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GENETIC DIVERSITY FOR EARLINESS, FIBRE QUALITY AND YIELD COMPONENTS IN COTTON (*GOSSYPIUM* SPP)

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ABSTRACT
Cotton is one of the most important source of natural fibre in the World. The crop is also an essential source of vegetable oil and animal feed. Genetic improvement of important agronomic traits including fibre yield and quality has been slow due to its narrow genetic base, and this necessitate the need to study and explore on the germplasm resources with the aim to identify and select novel lines which can be used as parents in hybridization programmes. One hundred cotton genotypes were evaluated from diverse sources in a 10 x 10 lattice design, replicated twice across two environments in 2020 wet season. Significant ($p<0.01$) genotypic variation was observed for plant height, number of sympodial branches, number of bolls, seed cotton yield and the degree of pest attack. The phenotypic coefficients of variations were higher than the corresponding genotypic coefficients of variations for the entire traits studied. Highest genotypic and phenotypic coefficients of variations were recorded by seed cotton yield (18.2 and 36.5), number of sympodial branches (34.0 and 34.3) and number of bolls per plant (27.5 and 30.5). Genotypes VIR-7112-HG-69-15, VIR-7072, LA-213-SEA-ISLAND LEAF, BULGARIA-996 and 30858 with rank summation indices of 243, 270, 313, 330, 332 and 368 respectively, were the best potential parents for hybridization when targeting genetic improvement while LINIA-7010 with rank summation index of 712 was the least promising. It could be concluded that significant genetic variation exists for important agronomic and fibre quality traits like seed cotton yield, number of bolls, plant height, number of sympodial branches, fibre length and fibre fineness and selection based on the aforementioned could make genetic improvement feasible.

Keywords: genetic diversity, cotton genotypes, coefficient of variation

INTRODUCTION
Cotton (*Gossypium* spp), the king of apparel fibre, since times immemorial popularly called "White gold" is the world most important fibre crop. It is a native to tropical and subtropical regions of the world including America, India and Africa (Kumar *et al*., 2017). It is considered as the leading fibre crop grown in more than 80 countries (Shakeel *et al*., 2011) and serves as an important source of ingredient for livestock feed and oil, with world consumption of approximately 27 million metric tons per year (Chen *et al*., 2007).

Genetic variation within cultivated cotton is narrow while improvement for most desired traits is slow due to the narrow genetic base of most modern cotton varieties (Akter *et al*., 2019). The study calls for the need to explore existing germplasm resource such as cultivated, primitive and wild species to identify sources of novel traits for improvement of agronomic traits of the crop. To exploit the variability in the germplasm, the collection has to be evaluated so as to select the novel lines which can be used as parents in hybridization or can be released as variety.

In an attempt to broaden the genetic base of Nigeria's national cotton breeding programme, a total of 459 new cotton germplasm lines were introduced from the USA into Nigeria in 2018 by the Institute for Agricultural Research (IAR), Ahmadu Bello University, Zaria (IAR, 2021).

The current narrow genetic base of Nigerian cotton germplasm makes it important and necessary to take advantage of the newly introduced genetic resource through their characterisation for desired attributes and identification of lines with outstanding traits for genetic improvement.

Although cotton development started in Nigeria since 1903 and right now grown in more than 24 states across the six geopolitical zones including the Federal Capital Territory (Abuja), production has however declined over the years due to many biotic and abiotic factors, narrow genetic base and less diverse cotton genotypes (Rathinavel, 2017). Average seed cotton yield is estimated at 600 Kg/ha, while the global average is about 2,230 kg/ha (USDA, 2019). The low yield of Nigerian cotton when compared to the world average is indeed a major constraint towards competitive cotton production in the country. Furthermore, Nigeria's average fibre/lint yield is 190 Kg/ha which is still low when compared with world average of 644 kg/ha (USDA, 2019). The development of high yielding and superior quality cotton genotypes is obligatory considering the demand and importance of the crop. As a result, the breeders are giving utmost attention towards development of high yielding superior genotypes (Mansoor and Paterson, 2012; Borland and Mayers, 2015). To broaden the genetic base of the varieties, genetically distant genotypes should be used to develop high yielding cotton genotypes (Shakeel *et al.,* 2015; Sun *et al.,* 2019). and while obtaining superior genotypes germplasm with wider genetic variation for hybridization and introduction of new germplasm, it is essential to exploit the available germplasm (Li *et al.,* 2008). Seed cotton yield depends on yield contributing traits and such traits could be improved through hybridization with superior germplasm. A thorough understanding of the nature of crops, association of different agronomic traits with yield and performance status is obligatory for breeders to control the yield limiting factors.

In order to recognize novel genotypes that can be utilized in further breeding programmes this study was conducted to evaluate genetic diversity, earliness, yield and fibre quality traits of 100 cotton genotypes germplasm.

