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## Genetic variability and diversity studies in rice (*Oryza sativa* L.) genotypes

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#### Abstract

The investigation was carried out to assess the extent of genetic variability and diversity for yield and yield related traits in fifty genotypes of rice. High heritability estimates along with high genetic advance as percent of mean and high GCV & PCV were recorded for number of tillers per panicle, number of filled grains per panicle, number of spikelets per panicle, test weight and L/B ratio. This indicates, by improvement of these characters would be more effective in crop improvement programme. The 50 genotypes were grouped into six clusters based on relative magnitude of  $D^2$  values. Among six largest one is cluster I which consisted of 45 genotypes, while remaining five clusters comprising with one genotype each (mono genotypic). The inter-cluster distance was observed maximum in cluster IV and VI followed by cluster III and VI indicated wide range of variation among the clusters formed. Hence, for efficient hybridization programme in rice the genotypes underlying in IV and VI clusters could be used. Grain yield per plant (g) (16.51%) recorded highest contribution towards genetic divergence.

**Keywords:** Rice, variability, diversity, heritability

#### Introduction

Rice (*Oryza sativa* L.) is the member of Oryzoideae sub-family of *Poaceae* (*Gramineae*) family. It is an important cereal crop which is grown successfully in humid to sub humid regions under subtropical and temperate climate. According to International Rice Research Institute, rice required for the world population in 2025 would be 800 million tons (Kubo and Purevdorj, 2004) [9]. The estimates of heritability help the plant breeder in determining the character for which selection would be beneficial. Heritability estimates along with genetic advance are more helpful in predicting the gain under selection (Johnson *et al.*, 1955) [7]. In any crop improvement programme genetic diversity plays considerable role in the development of superior recombinants (Manomani and Fazlullah Khan, 2003) [12]. The crosses between parents with maximum genetic divergence are generally the most responsive for genetic improvement (Arunachalam, 1981) [1]. Based on the above consideration the present study is conducted to analyse the genetic variability and diversity among 50 genotypes of rice.

#### Materials and Methods

The experimental material comprised of fifty germplasms of rice from different geographical origins which were maintained by Agricultural Research Station, Shirgaon. The current study was carried out at Agricultural Research Station, Shirgaon, Dist. Ratnagiri by adopting three replications in Randomized Block Design during the period June to November 2020 and quality analysis was done at Department of Soil Science and Agricultural Chemistry, College of Agriculture, Dr. B.S.K.K.V. Agriculture University, Dapoli. Dist. Ratnagiri (MS). Seed of all 50 genotypes were sown in seed bed on 19<sup>th</sup> June 2020 and after 24 days seedlings were transplanted in main field on 13<sup>th</sup> July 2020 with 20 cm distance between row to row and 15cm between plant to plant (20 cm x15 cm).

The data were recorded on five randomly selected plants per genotype per replication for recording observations on seventeen characters *viz.*: days to 50 per cent flowering, days to maturity, plant height (cm), number of tillers per plant, panicle length (cm), number of filled grains per panicle, number of spikelets per panicle, spikelet fertility (%), test weight (g), grain length (mm), grain breadth (mm), length/breadth ratio, grain yield per plant (g), straw yield per plant (g), harvest index (%), amylose content (%) and protein content (%).

The data available on individual characters were subjected to analysis of variance commonly applicable to the randomized block design (Panse and Sukhatme, 1985) [13].

The individual genotype grain sample was crushed into powder and nitrogen content in grain was recorded by micro Kjeldahl method. For recording protein content, total nitrogen in sample multiplied with 6.25 (multiplication factor). Amylose contents of the milled rice samples were estimated by the method suggested by Juliano (1964) [8] involving the spectrophotometer at 620 nm wave-length. The phenotypic and genotypic coefficients of variation (PCV, GCV) were computed as per method described by Burton and DeVane (1953) [3]. Heritability in broad sense was estimated for various character by formulae suggested by Lush (1949) and genetic advance was calculated in percent by the formula suggested by Johnson et al. (1955) [7]. Genetic diversity was estimated by Mahalanobis (1936) [11] D2 statistic technique as described by Rao (1952) [15].

