International Journal of Agriculture Sciences
ISSN: 0975-3710 & E-ISSN: 0975-9107, Volume 12, Issue 12, 2020, pp.-9991-9994.
Available online at https://www.bioinfopublication.org/jouarchive.php?opt=&jouid=BPJ0000217

Research Article

GENETIC DIVERSITY STUDIES AMONG UPLAND COTTON FOR MOROPHO-QUALITATIVE TRAITS

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Received: June 03, 2020; Revised: June 24, 2020; Accepted: June 25, 2020; Published: June 30, 2020

Abstract: The present investigation was conducted with the experimental material comprising of thirty-four genetically diverse and elite upland cotton lines collected from eleven locations of all over India. Data were collected by randomly selected sample plants per plot basis for important morpho-qualitative traits *viz*., days to 50 percent flowering, plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), number of seeds per boll, ginning outturn (%), seed index (g), lint index (%), 2.5% span length, fibre strength (g/tex), micronaire value (㎍/inch) and seed cotton yield per plant (g). The data obtained from the field experiment is subjected to the analysis of variance for various quantitative traits under study, which revealed the highly significant differences among the genotypes for all the fourteen traits under study indicating substantial genetic variability. The simultaneous test of significance based on Wilk's Criteria for the pooled effect of all the fourteen characters studied has shown highly significant differences among the thirty-four genotypes (x^2=1869.8080 at 462 d.f.). Therefore, D^2 values corresponding to 561 possible combinations among thirty-four genotypes found statistically significant. Analysis of variance revealed the significant differences among the thirty-four genotypes for all the traits studied, indicating the existence of considerable amount of genetic variability among them. On the basis of D^2 values for 561 possible pairs of the population of thirty-four genotypes were grouped into seven clusters, indicating the satisfactory magnitude of diversity in the genotypes. The selection of diverse parents belonging to diverse clusters for crossing programme for their exploitation to obtain the set of desirable segregants.

Keywords: *Cotton, Genetic Divergence, D^2 Analysis, Clustering, G. hirsutum* L

Citation: Ujjainkar V.V. and Patil V.D. (2020) Genetic Diversity Studies Among Upland Cotton for Moropho-Qualitative Traits. International Journal of Agriculture Sciences, ISSN: 0975-3710 & E-ISSN: 0975-9107, Volume 12, Issue 12, pp.- 9991-9994.

Academic Editor / Reviewer: Ammayappan L., Dr Zheko Radev

Introduction

Amongst the fibres, Cotton is under cultivation from ancient period as a source of a fibre in India. Cotton has a vital role in the national economy, being an important source of raw material (85 percent) to textile industry. Cultivation of cotton is more than eight million hectares in India and ranks first in the world in the area but third in production. Cotton refers to those species of genus Gossypium that bears the spinnable seed coat fibres. There are about 42 species of this genus, out of which only four species *viz*., *Gossypium arboreum, G. herbaceum, G.hirsutum* and *G.barbadense* are cultivated and rest are recognized as wild. The first two species *i.e. G. arboretum* and *G. herbaceum* are cytologically diploid (2n=2x=26) and native of Old World, termed as either Desi or Asiatic cotton. The remaining two *i.e., G.hirsutum* (American/Upland cotton) and *G.barbadense* (Sea land/ Egyptian or Tanguish cotton) are cytogentically tetraploids (2n=4x=52) and referred as New World Cotton.

The tetraploid cotton (*Gossypium hirsutum* L.) is the predominant cotton species grown and it contributes alone 90 percent to the global cotton production [26]. India is the only country in world where all the four cultivated species are grown for the commercial cultivation besides the hybrids.

Apart from fibre, cotton seed is also an important source of edible oil, meal and cattle feed. Refined cottonseed oil is one of the best edible oils, which is mainly consumed in many parts of the world including USA, China, Uzbekistan, India and Middle East. Cottonseed oil roughly has 2:1 ratio of unsaturated and saturated fatty acids. It consists of 18% Oleic acid, 52% linoleic acid and antioxidant *viz*., Palmitic and Stearic acids [2]. Development of superior varieties and exploitation of phenomenon of heterosis are the main breeding approaches followed for developing high yielding varieties in respect to cotton.

