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Genetic diversity studies in sesame (*Sesamum indicum* L.) genotypes

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Abstract
Present study prioritized on assessing genetic divergence in sesame (*Sesamum indicum* L.) against the 65 diverse germplasm, collected from different sources were planted at the Oil Seeds Research Station, Latur Research Farm, VNMKV, Latur (M.S.) during *kharif* 2016 in a Randomized Complete Block Design in two replications. With the help of Mahalanobis D^2 statistics, all the genotypes were clustered in 4 groups. Cluster I was the largest among all clusters comprising 60 germplasm, Cluster II comprising of 3 germplasm and Cluster III & IV were being mono-genotypic clusters. The trait 1000-seed weight (g) was contributed maximum (18.51%) towards diversity followed by days to maturity (16.30%), oil content (13.13%), number of seeds per capsule (11.88%), capsule length (11.59%), seed yield per plant (10.05%), number of branches (9.28%) in that order. The highest intra cluster distance was found in cluster II (13.55), followed by cluster I (10.87). The intra-cluster distance values were zero in the clusters, which had one genotype (III, IV) each. The maximum average inter-cluster distance was found between cluster I and IV (24.75). While minimum inter-cluster distance was observed between clusters I and III (15.88). Among 4 clusters, cluster III (Maduri) and IV (JLT-408) were most divergent to other clusters. Crossing between germplasms lying in clusters III and IV followed by clusters IV and II i.e. JLT-408, Maduri, UKNM-1067, TKG-306 and SWETA may be desirable for getting superior hybrids/recombinants.

Keywords: Sesame, D^2 statistics, genetic divergence

Introduction
Sesame is the prominent oilseed crop in the world consumption scenario and occupies 6th position after soybean, rapeseed, cottonseed, sunflower and groundnut. India occupies leading position in the area and production of sesame. In India, Sesamum is cultivated in an area of 1.78 million hectares, with a production of 0.81 million tons with productivity of 456 kg (2014-15). It is grown in marginal and sub-marginal lands to an altitude of 1200 meters, about 500 mm rainfall and with temperature requirement about 25-27 °C. It is grown as rain fed crop mainly in the states of Gujarat, West Bengal, Uttar Pradesh, Rajasthan, Madhya Pradesh, Andhra Pradesh, Maharastra, Tamilnadu, Odisha and Karnataka, which account for more than 96% of the total area and production. In Maharashtra it is cultivated in an area of 30.4 thousand hectares, with a production of 5.6 thousand tones with average productivity of 184 kg ha^{-1} (Oilseeds statistics A Compendium-2015 and Indian Institute of Oilseeds Research, Hyd.).

Sesame is grown mainly for its seeds that contain approximately 50% oil and 25% protein (Burden, 2005). With availability of antioxidants (sesamolin and sesamol) makes the oil most stable and suitable for culinary purpose. Sesamum oil possess high resistance to oxidative deterioration despite the presence of oleic and linoleic acids which are more prone to oxidation (about 80% of its total) of sesame oil, (Uzun *et al.*, 2007). Due to high stability of its oil with distinct sweet flavor, Sesamum is regarded as the 'Queen of Oilseeds', Sesame oil comprising 50% of the dry seed weight has been preferentially consumed in oriental food. Aside its being antioxidative, antihypertensive, hypocholesteremic, anticancer and immunoregulatory properties, sesame oil finds use in cosmetic, pharmaceutical, paint, detergent and pesticide industries. Sesame secured its position in various civilizations across the world and it's continuing still today. No "burger" in any famous confectionary across the world comes without sesame seeds topped on it. No meal in northern Europe completes without "Margoreta" an edible sweet made from sesame. A highly valued confectionary commodity, besides being the much sought after edible oil source world over, sesame has all the potential to emerge as an important commodity in International trade.

In spite of being the first oilseed crop known to man and its long history, sesame is a typically neglected crop or an "Orphan crop" or "Underutilized crop" because of lack of appreciable research efforts, in India and abroad.

Sesame is a self-pollinated crop, but very high cross pollination between 14-65 per cent has been recorded in some varieties in India. Hence the crop is classified under *often cross pollinated* group. Therefore, a considerable amount of genetic diversity may be expected in this crop. To obtain high heterotic effects and more variability, genetic divergence among parents is essential and the crossing programme involving genetically diverse parents is likely could be expected in the segregating generations.