## Result and Discussion

The results of analysis of variance are presented in table 1 showed significant differences for all the characters among treatments and non-significant variation among replications by t-test at 5% and 1% level of significance. Similar results were reported by Hefena *et al.* (2016) and Rashmi *et al.* (2017) [16].

The wide range of variation was observed for the characters days to 50% flowering (78.33 to 106 days), plant height (94.27 cm to 154.1 cm), number of filled grains per panicle (100.67 to 291.00), number of spikelets per panicle (115.33 to 349.67) and spikelet fertility (68.75% to 93.12%). Similar range of variation in these characters were reported by Rukmini Devi *et al.* (2017) [17] and Ishwarya Lakshmi *et al.* (2020) [6]. The genotypes viz., TULSI (78.33 days), RTN-214-1-1-1-2 (81 days), RTN-11-2-1-3 (82.067 days), ABHAYA (83 days) and EK-70 (84 days) were found to be earliest type for days to 50% flowering. Early flowering and early maturity are desirable for scheduling various cropping patterns and can be used as a donor parent in hybridization programme for evolving early maturity or short duration rice. Amylose content ranged from 16.09% in SYE-13-9-23-23 to 28.20% in RP-BIO-226. The protein content was observed highest in DRR-50-13 (8.26%) and lowest in KJT-1R (5.96%). The fifty rice genotypes were classified into different grain types based on the systematic classification of rice by Ramaiah (1969) [14]. Out of fifty genotypes, twenty-eight genotypes had long slender (LS) type grain, three had short slender (SS), four genotypes were having medium slender (MS), eight genotypes had Long Bold (LB) type grain and seven genotypes had short bold (SB) grain type. The medium slender grain type is most preferred grain type and higher yield than other types.

The total variability in each character can be partitioned into three components viz., phenotypic, genotypic and environmental. This helps to determine characters in which portion is heritable and non-heritable under study. The estimated data on genetic parameters revealed that genotypic and phenotypic variances were high for number of spikelets per panicle followed by number of filled spikelets per panicle, plant height, spikelet fertility, days to maturity and days to 50% flowering indicating wide variability for these characters. Rukmini Devi *et al.* (2017) [17] and Sadia *et al.* (2020) [18] also observed significant variability for these characters.

Among the all characters, higher estimates of PCV and GCV were observed for the characters like, number of filled grains per panicle (26.63, 26.13), number of tillers per plant (26.52,

26.12), number of spikelets per panicle (26.10, 25.22), test weight (21.33, 20.76) and L/B ratio (20.50, 20.21) respectively has given in table 3. This indicates the presence of broad genetic base among the genotypes taken for study and selection for these characters could help in genetic improvement of crop. These results were similar with experiments of Saha *et al.* (2019) [19]. Heritability estimates along with genetic advance are generally more helpful in the genetic gain under selection than heritability estimates alone. High heritability estimates and high genetic advance as percent of mean were recorded for number of tillers per panicle (97.00, 52.97), number of filled grains per panicle (96.30, 52.81), number of spikelets per panicle (93.40, 50.21) and test weight (94.70, 41.66).

The seventy genotypes were grouped into seven clusters as presented in table 3, which indicated a wide range of variation among the genotypes studied. The Cluster I was the largest which consisted of 45 genotypes, while remaining five clusters comprising with one genotype each. Clustering pattern suggesting that there is no relationship between genetic diversity and geographic, as genotypes chosen from same eco-geographical regions are found to be in different clusters. The variety having common genetic architecture may be grouped in same cluster irrespective with their origins. Similar results in rice were earlier confirmed by Chandra *et al.* (2007) [4] and Vennila *et al.* (2011) [21].

The cluster I was comprised of forty-five genotypes. These genotypes were better average for the plant height and protein content with respect to their population means. The cluster II comprised one genotype i.e., VDN-08-12. This cluster had better average plant height, number of spikelets per panicle, number of filled grains per panicle, grain length, L/B ratio, straw yield per plant, amylose content and grain yield per plant according to their population means respectively. The cluster III consisted one genotype i.e., KJT-3R. III. This genotype had superior average for all the characters except panicle length, grain length and L/B ratio with respect to their population means. The cluster IV comprised of only one genotype i.e., RTN-8 had better average for the all the studied characters except test weight, grain length, grain breadth and L/B ratio accordingly to their respective means. The cluster V comprised of KJT-3-1-12-5-35-1-4 genotype, which had better average for the characters spikelet fertility, test weight, grain breadth and amylose content. The cluster VI consisted of KJT-25-1-65-17-11-16 genotype. It had superior average for the characters panicle length, grain length and L/B ratio. The average values of these characters were exceeded their respective population mean (table 5).