Since long, cotton workers are seriously attempting to improve the cotton productivity to bridge the gap between demand and supply but a spectacular success is still awaited. However, India is credited to be the first country where hybrid cotton was on commercial scale way back in 1970 based on seed production by hand emasculation and pollination. But the productivity barriers are yet to heal up. The knowledge of nature and magnitude of genetic diversity present in the germplasm is most important pre-requisite for the success of any breeding programme. It is thus necessary to survey the variation present in the germplasm as the hybrids between diverse lines displays a greater heterotic effect than those between the closely related.

The genetic diversity of selected parents is not always based on the factors such as geographical diversity or place of release or ploidy level. Hence many statistical procedures *viz*., D^2 statistics, non-hierarchical Eucledian Cluster, Meteroglyph *etc*., are developed to measure the total variability present among the genotypes. Hence, the study on the assessment of genetic diversity based on morphological traits was taken up in upland cotton

Material and Methods

The present investigation was conducted with the experimental material comprising of thirty-four genetically diverse and elite upland cotton lines collected from eleven locations of all over India comprising of diverse agro-climatic zones.

The genetic divergence study was undertaken with thirty-four elite genotypes at experimental field of Cotton Research Unit, Dr Panjabrao Deshmukh Krishi Vidyapeeth, Akola in Completely Randomized Block Design (CRBD) with three replications.

Table-1 *Analysis of variance for various morphological characters of thirty-four elite cotton genotypes*

Source of variation	d.f.	Mean sum of squares [MSS]						
		Days to 50% flowering	Plant height (cm)	No. of monopodia per plant	No. of sympodia per plant	No. of bolls per plant	Boll weight (g)	No. of seeds per boll
Replication	2	49.0001^{NS}	136.406^{NS}	0.4833^{NS}	30.8310**	7.8203^{NS}	0.0348^{NS}	36.7519**
Genotypes	33	56.1427**	743.783**	1.3521**	29.8446**	36.1584**	0.4933**	28.1138**
Error	66	19.7070	73.7477	0.2234	4.7232	7.4079	0.0354	4.2307

Source of variation	d.f.	Mean sum of squares [MSS]						
		Ginning outturn (%)	Seed Index (g)	Lint Index (%)	2.5% span length (mm)	Fibre Strength (g/tex)	Micronaire value (µg/inch)	Seed Cotton yield per plant (g)
Replication	2	6.5429^{NS}	0.0442^{NS}	0.0901^{NS}	1.5547**	2.1484**	0.7409^{NS}	47.5859**
Genotypes	33	18.3802**	0.6478**	0.8553**	4.4178**	14.9687**	0.3026**	95.5537**
Error	66	2.2952	0.0160	0.0791	0.1949	0.2901	0.0253	10.5963