MATERIALS AND METHODS

Experimental Sites

The experiment was conducted in 2020 cropping season at two different locations, Institute for Agricultural Research (IAR) research field, Samaru Zaria, Kaduna State, Nigeria (northern guinea Savannah agro-ecological zone) on latitude 25.154865 and longitude 56.854692, and the second location was Malumfashi, Katsina State, Nigeria (Sudan Savannah agro-ecological zone) on latitude 11.761786 and longitude7.621555.

Plant material

The genetic materials consisted of 100 exotic cotton germplasm sourced from the United States Department of Agriculture (USDA) cotton repositories and other cotton elite/landrace of Nigerian origin. The list comprises four major cultivated species (Gossypium *hirsutum,* G. *barbadense,* G. *arboretum* and G. *herbaceum*) and other lines were of diverse origin.

Table 1: List of genotypes utilized in the study

Entry	Genotype	variety	Entry	Genotype	Variety
1	CH 253	*G. barbadense*	51	AUB NE-277	*G. hirsutum*
2	LMK-2	*G. barbadense*	52	HART 120-7	*G. hirsutum*
3	LINIA 7010	*G. barbadense*	53	AUB BR8	*G. hirsutum*
4	PALO VERDE	*G. barbadense*	54	ACALA SJ-2	*G. hirsutum*
5	PALMYRA 5	*G. barbadense*	55	DES 56	*G. hirsutum*
6	MENOUFI	*G. barbadense*	56	UKA J3(72)137	*G. hirsutum*
7	UC-3	*G. barbadense*	57	153-F	*G. hirsutum*
8	CH 252	*G. barbadense*	58	AUB BR7	*G. hirsutum*
9	GIZA 83	*G. barbadense*	59	TOMCOT SP-23	*G. hirsutum*
10	SEA ISLAND WHITE	*G. barbadense*	60	A-618	*G. hirsutum*
11	3199	*G. barbadense*	61	C2602	*G. hirsutum*
12	3960	*G. barbadense*	62	PAY MASTER 111-A	*G. hirsutum*
13	TADLA 29	*G. barbadense*	63	HAR U 585-12	*G. hirsutum*
14	3816	*G. barbadense*	64	TOMCOT SP-37H	*G. hirsutum*
15	PIMA S-6	*G. barbadense*	65	VIR 7147 OKRA LEAF 2	*G. hirsutum*
16	ADAN	*G. barbadense*	66	LA 213 SEA ISLANDLEAF	*G. hirsutum*
17	CHINA 10	*G. barbadense*	67	LA 887	*G. hirsutum*
18	TADLA 25	*G. barbadense*	68	WEST TEXAS ROUGH	*G. hirsutum*
19	3542	*G. barbadense*	69	LAH G-063	*G. hirsutum*
20	KARNAK 55	*G. barbadense*	70	VIR-7106 CR-142-45-7	*G. hirsutum*
21	TADLA 16	*G. barbadense*	71	PD 99035	*G. hirsutum*
22	2287	*G. barbadense*	72	UKA J3(72)036	*G. hirsutum*
23	TADLA 1	*G. barbadense*	73	REBA B50	*G. hirsutum*
24	UKA B2(72)193	*G. hirsutum*	74	VIR-7072	*G. hirsutum*
25	DES 24/CASCOT BR-1	*G. hirsutum*	75	BJA GLANDLESS NECTARIES	*G. hirsutum*
26	AUB OK F6-3	*G. hirsutum*	76	BULGARIA 436	*G. hirsutum*
27	GREGG/FOX 441 LANKART 3840	*G. hirsutum*	77	PD 98066	*G. hirsutum*
28	LANG-065	*G. hirsutum*	78	LONREN-2	*G. hirsutum*
29	VIR-7114 1780/N	*G. hirsutum*	79	AUBURN 73B-1	*G. hirsutum*
30	C6-5	*G. hirsutum*	80	BPA 68 C3 4030	*G. hirsutum*
31	S196	*G. hirsutum*	81	BULGARIA 996	*G. hirsutum*
32	A-637	*G. hirsutum*	82	TAM 1062	*G. hirsutum*
33	3342	*G. hirsutum*	83	S 845-12302 RESEL	*G. hirsutum*
34	AUB BR OK-7	*G. hirsutum*	84	UKA J2(72)817	*G. hirsutum*
35	LONREN-1	*G. hirsutum*	85	S-55	*G. hirsutum*
36	7107 CR-128-5-8	*G. hirsutum*	86	VIR-7067	*G. hirsutum*
37	S918-12302 RESEL	*G. hirsutum*	87	S-35	*G. hirsutum*
38	MISSDEL XP	*G. hirsutum*	88	VIR 7116	*G. hirsutum*
39	UK 64	*G. hirsutum*	89	STONE VILLE A	*G. hirsutum*
40	P-45	*G. hirsutum*	90	TERRA 207	*G. hirsutum*
41	TAM-2126	*G. hirsutum*	91	VIR-7113 HG-BR-8-N	*G. hirsutum*
42	UKA B1-(72)004	*G. hirsutum*	92	MALVI/ANI-1	*G. arboreum*
43	VIR-7112-HG-69-15	*G. hirsutum*	93	79-BH-97(MILL)	*G. arboreum*
44	IAC-RM 4-SM5	*G. hirsutum*	94	30858	*G. arboreum*

