flowering and days to maturity. Cluster VI, consisting of 4 genotypes exhibited highest cluster mean for number of fingers per ear, earhead width and earhead weight. Cluster VII, comprising of 2 genotypes potrayed highest cluster mean for finger length, finger width and earhead length. Cluster VIII, consisting of 5 genotypes showcased highest cluster mean for plant height. On the basis of above results it is evident that cluster III had highest maximum cluster means for most of the desirable characters *viz*., harvest index, 1000grain weight, protein content and grain yield per plant. Therefore, genotypes including in this cluster can be used for improvement of a large number of protein, seed yield and yield contributing characters, simultaneously. Earlier workers Bedis *et al*., 2007 [2] and Sahu *et al*., 2012 [18] also reported wide variability among clusters for yield and most of the yield contributing characters.

(d) Relative contribution of different characters towards divergence

Proportion of contribution of each character to total divergence presented in Table 4 and Figure1. Each character was ranked on the basis of percent contribution of that character.

The result showed that plant height contributed maximum (66.69%) to the total divergence among the fifty finger millet genotypes studied, followed by earhead weight (9.88%), finger length (8.90%), straw yield per plant (8.57%), earhead length (4.9%), days to maturity (0.49%), finger width (0.49%) and harvest index (0.08%). On contrary, days to 50% flowering, number of productive tillers per plant, number of fingers per ear, earhead width, protein content, 1000 grain weight and grain yield per plant had negligible contribution towards genetic divergence. According to the present study characters *viz*., plant height, earhead weight, finger length and straw yield per plant contribute to be important characters to the genetic divergence. Similar results were reported by Suryanarayana *et al.* (2014), Sapkal *et al*. (2019), Devaliya *et al*. (2017) [20, 17, 5].

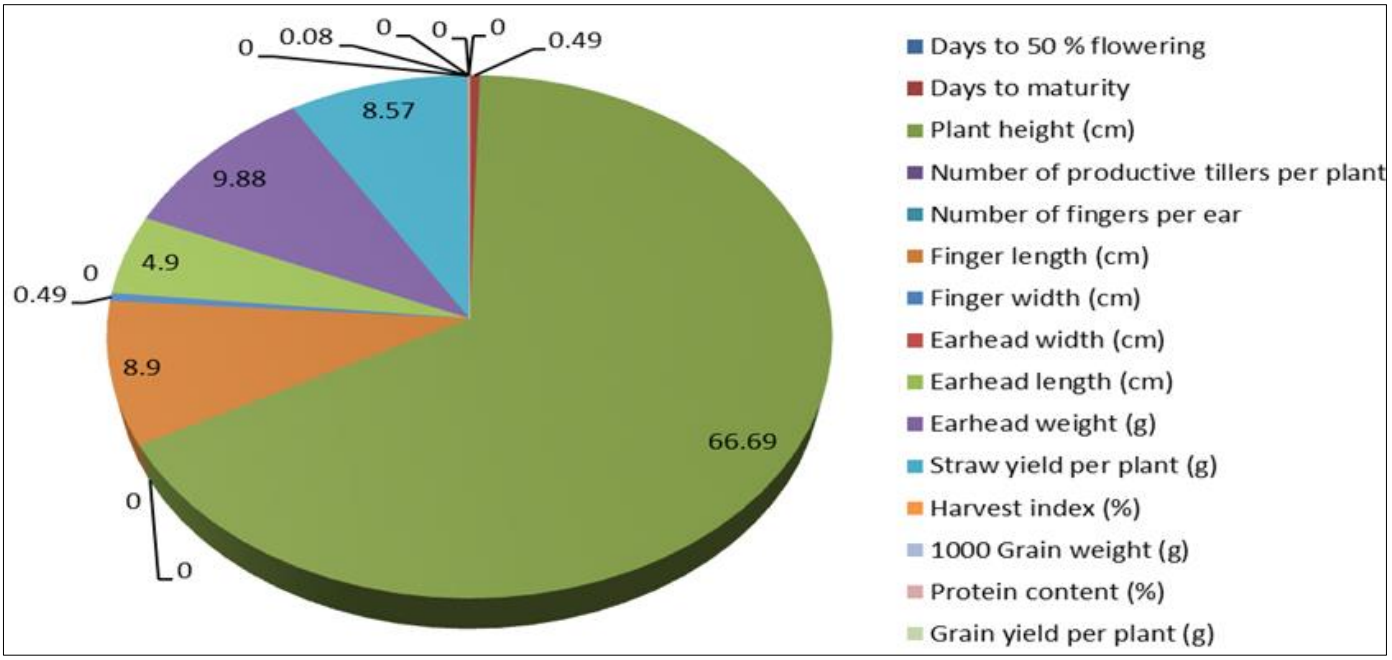

Fig 1: Pie chart depicting the contribution of each character to the genetic divergence of finger millet