**, ** Significant at 5% and 1% level of significance*

Table-2 *D^2 values of thirty-four elite cotton genotypes*

AKH–84635	0.00															
AKH-8835	269.76	0.00														
KH-118	84.14	295.43	0.00													
NH-545	326.49	136.60	364.94	0.00												
JLH-1594	131.85	249.83	201.02	403.56	0.00											
LRA-5166	97.62	253.46	94.47	308.58	296.27	0.00										
AKH-91	85.99	229.91	67.82	249.00	142.64	95.46	0.00									
NS-95	278.34	80.10	269.94	119.78	253.48	212.14	134.47	0.00								
AKH-44	138.93	132.30	87.47	205.64	209.70	77.53	52.18	76.15	0.00							
AKH-9312	112.39	210.37	54.34	274.85	244.37	47.91	53.77	144.04	20.53	0.00						
AKH-24	147.73	69.91	165.35	120.69	233.05	80.44	107.52	66.02	59.94	89.04	0.00					
AKH-62	243.44	84.74	270.00	144.26	278.92	207.21	159.53	66.60	79.82	143.96	97.28	0.00				
G Cot-10	245.25	167.42	192.11	154.15	310.72	173.02	129.85	92.03	103.88	130.55	73.49	203.29	0.00			
AKH-8801	100.01	109.25	95.92	153.31	190.51	95.83	74.88	106.27	38.32	52.44	46.94	114.00	70.84	0.00		
AH-107	166.24	444.52	127.77	462.47	217.68	292.03	122.44	379.94	186.98	186.70	342.25	354.59	341.56	190.74	0.00	
JK-119	97.18	158.20	104.64	173.89	246.17	87.14	107.05	184.37	106.19	108.63	52.09	192.85	88.07	53.82	267.86	0.00
GA-B	122.26	470.74	100.48	528.00	235.60	249.11	147.45	480.73	273.71	207.82	357.06	402.05	434.75	227.65	78.99	250.88
LCMS-5	101.84	170.64	84.15	192.94	146.06	118.33	59.47	138.01	64.41	82.57	85.93	154.98	80.47	39.46	166.50	58.95
LCMS-2	112.24	236.44	132.69	331.45	244.69	64.78	98.90	228.08	107.92	108.78	101.71	209.02	248.97	142.66	253.50	114.25
AKH-87	66.32	362.10	120.93	355.44	190.17	192.37	119.02	359.96	191.12	178.28	239.24	326.58	271.78	132.11	84.40	137.52
AKH-32	170.76	74.08	198.13	86.54	193.64	164.68	113.61	63.70	71.66	142.23	48.07	82.90	106.67	62.24	256.19	95.67
AKH-081	222.29	559.66	242.28	533.43	199.87	453.07	258.69	527.87	389.00	391.55	449.56	562.55	377.75	302.94	177.93	295.55
PH-93	140.85	360.95	193.27	324.71	105.16	311.11	98.16	293.86	218.34	249.52	281.54	287.28	303.65	193.95	96.94	234.22
AKH-053	182.02	544.18	214.21	649.55	129.48	406.79	212.81	540.07	353.02	340.10	462.60	517.00	513.90	329.42	117.17	361.41
AKH-023	159.59	452.26	127.05	435.68	243.98	304.74	147.82	430.19	234.84	233.27	348.19	384.04	342.09	201.32	58.53	221.42
IC-1547	85.29	165.30	103.02	151.27	187.29	80.43	68.05	132.10	74.02	90.19	57.90	152.70	85.64	53.17	220.38	37.89
AKH-1234	93.80	352.39	110.28	398.01	112.66	222.93	143.42	356.70	216.98	205.93	239.04	375.92	239.00	148.40	166.22	141.89
AKH-3436	71.84	342.83	76.77	363.32	229.51	45.85	50.05	243.98	97.69	63.36	137.71	249.27	193.24	122.69	183.50	112.97
SUMANGLA	134.20	443.08	148.19	513.79	239.60	275.52	175.50	447.34	246.58	227.59	328.59	402.99	375.98	230.80	106.13	209.92
NARSIMHA	75.12	231.63	89.80	267.94	268.78	28.74	81.08	195.90	60.61	47.45	92.25	163.84	192.96	79.37	214.17	97.01
VIKAS	199.01	360.63	147.19	394.25	136.33	328.87	113.34	276.85	178.80	189.32	291.05	300.58	245.59	172.59	92.21	248.89
SAHANA	121.84	139.51	101.70	173.28	192.68	157.67	118.39	190.66	88.83	111.59	102.44	156.96	173.69	56.69	159.41	77.10
AKH-8660	41.16	184.44	51.28	242.04	123.69	85.25	50.66	179.89	70.61	67.23	82.85	192.54	120.48	41.19	130.25	43.14
PS-348	127.16	381.18	130.06	409.19	311.03	198.23	165.90	426.45	198.80	186.19	271.84	310.97	396.30	189.77	118.56	181.48
Genotypes	AKH-84635	AKH-8835	KH-110	NH-545	JLH-1594	LRA-5166	AKH-91	NH-95	AKH-44	AKH-9312	AKH-24	AKH-62	G.COT 10	AKH-8801	AH-107	JK-119