The highest intra cluster distance was observed for cluster I (D=12.90), while remaining clusters showed no intra cluster distance being solitary, thereby suggesting highest degree of variability within cluster I. The solitary clusters designating their independent specification and significance due to the distinctive characters constituted by those genotypes. These genotypes may serve as potential base material for breeding programme.

The studies on inter-cluster distance indicated magnitude of genetic divergence between the clusters. It suggested that, how much these clusters were genetically diverse from each other. In present experiment, maximum inter cluster distance was observed between cluster IV and VI (1501.77) followed by cluster III and VI (1116.24) etc were presented in table 4. The genotypes which included in genetically diverse clusters could be used in hybridization programme for further crop

improvement in rice. Out of seventeen characters studied, grain yield per plant (16.51%) recorded highest contribution towards genetic divergence followed by harvest index (13.55%) and grain length (12.08%). Banumathy *et al.* (2010)

<sup>[2]</sup> and Solanki *et al.* (2019) <sup>[20]</sup> reported that the character grain yield per plant had highest contribution to genetic divergence.

**Table 1:** Analysis of variance for 17 characters in rice genotypes

Sr. No	Characters	Mean sum of squares		
		Replication (2)	Treatment (49)	Error (98)
1.	Days to 50% flowering	0.827	65.659**	4.745
2.	Days to maturity	0.287	80.635**	5.015
3.	Plant height (cm)	15.11	483.365**	10.739
4.	Number of tillers per plant	0.001	15.222**	0.157
5.	Panicle length (cm)	0.808	10.602**	1.648
6.	Number of filled grains per panicle	124.287	7025.739**	89.572
7.	Number of spikelets per panicle	3.86	9559.804**	220.588
8.	Spikelet fertility (%)	45.785	85.105**	37.438
9.	Test weight (g)	1.519	50.977**	0.93
10.	Grain length (mm)	0.004	2.019**	0.031
11.	Grain breadth (mm)	0.003	0.208**	0.001
12.	L/B ratio	0.026	1.24**	0.012
13.	Straw yield per plant (g)	0.097	54.191**	3.839
14.	Harvest index (%)	5.992	11.992**	5.21
15.	Amylose content (%)	0.852	20.852**	0.329
16.	Protein content (%)	0.199	1.969**	0.067
17.	Grain yield (g)	3.109	36.868**	2.737

\*\*Significant at 5% level.

(Figures in parenthesis denotes degrees of freedom)

**Table 2:** Estimates of genetic parameters for various characters of Rice genotypes

Sr. No.	Character	Mean	Range		PCV (%)	GCV (%)	h <sup>2</sup> b	GA	GAM (%)
			Min	Max					
1	Days to 50% Flowering	91.01	78.33	106.00	5.50	4.95	81.10	8.36	9.18
2	Days to maturity	120.71	102.67	135.00	4.55	4.16	83.40	9.45	7.83
3	Plant Height (cm)	121.10	94.27	154.10	10.71	10.37	93.60	25.02	20.66
4	Number of tillers per plant	8.58	5.87	15.75	26.52	26.11	97.00	4.55	52.97
5	Panicle Length (cm)	26.17	21.98	30.62	8.23	6.60	64.40	2.86	10.92
6	Number of filled grains per panicle	184.03	100.67	291.00	26.63	26.13	96.30	97.19	52.81
7	Number of spikelets per panicle	221.22	115.33	349.67	26.10	25.22	93.40	111.07	50.21
8	Spikelet Fertility (%)	83.68	68.75	93.12	4.76	4.76	29.80	4.48	5.36
9	Test Weight (g)	19.67	10.81	27.71	21.33	20.76	94.70	8.19	41.66
10	Grain Length (mm)	6.61	5.23	8.80	12.61	12.32	95.50	1.64	24.81
11	Grain Breadth (mm)	2.13	1.58	2.79	12.45	12.32	98.00	0.54	25.14
12	Length/ Breadth Ratio	3.17	2.18	5.21	20.50	20.22	97.20	1.30	41.05
13	Straw yield per plant (g)	26.46	16.92	37.47	17.16	15.48	81.40	7.61	28.77
14	Harvest Index (%)	42.91	38.86	46.53	6.37	3.50	30.30	1.70	3.97
15	Amylose content (%)	23.66	16.09	28.20	11.32	11.06	95.40	5.26	22.25
16	Protein content (%)	7.03	5.96	8.26	11.92	11.33	90.50	1.56	22.21
17	Grain yield per plant (g)	19.94	13.19	26.76	18.84	16.92	80.60	6.24	31.29

