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S Pavan Kumar
Department of Genetics and
Plant Breeding, College of
Agriculture, PJTAU,
Rajendranagar, Hyderabad,
Telangana, India

D Padmaja
AICRP on Forage Crops Unit,
Agricultural Research
Institute, PJTAU,
Rajendranagar, Hyderabad,
Telangana, India

K Sumalini
Department of Genetics and
Plant Breeding, College of
Agriculture, PJTAU,
Rajendranagar, Hyderabad,
Telangana, India

J Aruna Kumari
AICRP on Forage Crops Unit,
Agricultural Research
Institute, PJTAU,
Rajendranagar, Hyderabad,
Telangana, India

Corresponding Author:
S Pavan Kumar
Department of Genetics and
Plant Breeding, College of
Agriculture, PJTAU,
Rajendranagar, Hyderabad,
Telangana, India

Genetic divergence and cluster analysis for yield and yield contributing traits in fodder cowpea (*Vigna unguiculata* (L.) Walp.) genotypes

S Pavan Kumar, D Padmaja, K Sumalini and J Aruna Kumari

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Abstract

The present study was undertaken to assess the genetic divergence among 50 fodder cowpea (*Vigna unguiculata* (L.) Walp.) genotypes during Rabi 2025-26 at the AICRP on Forage Crops Unit, Agricultural Research Institute, Rajendranagar, Hyderabad. The experiment was conducted in an alpha lattice design with two replications and observations were recorded on nineteen morphological, yield and quality traits. Genetic divergence was estimated using Mahalanobis D² statistics and the genotypes were grouped following Tocher's method. The fifty genotypes were classified into seven clusters, with Cluster I comprising 25 genotypes and Cluster II comprising 20 genotypes, while the remaining five clusters were solitary. The highest inter-cluster distance was observed between Clusters IV and V, indicating wide genetic divergence among these genotypes. Cluster VI recorded the highest green fodder yield and dry fodder yield, whereas Cluster IV exhibited superior seed yield and 100-seed weight. Of all the traits, green fodder yield contributed the maximum towards total genetic divergence, followed by vine length, crude protein and seed yield. Genotypes viz., UPC 24-1, MFC-18-5 and FSCP 2024-1 were found promising and genetically diverse could be effectively utilized in hybridization programmes for development of high-yielding and nutri-rich fodder cowpea varieties.

Keywords: Fodder cowpea, Mahalanobis D² statistics, Genetic divergence, Tocher's method, green fodder yield

Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.) is an important multipurpose legume cultivated in tropical and subtropical regions for food, fodder, vegetable and green manure purposes. Globally, the crop occupies 15.19 million ha with an annual production of 9.77 million tonnes and an average productivity of 643.5 kg ha⁻¹ (FAOSTAT, 2024) [4]. In India, cowpea is cultivated over approximately 0.32 million ha with an annual production of about 0.20 million tonnes (Indiastat, 2024) [6]. India possesses the world's largest livestock population, with a total of 535.78 million livestock as per the 20th Livestock Census (2019) [3] and continues to face deficits in green fodder, dry fodder and concentrate feed, highlighting the need for high-yielding and nutritionally superior fodder crops (DAHD, 2019; ICAR-IGFRI, 2024) [5]. In Telangana, fodder cowpea has considerable potential owing to the expanding dairy sector and increasing demand for quality fodder, particularly during the rabi season, when favourable climatic conditions promote better vegetative growth and fodder quality. Fodder cowpea is valued for its rapid growth, high biomass production, superior nutritional quality (13-17% crude protein), excellent palatability and its ability to fix substantial atmospheric nitrogen through symbiosis with *Rhizobium* species, thereby contributing to sustainable livestock production and soil fertility improvement (Tarawali *et al.*, 1997a; Singh *et al.*, 2003; Peoples *et al.*, 2009) [16, 14, 10].

The success of any crop improvement programme depends on the availability and effective utilization of genetic variability. Assessment of genetic divergence among germplasm facilitates the identification of genetically diverse parents capable of producing superior recombinants and broadening the genetic base for improving economically important traits (Allard, 1960) [1]. Among the multivariate techniques, Mahalanobis D² statistics is widely used for estimating genetic divergence because it simultaneously considers several quantitative traits (Mahalanobis, 1936) [7].