Genetic diversity between populations/genotypes indicate the differences in gene frequencies.

For identifying such diverse parents for crossing, multivariate analysis using Mahalanobis D^2 statistical method (1936) [6] has been used in several crops. This is a widely using tool to study genetic divergence at inter varietal and sub-species level in classifying the crop plants.

Materials and Methods

The experiment was laid out in *kharif* 2016 at Oil Seed Research Station, Latur. The Research station is located on the South-East to Latur Dist. (Maharashtra), India during Kharif-2016. Sixty-five diverse genotypes of sesame including four check varieties Swetha, JLT-408, G-1 and Madhuri were included in the present study. The details of genotypes are enlisted in Table 1.

The 65 sesame genotypes were sown on 1st July, 2016 in a Randomized Block Design with two replications. Each genotype in each replication was sown by dibbling the seeds in one row plot of 9.0 m length, adopting a spacing of 45 cm between rows and 10 cm between the hills. Thinning of seedlings was carried out after 10 days of sowing by keeping one seedling per hill. The recommended cultural practices were adopted in respect of irrigation, weeding and fertilization. Plant protection measures were taken up as and when required. The genotypes were harvested as and when they attained physiological maturity. Eleven biometrical traits of sesame were recorded on five randomly selected plants in each of the accession per replication. The mean values were utilized for statistical analysis.

Statistical analysis

The mean values were utilized for statistical analysis. The Mahalanobis D^2 analysis was performed by using the software SPSS version 17.0.

Results

The observations recorded in sesame accessions on eleven characters *viz*., days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of capsules per plant, capsule length (cm), capsule width (cm), number of seeds per capsule, 1000- seed weight (g), oil content (%) and seed yield per plant (g), indicating the presence of considerable genetic variability among the experimental germplasm under study.

Genetic Divergence using mahalanobis D^2 analysis Clustering Patterns of 65 sesame collections

The quantitative assessment of genetic divergence was made by adopting Mahalanobis D^2 statistic for yield and its contributing characters. Genetic divergence was estimated for sixty-five sesame genotypes and the results obtained from the study are presented below.

Wilk's 'V' criterion test

Wilk's 'V' (statistic) criterion was used to test the significant differences between the groups based on the pooled effects of all the characters. The significance of 'V' (statistic) value was tested by % at 704 degrees of freedom. The 'V' statistic value obtained was highly significant. Therefore, when all the characters were simultaneously considered, the genotypes said to be significantly differed.

The significance of sixty-five genotypes in the analysis of variance of dispersion clearly indicated the significant pooled effect of all the characters studied between different genotypes. Therefore, further analysis was made to estimate D^2 analysis.

Mahalanobis generalized distance D^2 values

In order to assess the genetic diversity among sixty-five genotypes, D^2 statistic was used following the procedure given by Rao (1952) [8], since the entire 11 yield component characters were correlated, they were transformed into uncorrelated linear combination through pivotal condensation method.

Grouping of genotypes into various clusters

Sixty-five genotypes were grouped into four clusters based on D2 values using Tocher's method (Rao, 1952) [8] such that the genotypes belonging to same cluster had an average smaller D2 values than those belonging to different clusters. The distribution of genotypes into various clusters has been presented in Table 2 and Fig 1 out of four clusters, cluster I was the largest comprising of sixty genotypes followed by cluster II with three genotypes, clusters III and IV were mono-genotypic clusters, suggesting the existence of high degree of heterogeneity among the genotypes.

Average inter and intra cluster distances

The inter cluster distance was higher than intra cluster distance (Table 3), indicating the presence of wide genetic diversity among the genotypes under study. The intra-cluster D^2 values varied from 0.00 to 13.55. The maximum intra-cluster distance was found in cluster II (13.55), followed by cluster I (10.87). The intra-cluster distance values were zero in the clusters, which had one genotype (III, IV) each.

The maximum average inter-cluster distance was found between cluster I and IV (24.75). While minimum inter-cluster distance was observed between clusters I and III (15.88). Among 4 clusters, cluster III (Maduri) and IV (JLT-408) were most divergent to other clusters.