**Table 3:** Distribution of 50 genotypes into SIX different clusters

Cluster	Number of genotypes include	Genotypes and their source/origin	
I	45	VDN-10-18	RTN-7
		RTN-8-1-22	DRR-363-5
		RTN-15-2-1-1	IR-64
		KOLAMBA-540	DRR-50-13
		SYE-404-41-31	DRR-215
		RTN-27-1-12	DRR-86-18
		RTN-95-2-1-7-1	BL-184AR
		RTN-50-1-1-1	RTN-11-2-1-3
		RTN-69-1-1-8	NP-26
		SYE-13-9-23-23	GR-11
		KJT-29-2-36-6-17-1-5	SKL-22-63-21
		DRR-86-8	PR-114
		KJT-25-1-29-14-24-1-5	EK-70
		AJAYA	NAUR-1
		RTN-214-1-1-1-2	DRR-50-12

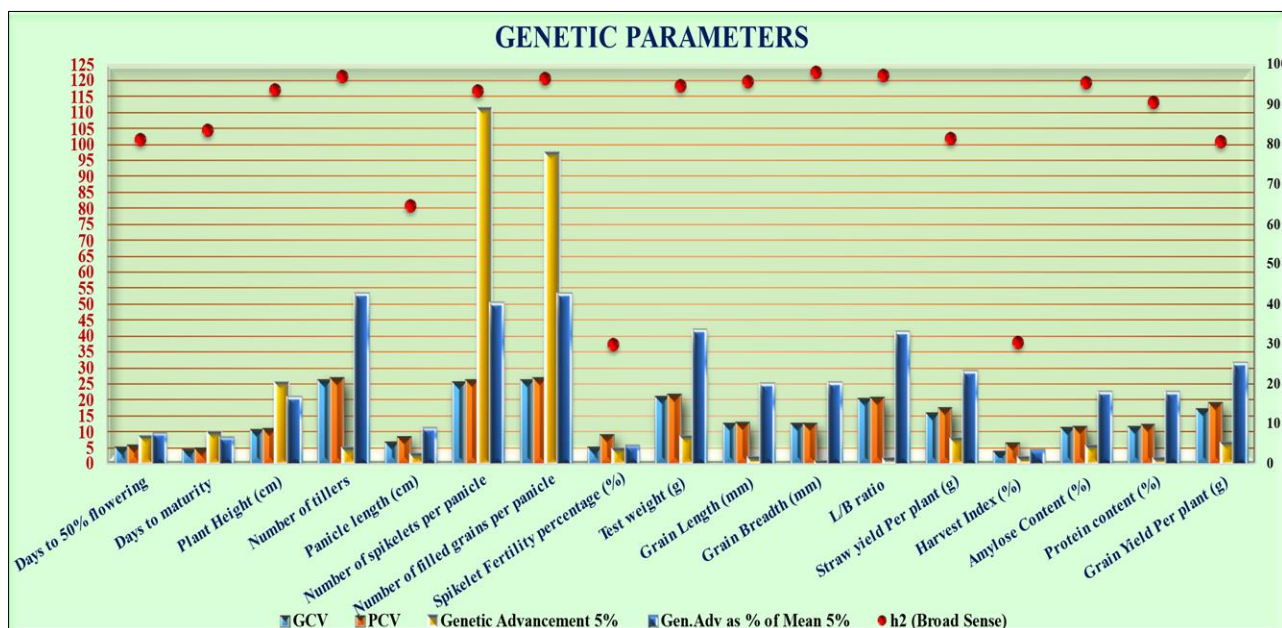
		IR-26	TULSI
		DRR-50-10	RTN-711
		ABHAYA	RP BIO-170
		PLG-1	RTN-4
		RP-BIO-226	KJT-1R
		PKV GANESH	PR-118
		GR-103	RTN-6
		RTN-13-1	
II	1	VDN-08-12	
III	1	KJT-3R	
IV	1	RTN-8	
V	1	KJT-3-1-12-5-35-1-4	
VI	1	KJT-25-1-65-17-11-16	