LCMS-5	0.00															
LCMS-2	168.88	0.00														
AKH-87	101.50	187.33	0.00													
AKH-32	75.41	150.91	198.86	0.00												
AKH-081	181.92	461.27	125.42	355.64	0.00											
PH-93	129.47	256.73	96.72	185.91	124.65	0.00										
AKH-053	243.11	333.45	119.61	397.66	137.49	106.92	0.00									
AKH-023	163.14	266.11	65.70	273.44	131.56	96.00	139.38	0.00								
IC-1547	23.60	130.60	113.23	57.08	241.61	162.07	308.00	208.86	0.00							
AKH-1234	71.54	259.61	78.17	221.02	62.99	120.45	126.27	139.04	112.02	0.00						
AKH-3436	106.87	78.93	141.07	188.41	317.05	197.42	284.76	217.58	90.13	162.92	0.00					
SUMANGLA	195.71	195.41	70.18	301.18	188.93	177.80	130.05	88.84	219.93	164.24	191.55	0.00				
NARSIMHA	118.47	58.07	140.16	128.93	406.99	245.78	358.14	214.62	80.98	224.93	61.80	201.98	0.00			
VIKAS	114.96	326.16	175.73	233.95	148.62	96.76	156.20	159.62	198.34	124.59	201.59	207.55	301.36	0.00		
SAHANA	67.00	139.52	108.06	80.14	269.57	171.20	251.90	158.87	81.31	139.73	178.09	164.11	122.77	174.27	0.00	
AKH-8660	30.05	98.36	64.18	94.31	187.40	130.98	188.60	143.97	36.50	65.12	66.34	119.88	79.86	123.87	53.07	0.00
PS-348	199.67	128.63	85.33	244.96	331.92	194.17	211.87	100.51	198.20	223.96	175.37	104.95	127.91	281.73	105.58	132.49
Genotypes	LCMS 5	LCMS-2	AKH-87	AKH-32	AKH-081	PH-93	AKH-053	AKH-023	IC-1547	AKH-1234	AKH-3436	Sumgla	Narsimbha	Vikas	Sahana	AKH-8660	PS-348

Table-3 *Grouping of thirty-four genotypes into different clusters*

Cluster No.	I	II	III	IV	V	VI	VII
No of Genotypes	1	6	5	4	6	5	7
Genotypes grouped under cluster	LCMS – 2	KH – 118	AKH – 84635	AKH – 87	AKH – 8835	AH – 107	NH – 545
		AKH – 91	LRA – 5166	AKH – 081	JLH – 1594	GA – B	AKH – 24
		AKH – 9312	IC – 1547	AKH – 1234	NS – 95	PH – 93	GCot – 10
		LCMS – 5	AKH – 3436	SUMANGALA	AKH – 44	AKH – 023	AKH – 8801
		AKH – 053	NARSIMHA		AKH – 62	PS – 348	JK – 119
		VIKAS			AKH – 32		SAHANA
							AKH – 8660

Table-4 *Average Intra and Inter-cluster distances*

Cluster	I	II	III	IV	V	VI	VII
I	0.0000	24.0002	13.4395	30.1840	19.3952	30.5256	17.0321
II		6.9063	10.7190	14.0101	12.4468	13.5866	7.2684
III			5.3130	15.3115	14.0550	18.9834	8.6907
IV				7.5460	32.6155	10.8175	11.7512
V					8.1225	28.1827	14.1827
VI						8.0032	16.1926
VII							7.9411

***Diagonal figures indicate the intra-cluster distance*

The all recommended cultivation practices were applied to grow the healthy crop. Data were collected by randomly selected sample plants per plot basis for various economical as well as morpho-qualitative traits *viz*., days to 50 percent flowering, plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), number of seeds per boll, ginning outturn (%), seed index (g), lint index (%), 2.5% span length, fibre strength (g/tex), micronaire value (□g/inch) and seed cotton yield per plant (g). The data obtained from above observations were subjected to statistical analysis *viz*., analysis of variance, estimation of D^2 values, grouping of genotypes into different clusters and selection of parents for hybridization programme based on clustering pattern. The analysis of variance was performed to test the significance of differences among the genotypes for all the traits under study. The analysis of variance was carried out as per standard method [15, 28] for all the characters under investigation.