Cluster I exhibited maximum divergence with cluster IV (24.75), followed by cluster II (17.90) and cluster III (15.88).

Cluster II had maximum divergence with cluster I (17.90) followed by cluster IV (17.82) and cluster III (17.68).

Cluster III displayed maximum divergence with cluster II (17.68) and followed by cluster I (15.88) and cluster IV (15.42).

Maximum divergence of cluster IV expressed with cluster I (24.75) followed by cluster II (17.82) and cluster III (15.42).

Contribution of Various quantitative and qualitative Characters towards total genetic divergence Rank method of D^2 analysis

The cluster means for each of eleven characters are presented in Table 4 It can be seen from the data that considerable differences existed for all the characters under study.

Cluster-I

Cluster-I showed low mean for capsule length (2.43 cm), number of capsules per plant (47.12), number of seeds per capsules (71.05), 1000 seed weight (2.62 g), seed yield per plant (8.72 g) and oil content (42.32%).

The genotypes with low mean values for characters above mentioned are grouped in this cluster.

Cluster-II

Cluster II showed high mean values for days to maturity (88.50), plant height (105.40 cm) and number of branches per plant (3.65).

The genotypes with high plant height, more number days to maturity and number of branches per plant were grouped in this cluster.

Cluster-III

Cluster III shown low mean values for days to 50% flowering (33.0), days to maturity (74.0) and number of branches per plant (2.20). The high mean values are observed for characters capsule width (0.68) and number of seeds per capsule (33.40).

The genotypes which shown low mean values for days to 50% flowering, days to maturity, number of branches per plant and high mean values for capsule width and number of seeds per capsule were grouped in this cluster.

Cluster-IV

Genotypes in this cluster had high mean values for days to 50% flowering (38.50), capsule length (2.67 cm), number capsules per plant (85.25), seed yield per plant (25.98 g), 1000 seed weight (3.78 g) and oil content (49.31%) and observed low mean values for capsule width (0.64) and plant height (89.15).

Cluster-IV was formed with genotypes having high days to 50% flowering, capsule length, number of capsules per plant, seed yield per plant, 1000 seed weight, and oil content.

Relative contribution of characters towards genetic divergence

The utility of D^2 statistics as a potential tool to quantify the extent of divergence in biological populations at genetic level is further enhanced by its applicability to estimate the relative contribution of the various plant characters to total genetic divergence. The number of times that each of ten characters appeared in first rank and its respective per cent contribution towards genetic divergence is presented in Table 5.

The results showed that the contribution of 1000 seed weight was the highest towards genetic divergence (18.51%) by taking 385 times ranking first, followed by days to maturity (16.30%) by 339 times, oil content (13.13%) by 279 times, number of seeds per capsule (11.88%) by 247 times, capsule length (11.59%) by 241 times, seed yield per plant (10.05%) by taking 209 times, number of branches per plant (9.28%) by 193 times, days to maturity (2.89%) by 55 times, days to 50% flowering (1.80%) by 34 times and seed yield per plant (1.00%) by 19 times to the genetic divergence in decreasing order.

Out of eleven characters studied, seven characters namely 1000 seed weight, days to maturity, oil content, number of seeds per capsule, capsule length, seed yield per plant and number of branches per plant together contributed 90.74% towards total divergence. Therefore, these characters should be given prominance during hybridization and selection of segregating populations.

Discussion

Based on D^2 analysis the pattern of distribution of 65 genotypes into 4 clusters was at random with maximum number of genotypes (60) in cluster I, Cluster II possessed 3 genotypes, Cluster III and Cluster IV consisted single genotypes each *viz.,* Maduri and JLT-408 respectively. The pattern of distribution of genotypes from different eco-geographical regions into different clusters with different divergence values was at random supporting that geographical diversity is not related to genetic diversity. The main forces other than geographical origin responsible for this genetic diversity may be natural and artificial selection, exchange of breeding material, genetic drift and environmental variation. Similar conclusions were drawn by Chandra Mohan *et al.* (2014) [2] and Abate and Mekbib (2015) [1].