**Table 4:** Average intra and inter cluster values in 6 clusters (D) = ( $\sqrt{D^2}$ ) in rice genotypes

Clusters	I	II	III	IV	V	VI
I	12.90	17.21	19.73	21.37	17.76	25.46
II		0	21.88	25.30	21.41	15.85
III			0	18.43	16.70	33.41
IV				0	30.14	38.75
V					0	26.09
VI						0

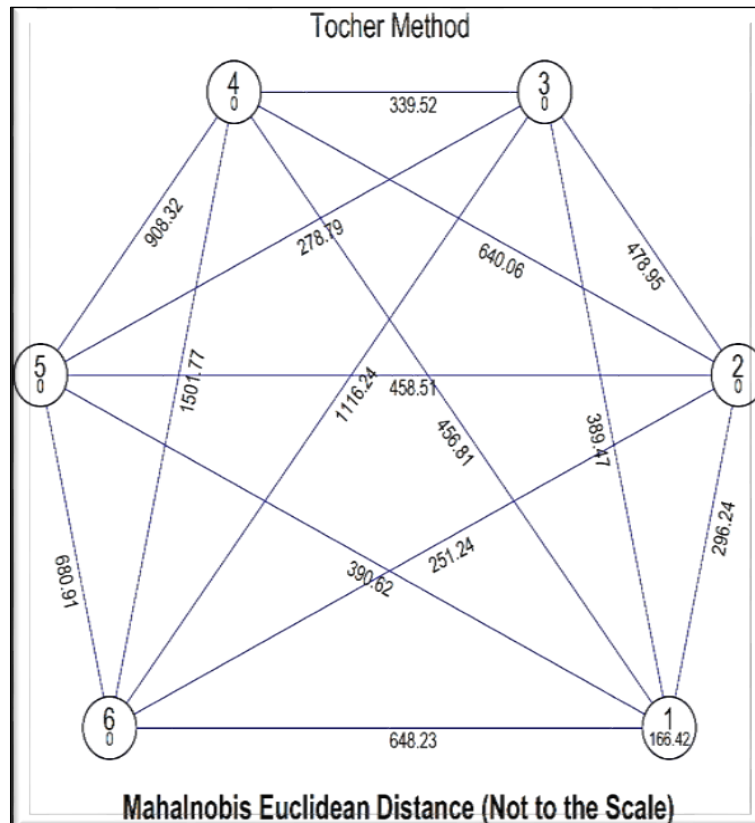
**Table 5:** Cluster mean performance of 17 characters in 50 genotypes of rice

S. N.	Characters	Clusters						Population means	Percent contribution
		I	II	III	IV	V	VI		
1	Days to 50% Flowering	90.59	92.33	96.33	106	88.33	91	94.10	0.33%
2	Days to maturity	120.33	120.67	125.33	135	119	120.33	123.44	0.16%
3	Plant Height (cm)	121.34	122.6	125.7	125.23	100.67	120.47	119.33	5%
4	Number of tillers per plant	8.4	10.53	12.36	15.75	5.93	6.67	9.94	7%
5	Panicle Length (cm)	26.06	25.44	25.63	28.77	26.57	29.34	26.97	2%
6	Number of spikelets per panicle	219.19	259.33	270	326	183.67	158.67	236.14	3%
7	Number of filled grains per panicle	181.73	211	246	282.33	158	126.33	200.90	2.69%
8	Spikelet Fertility (%)	83.52	81.45	91.39	86.67	86.16	80.09	84.88	2%
9	Test Weight (g)	19.358	18.65	27.71	18.45	24.27	13.46	20.32	7%
10	Grain Length (mm)	6.56	7.64	6.8	5.87	6.67	8.26	6.97	12.08%
11	Grain Breadth (mm)	2.12	1.64	2.74	2.07	2.79	1.58	2.16	7%
12	Length/ Breadth Ratio	3.13	4.67	2.49	2.84	2.39	5.21	3.46	1%
13	Straw yield per plant (g)	26.37	29.4	28.37	31	26.35	21.13	27.10	8%
14	Harvest Index (%)	42.83	42.95	46.53	46.28	43.34	39.1	43.51	13.55%
15	Amylose content (%)	23.45	26.73	26.06	25.45	27.27	21.87	25.14	6%
16	Protein content (%)	7.08	6.15	7.43	6.94	6.03	6.04	6.61	6.69%
17	Grain yield per plant (g)	19.77	22.17	24.71	26.71	20.16	13.58	21.18	16.51%