The technique groups genotypes into distinct clusters and provides information on inter-and intra-cluster distances, cluster mean performance and the contribution of individual characters towards total divergence. Genotypes belonging to widely separated clusters are considered more diverse and are expected to produce superior segregants when used in hybridization programmes (Rao, 1952) ^[13].

Considering the increasing demand for quality green fodder, the existing fodder deficit and the limited information on genetic divergence in fodder cowpea under rabi conditions, the present investigation was undertaken to assess the genetic divergence among diverse fodder cowpea genotypes using Mahalanobis D² analysis and to identify genetically diverse and agronomically superior parents for future fodder cowpea improvement programmes.

Materials and Methods

The present investigation was conducted during Rabi 2025-26 at the All India Coordinated Research Project (AICRP) on Forage Crops Unit, Agricultural Research Institute (ARI), Rajendranagar, Hyderabad, Telangana. The experimental material comprised 50 fodder cowpea genotypes, including 49 germplasm accessions obtained from the National Bureau of Plant Genetic Resources (NBPGR), New Delhi and one released variety, Vijaya, used as the standard check.

The experiment was laid out in an alpha lattice design with two replications. Each genotype was grown in two rows of 3 m length, maintaining a spacing of 30 cm × 10 cm. Recommended agronomic practices were followed throughout the crop season.

Observations were recorded on nineteen morphological, yield and quality traits, viz., days to 50 percent flowering, plant height, number of primary branches per plant, number of leaves per plant, leaf length, leaf width, leaf-to-stem ratio, vine length, number of seeds per pod, pod length, 100-seed weight, seed yield, green fodder yield, dry fodder yield, dry matter content, crude protein, crude fibre, calcium and phosphorus.

Genetic divergence among the genotypes was estimated using Mahalanobis D² statistics (Mahalanobis, 1936) ^[7] and clustering was performed following Tocher's method (Rao, 1952) ^[13]. Cluster means, intra-and inter-cluster distances and the contribution of individual characters towards total genetic divergence were computed. Statistical analyses were carried out using WINDOSTAT version 9.3 at the Computer Centre, PJTAU, Rajendranagar, Hyderabad.

Results and Discussion

Grouping of Genotypes into Clusters

The genetic divergence among the fifty fodder cowpea genotypes was estimated using Mahalanobis D² statistics based on nineteen morphological, yield and quality traits. Based on Tocher's clustering method, the genotypes were grouped into seven distinct clusters (Table 1). Cluster I was the largest, comprising 25 genotypes, followed by Cluster II with 20 genotypes, whereas Clusters III, IV, V, VI and VII each consisted of a single genotype.

The occurrence of two large clusters together with five monogenotypic clusters indicated the presence of considerable genetic diversity among the experimental material. The solitary clusters represent genetically distinct genotypes possessing unique combinations of desirable characters, which may serve as valuable parents in hybridization programmes for broadening the genetic base and generating superior recombinants.

The clustering pattern observed in the present investigation suggested that the grouping of genotypes was independent of their geographical origin, indicating that genetic diversity was influenced mainly by genetic constitution and selection rather than geographical distribution. Similar findings were reported by Mohan Kumar and Gangaprasad (2017) ^[8], Pokar *et al.* (2019) ^[11], Rai *et al.* (2020) ^[12], Belay and Fisseha (2021) ^[2] and Vaggar *et al.* (2022) ^[17], who also observed that genotypes from different geographical regions were distributed across different clusters, reflecting the absence of a clear relationship between geographical origin and genetic divergence.

Table 1: Grouping of fifty fodder cowpea genotypes into seven clusters, *rabi* 2025-26

Cluster	No. of genotypes	Genotypes
Cluster I	25	MFC-09-1, Vijaya, EC-458473, EC-458402, MFC-18-6, EC-402159, MFC-18-2, 1-1-23, 1-1-97-1, MFC-20-4, 1-1-99-2, 1-1-74-2, MFC-9-3, PFC 54, 1-1-83-1, 1-1-22-5, 1-1-30, 1-1-34, 1-1-65, 1-1-7, 1-1-16-1, BL 24-4, 1-1-74, 1-1-84-2, 1-1-58
Cluster II	20	MFC-18-4, 1-1-18, UPC-8705, 1-1-89, EC-394839, 1-1-22-2, EC-458411, EC-458418, 1-1-44-1, UPC-5286, EC-170584, 1-1-49, 1-1-38, 1-1-71, 1-1-11-3, BL 24-1, BL 24-3, EC-458485, 1-1-54, EC-075180
Cluster III	1	MFC-18-8
Cluster IV	1	UPC 24-1
Cluster V	1	MFC-18-5
Cluster VI	1	FSCP 2024-1
Cluster VII	1	BL 24-2