The genotypes of common geographic origin or same location also were grouped into different clusters as evidenced by the distribution of genotypes from Jabalpur (M.P) into different clusters. K-5170, DCR-1794, SI-5354, VB-7901, SI-75 and EC-357308 were grouped in cluster I, while PS-201 and DCB-1799 into cluster II and III, respectively. The results are in accordance with Ganesh and Thangavelu (1995) [3] and Gangadhara Rao (2004) [5].

The results on character wise contributed towards total genetic divergence shows that no single trait had a great contribution to total divergence. Relative contribution of 1000-seed weight (g) was maximum (18.51%) towards diversity followed by days to maturity (16.30%), oil content (13.13%), number of seeds per capsule (11.88%), capsule length (11.59%), seed yield per plant (10.05%), number of branches (9.28%) in that order. While the contribution of other four characters towards divergence was negligible. These results are in agreement with Sudhakar *et al.* (2006), Parameshawarappa *et al.* (2009), they reported higher contribution of 1000-seed weight (g), seed yield per plant, number of branches per plant and plant height towards divergence. Similar track of findings was reported by Tripathy *et al.* (2013) [9] for 1000-seed weight (g), Gangadhara *et al.* (2012) [4] for oil content and seeds per capsule. No report suggested contribution of days to maturity is maximum towards diversity. It was suggested that characters with maximum contribution towards diversity should also be given due consideration for sesame improvement.

The inter-cluster D^2 values were higher than the intra-cluster D^2 values. The maximum inter-cluster distance was observed between cluster I and IV (24.75) followed by cluster I and II (17.90) and least inter-cluster value was observed between I and III (15.88) followed by cluster II and III (17.68). Out of 4 clusters formed, two clusters III and IV are solitary and had no intra-cluster distances. Based on these studies crosses may be attempted between the genotypes of cluster III (Maduri) and cluster IV (JLT-408) to obtain new desirable recombinants in sesame. On the other hand, minimum

distance occurred between cluster III and cluster IV (15.42) indicated almost parallel diversity among the genotypes included in this clusters. Maximum intra-cluster D^2 value was observed in cluster-IV (24.75) followed by cluster-II (17.90). The highest intra cluster distance in cluster-II indicates the presence of wide genetic diversity among the genotypes (UKNM-1067, TKG-306 and SWETA) within the cluster.

There was a wide range of cluster mean values among the characters studied, indicating the presence of variation among genotypes studied. Cluster-IV with single genotype *viz.*, JLT-408 had highest mean values for six characters *viz.*, days to 50% flowering, capsule length, number of seeds per capsule, seed yield per plant, 1000-seed weight (g), and oil content. While cluster III with single genotype (Maduri) had highest value for capsule width and number of seeds per capsule and cluster II (UKNM-1067, TKG-306 and SWETA) had highest values for days to maturity, plant height and number of branches per plant. So genotypes in these clusters can be used for creating variability for these yield component traits.

Based on multivariate analysis, the two clusters IV and III with single genotypes JLT-408 and Maduri respectively scored high mean values for 8 characters which are considered as important economic attributes. As the magnitude of heterosis depends largely on the degree of genetic diversity of parental lines, the genotypes JLT-408 belonging to cluster IV and Maduri from cluster III can be used to derive a broad spectrum of genetic variability in the segregating generations for seed yield per plant.

Table 1: Details of sixty-five genotypes of sesame.