D^2 Analysis

The inverse matrix of original genotypic variance covariance matrix was computed to derive the relationship by which the original character mean (X1-X14) were transformed to an uncorrelated set of variables Y1-Y14. In term of variance and covariance, the D^2 values were obtained as follows [12]. The D^2 value obtained for a pair of population is taken as the calculated value of X^2 and is tested against the tabulated value of X^2 for 'p' degrees of freedom, where 'p' is the number of characters. The grouping of genotypes was done by Tocher's method [18]. The criterion used in clustering was that any two varieties belonging to the same cluster should at least on an average show smaller D^2 values than those belonging to different clusters. The average inter-cluster distance was calculated using all possible D^2 values between genotypes included in any two clusters. The cluster means were calculated for individual character on the basis of mean performance of the genotypes included in that cluster.

Result and Discussion

The data obtained from the field experiment is subjected to the analysis of variance for various quantitative traits under study. The ANOVA table [Table-1] revealed the highly significant differences among the genotypes were observed for all the fourteen traits under study indicating substantial genetic variability. The analysis of divergence to classify the available breeding material into useful groups. This is used as a measure of the statistical distance between the populations [27]. This approach has been followed by several workers [8, 17, 23, 1, 21, 25 and 30] in cotton whereas many others in various agricultural crops. Analysis of variance revealed the significant differences among the thirty-four genotypes for all the traits studied, indicating the existence of considerable amount of genetic variability among them. The simultaneous test of significance based on Wilk's Criteria for the pooled effect of all the fourteen characters studied has shown highly significant differences among the thirty-four genotype (X^2=1869.8080 at 462 d.f.). Therefore, D^2 values corresponding to 561 possible combinations among thirty-four genotypes have been presented in [Table-2], the D^2 values were found statically significant. The concept of genetic diversity is very important in differentiating a population. It is a prerequisite for initiating a hybridization programme because the choice of potent and diverse parents determines the success of such programmes. Selection of diverse parents in crossing programme serves the purpose of combining desirable genes to obtain superior recombination. Selection of parents based on per se performance, eco–geographical diversity had a limited success in past. However, several methods of multivariate analysis and metroglyph analysis have been found to be useful in selecting parents in crossing programme. The application of D^2 statistics in estimation of genetic diversity [18]. Systematic crop breeding programme has a vital role of genetic diversity based on the hypothesis that hybrids among the parental lines of diverse origin generally exhibit greater heterosis in relation to closely related parents. Genetic diversity arises either due to geographical separation or genetic barriers to cross-ability. Assessment of the genetic divergence by the use of D^2 statistics is useful in choosing the parents for many breeding objectives [14]. The 'Tocher's Method' was employed for grouping of the genotypes collected from various locations of the country into diverse cluster and presented in [Table-3] and [Fig-1]. All thirty-four genotypes were grouped into seven clusters. Cluster VII was largest involving seven genotypes *viz*., NH–545, AKH–24, GCot–10, AKH–8801, JK–119, Sahana and AKH–8660. The cluster no II and Cluster V shared six genotypes each. The cluster II constituted by KH–118, AKH–91, AKH–9312, LCMS–5, AKH–053 and Vikas. Whereas, the cluster (V) involved six genotypes *viz*., AKH–8835, JLH–1594, NS–95, AKH–44, AKH–62 and AKH–32. The cluster III and VI comprised of five genotypes each. The cluster III comprised, AKH–84635, LRA–5166, IC–1547, AKH–3436 and Narsimha genotypes. The genotypes AH–107, GA–B, PH–93, AKH–023 and PH–348 were grouped in cluster VI. The cluster IV comprised of four genotypes *viz*., AKH–87, AKH–081, AKH–1234 and Sumangala. The cluster I was comprised of only one genotype *i.e*. LCMS–2. The average intra and inter cluster statistical distances are presented in [Table-4]. The intra cluster distance ranged from 0 (Zero) to 8.1225. The cluster V recorded the maximum intra-cluster distance (D=8.1225) followed by cluster VI (D=8.0032) whereas, cluster I recorded zero intra-cluster distance as it comprises only one genotype. The average inter-cluster distance was maximum between cluster IV and V (D=32.6155) followed by distance between Cluster I and VI (D=30.5256) and between cluster I and IV (D=30.1840) respectively. The analysis of divergence to classify the available breeding material into useful groups. This is used as a measure of the statistical distance between the populations [27]. This approach has been followed by several workers in cotton [29, 16, 19, 8, 17, 5, 13, 25] whereas many others in various agricultural crops [7]. Analysis of variance revealed the significant differences among the thirty-four genotypes for all the traits studied, indicating the existence of considerable amount of genetic variability among them. On the basis of D^2 values for 561 possible pairs of the population of thirty-four genotypes were grouped into seven clusters, indicating the satisfactory magnitude of diversity in the genotypes. The cluster VII was a largest one, comprised maximum number of genotypes *i.e*. seven followed by cluster IInd and Vth comprising six genotypes each. While the cluster I was the smallest one, as it comprises only one genotype. Although the maximum number of genotypes were from Akola station, were scattered in all the clusters along with genotypes of other origin indicating there is no relationship between geographical diversity and genetic one, as earlier reports [4, 3, 29, 20, 9, 10,1, 6]. The practical significance of grouping the genotypes into different clusters and computing statistical distances between them are discussed here. While planning a crossing programme the consideration of statistical distances between the clusters as the index of genetic diversity is required [Table-4]. Hence the crosses between the genotypes belonging to the clusters having higher magnitude of average inter cluster distances may yield better segregants. The mean statistical distance may be considered arbitrarily as a guide line [4].