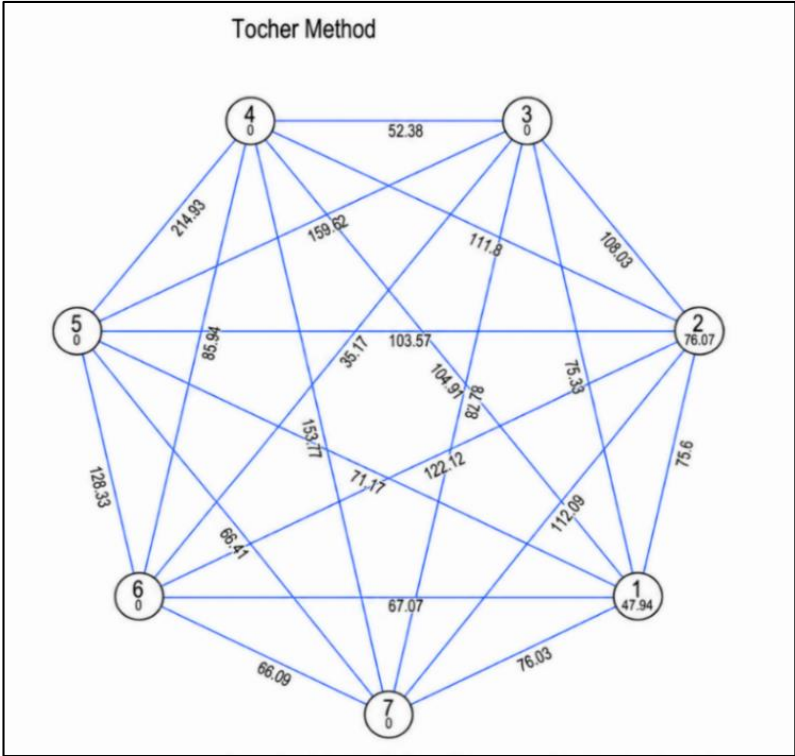


Fig 1: Mahalanobis Euclidean Distance among fifty genotypes of fodder cowpea

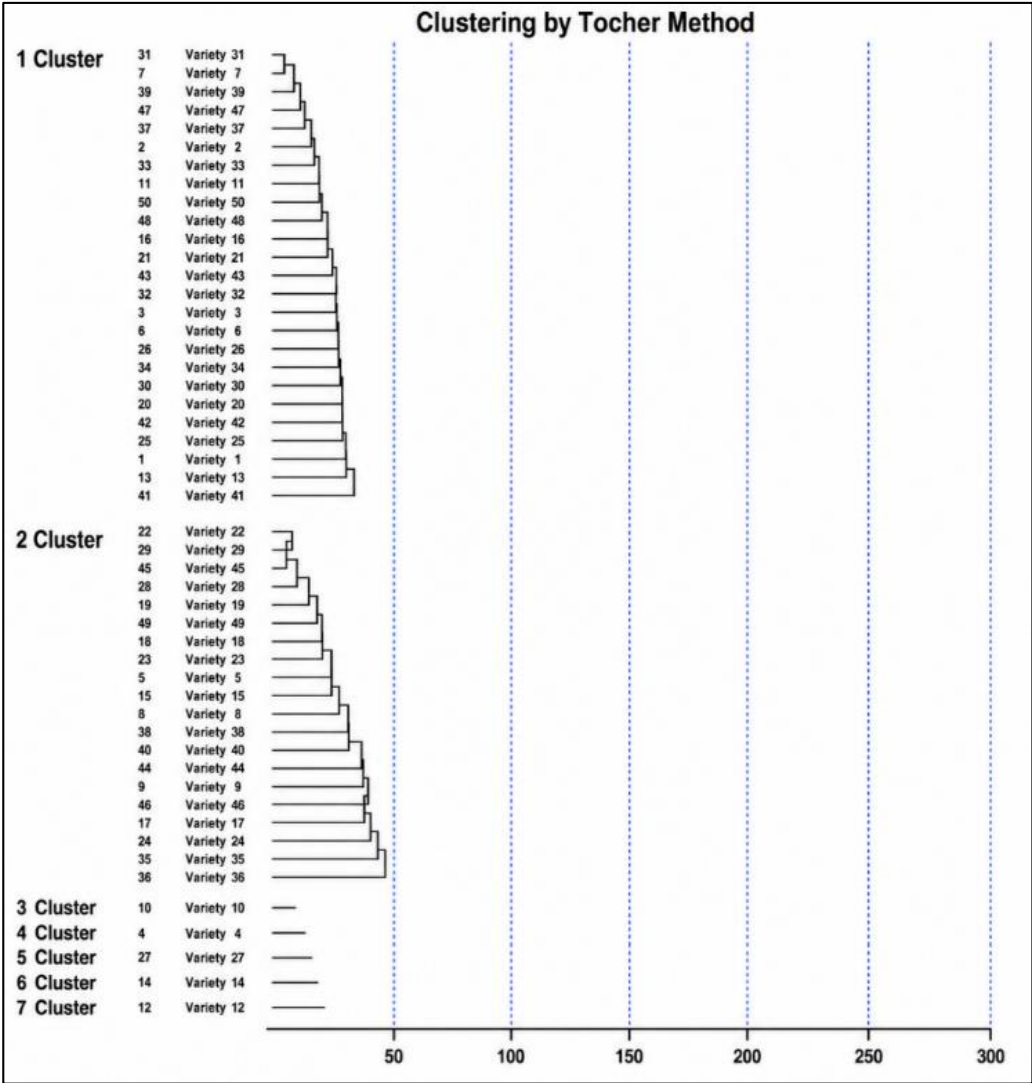


Fig 2: Dendrogram showing clustering of fodder cowpea genotypes

Intra-and Inter-cluster Distances

The average intra and inter-cluster distances within and between the seven clusters are presented in Table 2. Estimation of these distances provides useful information on the magnitude of genetic divergence and helps in identifying diverse parents for hybridization. Generally, crosses between genotypes from widely separated clusters are expected to produce greater heterosis and wider variability in the segregating generations.

Among the multi-genotypic clusters, Cluster II recorded the highest intra-cluster distance (76.07), followed by Cluster I (47.94), indicating greater variability within Cluster II. The monogenotypic Clusters III, IV, V, VI and VII exhibited zero intra-cluster distance.

The highest inter-cluster distance was observed between Cluster IV and Cluster V (214.93), followed by Cluster III

and Cluster V (159.62) and Cluster IV and Cluster VII (153.77), indicating wide genetic divergence among these clusters. Therefore, hybridization between genotypes such as UPC 24-1 (Cluster IV) and MFC-18-5 (Cluster V) may be