S. No	Genotype	Source	S. No	Genotype	Source
1	SI-413-A	P.C. Unit, Jabalpur.	34	IC-42200	P.C. Unit, Jabalpur.
2	SI-205-61	P.C. Unit, Jabalpur.	35	IC-23233	P.C. Unit, Jabalpur.
3	SI-199-2-84	P.C. Unit, Jabalpur.	36	NIC-16220	P.C. Unit, Jabalpur.
4	SI-1147	P.C. Unit, Jabalpur.	37	EC-231-2-84	P.C. Unit, Jabalpur.
5	IS-299A	P.C. Unit, Jabalpur.	38	EC-370840	P.C. Unit, Jabalpur.
6	ES-44	P.C. Unit, Jabalpur.	39	EC-209	P.C. Unit, Jabalpur.
7	ES-146-1-84	P.C. Unit, Jabalpur.	40	EC-89111	P.C. Unit, Jabalpur.
8	ES-113-18-84	P.C. Unit, Jabalpur.	41	EC-377015	P.C. Unit, Jabalpur.
9	EC-370936	P.C. Unit, Jabalpur.	42	SI-983	P.C. Unit, Jabalpur.
10	IC-204001	P.C. Unit, Jabalpur.	43	OSC-3209	P.C. Unit, Jabalpur.
11	GM-NIC- 7909	P.C. Unit, Jabalpur.	44	DS-21	P.C. Unit, Jabalpur.
12	GM-NIC- 7913	P.C. Unit, Jabalpur.	45	EC-101396	P.C. Unit, Jabalpur.
13	GM-NIC- 8202	P.C. Unit, Jabalpur.	46	SI-5354	P.C. Unit, Jabalpur.
14	GM-NIC- 8631	P.C. Unit, Jabalpur.	47	IS-424	ORS, Latur.
15	GM-NIC- 8934	P.C. Unit, Jabalpur.	48	SI-3168	ORS, Latur.
16	GM-NIC- 16146	P.C. Unit, Jabalpur.	49	KMR-69	ORS, Latur.
17	GM-NIC- 16226	P.C. Unit, Jabalpur.	50	KMR-114	ORS, Latur.
18	GM-NIC- 16330	P.C. Unit, Jabalpur.	51	GT-3	ORS, Latur.
19	GM-NIC- 16332	P.C. Unit, Jabalpur.	52	SI-1003	ORS, Latur.
20	GM-NIC- 8254	P.C. Unit, Jabalpur.	53	YLM-17	ORS, Latur.
21	NIC-7855	P.C. Unit, Jabalpur.	54	EC-303423	ORS, Latur.
22	NIC-7903	P.C. Unit, Jabalpur.	55	PKDS-8	ORS, Latur.
23	NIC-10621	P.C. Unit, Jabalpur.	56	JLT-07	ORS, Latur.
24	NIC-16114	P.C. Unit, Jabalpur.	57	TKG-22	ORS, Latur.
25	NIC-16324	P.C. Unit, Jabalpur.	58	EC-S-0523A	ORS, Latur.
26	NIC-16104	P.C. Unit, Jabalpur.	59	EC-S-0223	ORS, Latur.
27	NIC-8263	P.C. Unit, Jabalpur.	60	TKG-306	ORS, Latur.
28	EC-310439	P.C. Unit, Jabalpur.	61	IS-207	ORS, Latur.
29	ES-42-2-84	P.C. Unit, Jabalpur.	62	JLT-408	ORS, Latur.
30	K-5170	P.C. Unit, Jabalpur.	63	MADURI	ORS, Latur.
31	UKNM-1067	P.C. Unit, Jabalpur.	64	G-1	ORS, Latur.
32	UKNM-2386	P.C. Unit, Jabalpur.	65	SWETA	Local selection from Telangana
33	IC-41962	P.C. Unit, Jabalpur.			

Table 2: Grouping of 65 sesame genotypes into Clusters

Cluster no.	No. of genotypes included	Genotypes in cluster
I	60	GM-NIC- 16146,K-5170, TKG-22, SI-413-A, ES-113-18-84, NIC-10621, NIC-8263, SI-1147, SI-199-2-84, GM-NIC- 8254, ES-42-2-84, EC-209, EC-S-0223, EC-231-2-84, EC-89111, NIC-16114, NIC-16324, GM-NIC- 7909, GM-NIC- 16332, GM-NIC- 7913, GM-NIC- 16226, ES-44, NIC-7903, KMR-114, JLT-07, GM-NIC- 16330, EC-S-0523A, IS-299A, IC-41962, ES-146-1-84, UKNM-2386, EC-370936, PKDS-8, SI-983, NIC-16220, IC-23233, NIC-16104, OSC-3209, KMR-69, IC-204001, IC-42200, GM-NIC-8202, DS-21, IS-207, GM-NIC- 8934, SI-205-61, YLM-17, EC-101396, EC-310439, EC-377015, GM-NIC- 8631, EC-303423, SI-5354, SI-3168, SI-1003, EC-370840, NIC-7855, IS-424, GT-3, G-1.
II	3	UKNM-1067, TKG-306 and SWETA
III	1	MADURI
IV	1	JLT-408

Table 3: Intra (diagonal) and inter-cluster average of D and D^2 values of 65 Sesame genotypes.