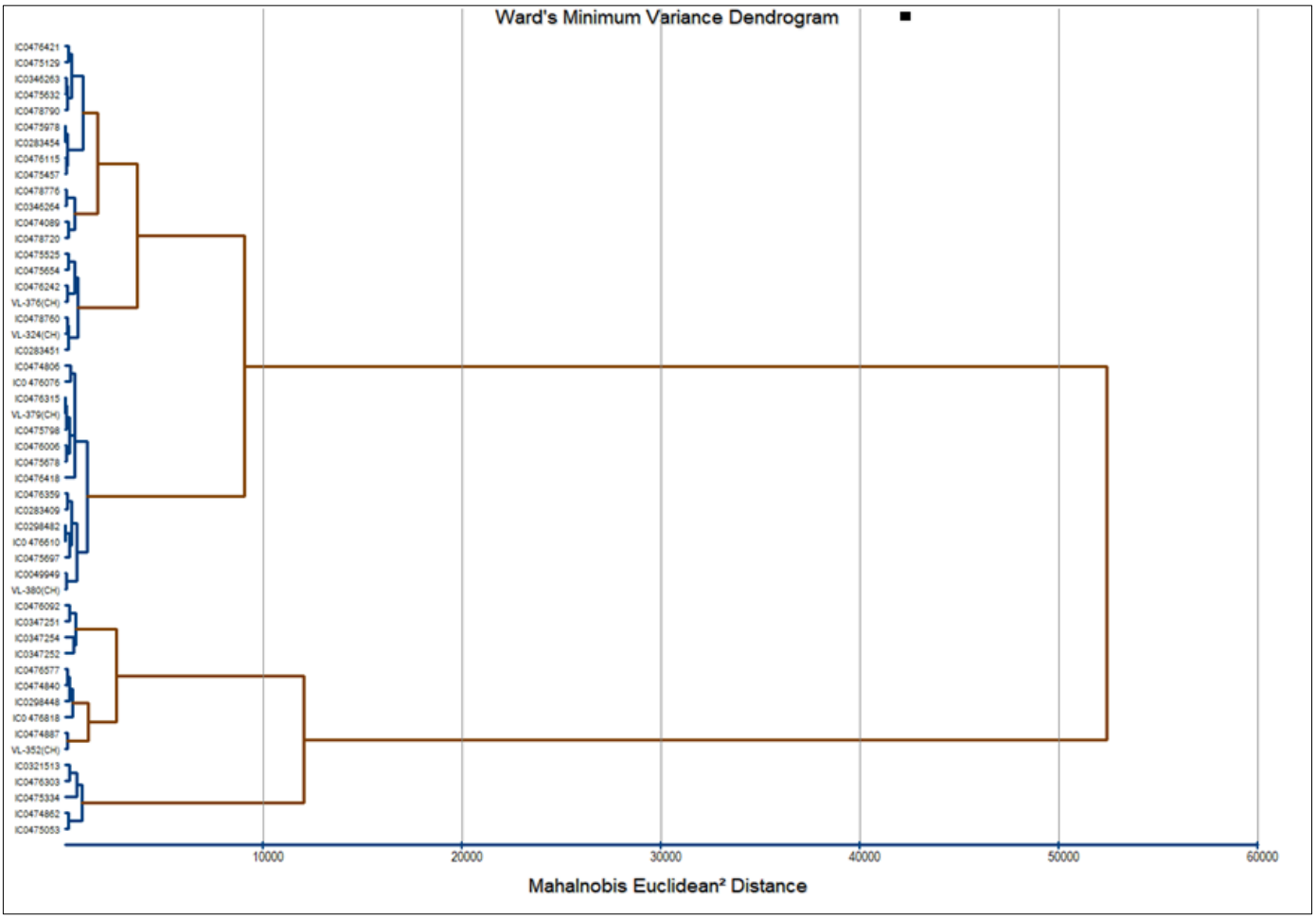

Fig 2: Dendrogram (cluster diagram) showing the relationship among 50 finger millet genotypes developed by Tocher method based on 15 quantitative characters

Conclusion

Genotypes grouped into the same cluster presumably diverge little from one another as the aggregates of characters measured. The maximum inter-cluster distances for grain yield were recorded between Cluster IV & VIII and Cluster III and VIII respectively, indicates the presence of wide diversity between these clusters. Therefore, genotypes from these clusters can be selected for hybridization programme to get desirable recombinants. Plant height contributed the maximum per cent towards genetic divergence in fifty genotypes of finger millet, indicates the presence of wide variability for these traits among the studied genotypes.

Considering the high inter-cluster distances, cluster means and mean performance of genotypes, crossing of entry of clusters III with entries of cluster VI and VII would be fruitful for obtaining transgressive segregants for developing high yielding, high protein containing and better quality finger millet varieties in forth coming crop improvement programmes.

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