useful for generating superior recombinants. In contrast, the lowest inter-cluster distance was recorded between Cluster III and Cluster VI (35.17), indicating close genetic similarity between these genotypes.

The higher inter-cluster distances compared with intra-cluster distances indicate the presence of substantial genetic diversity among the genotypes. Similar results were reported by Patel *et al.* (2017) ^[9], Pokar *et al.* (2019) ^[11], Rai *et al.* (2020) ^[12], Belay and Fisseha (2021) ^[2] and Vaggar *et al.* (2022) ^[17], who emphasized that hybridization between genetically divergent clusters enhances the chances of obtaining superior recombinants.

Table 2: Average intra and inter-cluster D² values among the genotypes of fodder cowpea, *rabi* 2025-26

Clusters	I	II	III	IV	V	VI	VII
Cluster I	47.94	75.60	75.33	104.91	71.17	67.07	76.03
Cluster II	75.60	76.07	108.03	111.80	103.57	122.12	112.09
Cluster III	75.33	108.03	0.00	52.38	159.62	35.17	82.78
Cluster IV	104.91	111.80	52.38	0.00	214.93	85.94	153.77
Cluster V	71.17	103.57	159.62	214.93	0.00	128.33	66.41
Cluster VI	67.07	122.12	35.17	85.94	128.33	0.00	66.09
Cluster VII	76.03	112.09	82.78	153.77	66.41	66.09	0.00

Diagonal values (bold) represent intra-cluster distances; off-diagonal values represent inter-cluster distances.