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	10.87	17.90	15.88	24.75
Cluster II		13.55	17.68	17.82
Cluster III			0.00	15.42
Cluster IV				0.00

Table 4: Cluster means for 11 characters in 65 Sesame genotypes.

Cluster	Days to 50% flowering	Days to maturity	Capsule length	Capsule width	Plant height	Number of branches per plant	Number of capsules per plant	Number of seeds per capsule	Seed yield per plant	1000 seed weight	Oil content (%)
Cluster I	37.22	82.71	2.43	0.65	95.24	3.60	47.12	71.05	8.72	2.62	42.32
Cluster II	38.33	88.50	2.59	0.66	105.40	3.65	51.65	75.50	13.59	3.47	46.59
Cluster III	33.00	74.00	2.66	0.68	93.50	2.20	74.50	93.40	21.17	3.03	48.10
Cluster IV	38.50	78.50	2.67	0.64	89.15	2.90	85.25	80.60	25.98	3.78	49.31

Table 5: Relative contribution of different characters to genetic diversity in sesame genotypes.

S. No.	Character	Times ranked 1st	Contribution (%)
1	Days to 50% flowering	56	2.69%
2	Days to maturity	339	16.30%
3	Capsule length	241	11.59%
4	Capsule width	18	0.87%
5	Plant height	41	1.97%
6	Number of branches per plant	193	9.28%
7	Number of capsules per plant	78	3.75%
8	Number of seeds per capsule	247	11.88%
9	Seed yield per plant	209	10.05%
10	1000 seed weight	385	18.51%
11	Oil content (%)	279	13.13%

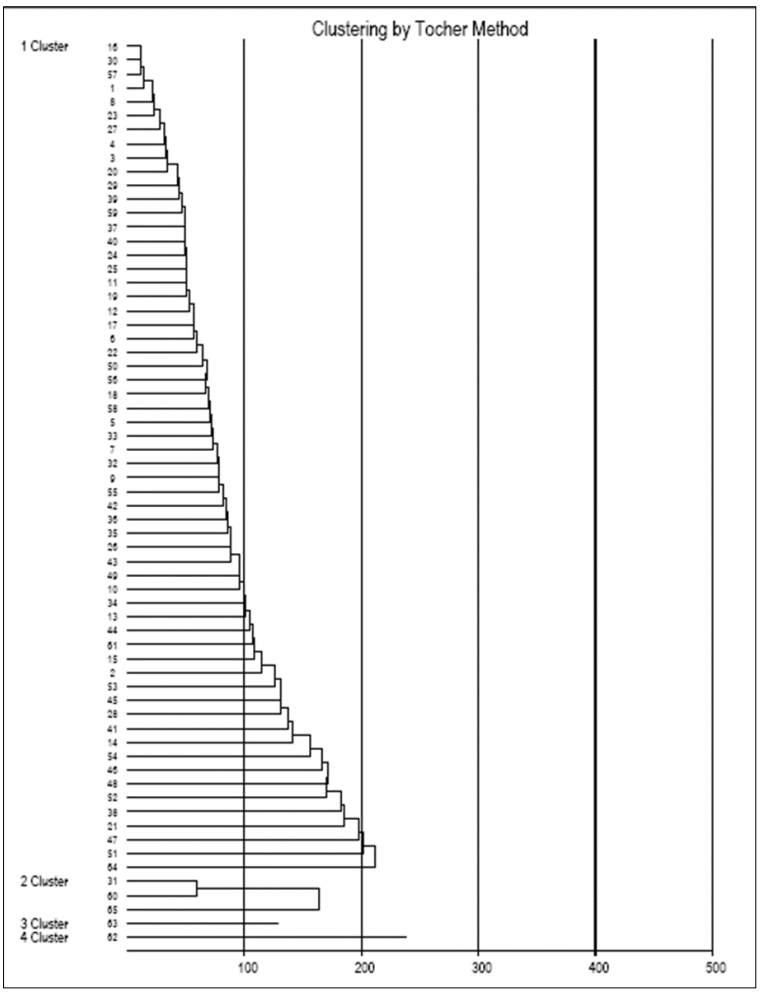

Fig 1: The distribution of genotypes into various clusters has been presented

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