In the present study, all possible combinations beyond the mean statistical distance (D = 19.38), formed from seven different clusters have been arranged in descending order of magnitude of genetic distances and promising parents have been identified. The maximum inter-cluster distance (32.6155) was observed between Cluster IV and Cluster V, followed by Cluster I and Cluster VI (30.5256) and Cluster I and Cluster IV (30.1840).

The selection of diverse parents belonging to diverse clusters based on morphological observations for crossing programme for desirable segregants have been suggested by the earlier worker in cotton [19, 8, 17, 23, 21 and 25]. Further it is revealed that yield is complex characters needs to be improved by applying trait specific selection therefore, the relationship among yield contributing traits is important for ensuring improvement of productivity and profitability [31].

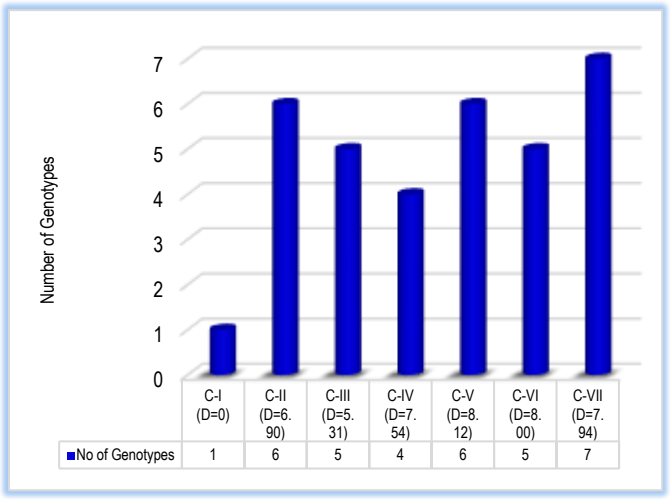

Fig-1 Cluster-wise distribution of Cotton Genotypes

Application of research: Selection of diverse parents for cotton improvement programme.

Research Category: Genetics and Plant Breeding, Cotton Breeding.

Abbreviations: ANOVA- Analysis of Variance

Acknowledgement / Funding: Authors are thankful to research facilities and support provided by the Senior Research Scientist, (AICRP on Cotton), Cotton Research Unit and Department of Agricultural Botany, College of Agriculture, Dr Panjabrao Deshmukh Krishi Vidyappeth, Akola, 444 104, Maharashtra, India.

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University: Dr Panjabrao Deshmukh Krishi Vidyapeeth, Akola 444 104, Maharashtra, India.
Research project name or number: Molecular analysis of polymorphism, heterosis and combining ability in cotton (*Gossypium hirsutum* L.)

Author Contributions: All authors equally contributed

Author statement: All authors read, reviewed, agreed and approved the final manuscript. Note-All authors agreed that- Written informed consent was obtained from all participants prior to publish / enrolment

Study area / Sample collection: Cotton Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola 444 104, Maharashtra

Cultivar / Variety / Breed name: Cotton (*Gossypium hirsutum* L.)

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.
Ethical Committee Approval Number: Nil

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