Cluster Mean Performance

The cluster mean values for nineteen morphological, yield and quality traits are presented in Table 3. Cluster mean analysis identifies clusters with desirable combinations of economically important traits and facilitates the selection of suitable parents for hybridization.

Among the seven clusters, Cluster I exhibited intermediate mean values for most traits, while Cluster II recorded the lowest mean values for plant height (53.83 cm), vine length (123.90 cm) and dry fodder yield (4.06 t ha⁻¹). Cluster III was the earliest in flowering (41.65 days) and recorded the highest values for number of seeds per pod (13.38), pod length (17.97 cm), dry matter content (23.46%) and crude protein (19.93%), along with the lowest crude fibre content (27.68%).

Cluster IV recorded the highest mean values for 100-seed weight (15.65 g), seed yield (1034.99 kg ha⁻¹) and phosphorus content (0.31%), whereas Cluster V exhibited

the highest vine length (193.95 cm) but comparatively lower values for several yield-related traits. Cluster VI had highest mean for green fodder yield (32.78 t ha⁻¹), dry fodder yield (5.76 t ha⁻¹), leaf width (8.50 cm) and crude fibre (30.83%), while Cluster VII had the highest values for plant height (68.61 cm), number of primary branches (7.85), number of leaves per plant (59.76), leaf length (15.37 cm), leaf-to-stem ratio (1.75) and calcium content (1.10%).

On the whole, the cluster mean analysis revealed substantial variation among the clusters. Cluster VI was identified as the best donor for fodder yield, Cluster IV for seed yield and Cluster III for crude protein, indicating their potential use in fodder cowpea improvement programmes. The usefulness of cluster mean analysis in identifying superior and genetically diverse parents for hybridization has also been emphasized in cowpea by Mohan Kumar and Gangaprasad (2017) ^[8], Patel *et al.* (2017) ^[9], Pokar *et al.* (2019) ^[11], Belay and Fisseha (2021) ^[2] and Vaggar *et al.* (2022) ^[17].

Table 3: Cluster means for nineteen agro-morphological traits in fodder cowpea, *rabi* 2025-26

Cluster	DFF	PH	NPB	NLP	LL	LW	L/S	VL	NSP	PL	100SW	SY	DFY	DMC	CP	CF	Ca	P	GFY
Cluster I	44.81	60.70	6.53	55.05	11.21	6.86	1.42	156.96	9.59	14.49	14.38	824.82	5.27	22.68	19.72	29.50	1.07	0.28	24.75
Cluster II	47.17	53.83	5.86	49.31	11.27	7.01	1.40	123.90	10.20	14.35	14.10	835.19	4.06	21.40	19.66	28.09	1.05	0.27	20.59
Cluster III	41.65	59.66	7.81	55.01	13.59	7.85	1.72	154.52	13.38	17.97	13.91	963.24	5.68	23.46	19.93	27.68	0.96	0.27	28.21
Cluster IV	45.04	57.27	6.60	47.82	10.90	6.18	1.00	128.72	12.96	16.42	15.65	1034.99	5.05	21.13	18.09	29.45	0.99	0.31	25.86
Cluster V	52.04	63.55	5.56	54.28	7.12	4.89	1.58	193.95	9.09	12.86	12.10	692.88	4.62	19.63	18.54	29.85	0.94	0.25	20.05
Cluster VI	42.75	68.34	7.42	55.71	11.83	8.50	1.58	162.67	9.88	16.58	15.41	950.63	5.76	21.83	15.92	30.83	1.00	0.27	32.78
Cluster VII	52.52	68.61	7.85	59.76	15.37	6.77	1.75	161.85	11.51	15.06	12.26	959.09	5.38	18.12	17.40	27.88	1.10	0.27	23.42

DFF-Days to 50 percent flowering, PH-Plant height (cm), NPB-No. of primary branches/plant, NLP-No. of leaves/plant, LL-Leaf length (cm), LW-Leaf width (cm), L/S-Leaf stem ratio, VL-Vine length (cm), NSP-Number of seeds per pod, PL-Pod length (cm), 100SW-100-seed weight (g), SY-Seed yield (kg/ha), DFY-Dry fodder yield (t/ha), DMC-Dry matter content (%), CP-Crude protein (%), CF-Crude fibre (%), Ca-Calcium (%), P-Phosphorus (%), GFY-Green fodder yield (t/ha).