**Fig 1:** GCV, PCV, Genetic advancement 5%, Gen. Adv as % of mean 5% and heritability (h<sup>2</sup> BS) in rice





Note: This Cluster diagram is drawn for  $D^2$  values

Fig 2: Cluster diagram (Tocher Method)

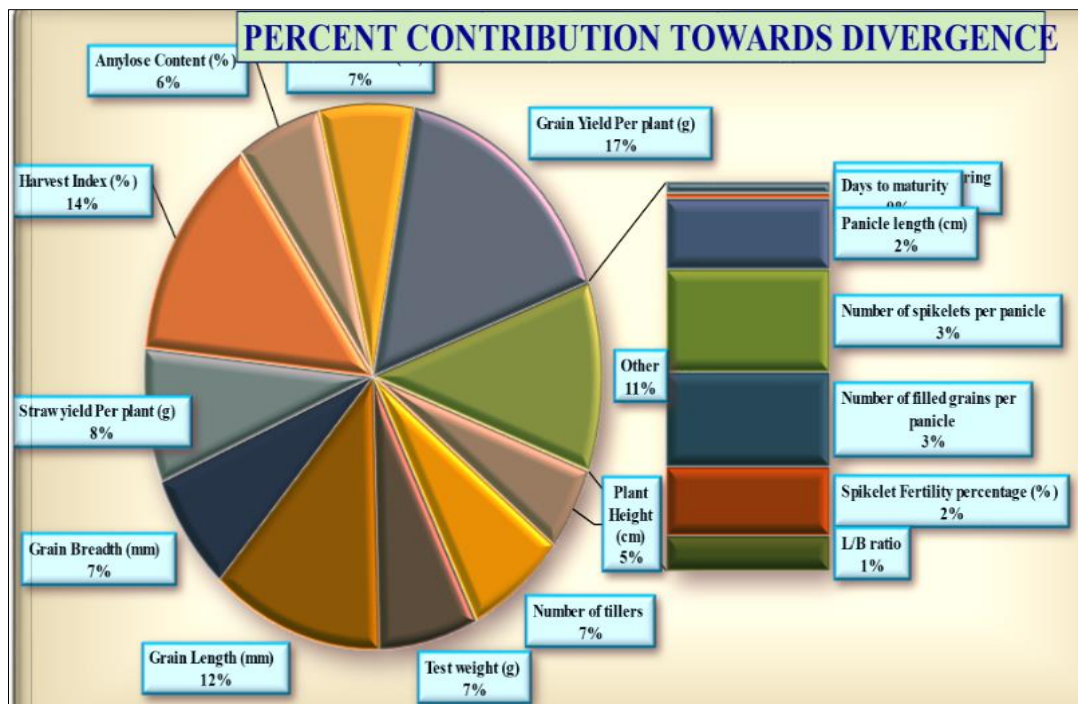


Fig 3: Percent contribution towards divergence

### Conclusion

In conclusion, it is to be stated that, significant range of variability was existing among the genotypes studied for the different quantitative characters. From the present research experiment, it is evident that the wide range of variability for different traits coupled with high heritability and high genetic advance as percentage of mean for important yield traits like number of filled grains per panicle, number of spikelets per panicle, number of tillers per panicle, test weight, L/B ratio;

hence selections based on the traits could improve productivity in rice directly. The present experiment further revealed through  $D^2$  statistics that cluster IV and cluster VI are most diverse to each other. Therefore, genotypes present in these clusters viz., RTN-8 and KJT-25-1-65-17-11-16 are suggested to provide a broad-spectrum variability in segregating generations and may be used as parents for future hybridization programme to develop desirable genotypes.

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