Contribution of Individual Characters towards Genetic Divergence

The contribution of individual characters towards total genetic divergence is presented in Table 4. Traits with

higher contribution are considered more important for differentiating genotypes and selecting suitable parents for hybridization.

Among the nineteen characters, green fodder yield contributed the highest (21.31%), followed by vine length (12.90%), crude protein (11.59%), seed yield (7.18%) and crude fibre (6.94%), indicating that these traits were the major contributors to genetic divergence. While traits viz., pod length (6.04%), phosphorus (5.22%), leaf-to-stem ratio (4.65%), 100-seed weight (4.57%) and number of seeds per pod (4.00%), dry matter content (2.94%), leaf width (2.69%), days to 50 percent flowering (2.61%) and number of leaves per plant (2.45%) contributed relatively low to the total genetic divergence.

The lowest contribution to the total genetic divergence was observed for plant height and calcium each (0.65%), followed by leaf length (0.98%), number of primary branches per plant (1.06%) and dry fodder yield (1.55%). Similar findings were reported by Patel *et al.* (2017) [9], Pokar *et al.* (2019) [11], Vaggar *et al.* (2022) [17] and Borah and Fazlullah Khan, although the magnitude and ranking of the contributing traits varied depending on the genetic material evaluated.

Table 4: percent contribution of different traits towards total genetic divergence in fodder cowpea, *rabi* 2025-26

S. No.	Trait	Times ranked 1st	Contribution (%)
1	Days to 50% flowering	32	2.61
2	Plant height (cm)	8	0.65
3	No. of primary branches/plant	13	1.06
4	No. of leaves/plant	30	2.45
5	Leaf length (cm)	12	0.98
6	Leaf width (cm)	33	2.69
7	Leaf stem ratio	57	4.65
8	Vine length (cm)	158	12.90
9	Number of seeds per pod	49	4.00
10	Pod length (cm)	74	6.04
11	100-seed weight (g)	56	4.57
12	Seed yield (kg/ha)	88	7.18
13	Dry fodder yield (t/ha)	19	1.55
14	Dry matter content (%)	36	2.94
15	Crude protein (%)	142	11.59
16	Crude fibre (%)	85	6.94
17	Calcium (%)	8	0.65
18	Phosphorus (%)	64	5.22
19	Green fodder yield (t/ha)	261	21.31

Conclusion

The present study was conducted to assess the extent of genetic divergence among fifty fodder cowpea genotypes using Mahalanobis D² statistics for nineteen morphological, yield and quality traits. The analysis revealed significant genetic diversity among the evaluated genotypes and using Tocher's method, genotypes were grouped into seven distinct clusters. The occurrence of two large clusters together with five solitary clusters indicated the presence of genetically diverse genotypes possessing unique combinations of desirable traits. The highest inter-cluster distance was observed between Clusters IV and V, suggesting that hybridization between genotypes belonging to these clusters would be useful for generating superior recombinants with greater variability.

Cluster mean analysis identified Cluster VI as the most promising for green fodder yield and dry fodder yield, Cluster IV for seed yield and 100-seed weight and Cluster III for crude protein content. Among the nineteen traits studied, green fodder yield contributed the highest towards

total genetic divergence, followed by vine length, crude protein and crude fibre, indicating their major role in differentiating the genotypes. Based on genetic divergence and cluster mean performance, the genotypes UPC 24-1, MFC-18-5 and FSCP 2024-1 were identified as promising and genetically diverse parents for hybridization programmes aimed at improving fodder yield and nutritional quality in cowpea.

The results of the present investigation demonstrated the existence of ample genetic variability in the experimental material and provides valuable information for parent selection in fodder cowpea breeding programmes. Further evaluation of the identified superior genotypes across diverse environments, supplemented with molecular characterization, would facilitate their effective utilization in developing high-yielding and nutritionally superior fodder cowpea varieties.

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