Table 1 continuation

45	AUB G1-201	*G. hirsutum*	95	DESI 88	*G. arboreum*
46	PAYMASTER 92	*G. hirsutum*	96	YONGLING	*G. herbaceum*
47	PD 4461	*G. hirsutum*	97	VAR-DIGVIJAY	*G. herbaceum*
48	B4 18 FERTILITY RESTORER GENE	*G. hirsutum*	98	SAMCOT 8	*G. herbaceum*
49	VIR-7205 LA OKRA LEAF-2	*G. hirsutum*	99	SAMCOT 9	*G. herbaceum*
50	A 46	*G. hirsutum*	100	SAMCOT 10	*G. herbaceum*

Experimental Design

The experiment was laid out in a 10 x 10 balanced lattice design with two replications. Each replication consisted of ten blocks each with ten genotypes. Each genotype was grown in one row plot of 10 m length. A spacing of 90 by 45 cm inter and intra row was used.

Agronomic and Cultural Practices

All cultural and agronomic practices according to the IAR recommendations for cotton were adopted (CDC, 2007). Three to four seeds were sown per hill and thinning was done to reduce population to two plants per stand at three weeks after sowing (WAS). Butachlor (active ingredient butachlor) was applied as pre-emergence herbicide at the rate of 4 litres per hectare. Three supplemental hoe weeding were done with the first at 3 WAS, the second and third at 6 and 9 WAS respectively. Fertilizer application and pest control were done as reported by Yahaya (2017). Sixty-five kg/ha of nitrogen in the form of Urea (46% N) was applied**.**

The application was in split doses – with the first and second half applied at 3 and 8 weeks after sowing respectively. Phosphorus (P) was applied in the form of single super phosphate (P_2O_5) at the rate of 35 kg/ha whereas 30 kg/ha of potassium was also applied in the form of muriate of potash (K_2O). The P_2O_5 and K_2O were applied after the first weeding (at 3 WAS) into shallow grooves 8-10cm away from the plants. Lambda-Cyhalothrin (Karate), a non-persistent insecticide, was sprayed at 8-9 weeks after sowing at the rate of 400 ml/ha to control extra early pests (aphids and white-flies).

Data were collected on 11 characters that consisted of both agronomic and fibre quality traits. Data were recorded on five randomly selected plants per entry from all blocks across the replications. The characters measured includes stand count at emergence, stand count at harvest, plant height, days to 50% flowering, days to 50% square, number of sympodial branches per plant, number of bolls per plant, boll weight, seed cotton yield per plant, degree of pest attack, fibre length and micronaire.

Data Analysis

Data collected from the two field environments were analysed. Analysis of variance was done (ANOVA) using the SAS software (SAS institute Inc. 2004). Thereafter, Fisher's protected least significant difference (LSD) test was used to make comparisons between treatments means (Gomez and Gomez, 1984). The statistical model used for the analysis for two environments was based on the Linear model for lattice design.

Coefficient of variation was computed and then used to compare variability of each character studied. Phenotypic and genotypic coefficients of variance were estimated (Burton and Devane, 1953) to quantify the genetic variance among the genotypes.

Phenotypic and genotypic variances were estimated using the formula below;

$$V_g = \frac{MS_g - MS_e}{r}$$

$$V_p = V_g + MS_e$$

Where V_g= genotypic variance, V_p = phenotypic variance, MS_g = mean square of genotypes, MSe = mean square of errors, r = number of replications.

$$GCV = \frac{\sqrt{V_g}}{\bar{X}} * 100$$

$$PCV = \frac{\sqrt{V_p}}{\bar{X}} * 100$$

GCV= genotypic coefficient of variance
PCV= phenotypic coefficient of variance
$\sqrt{V_g}$ = genotypic standard deviation
$\sqrt{V_p}$ =phenotypic standard deviation
$\bar{X}$ = general mean of the character.

RESULTS AND DISCUSSION

The existence of significant ($p \leq 0.05$) and highly significant differences in the traits as observed in the present study suggests the presence of considerable genetic variability among the cotton genotypes (Table 2). The genotypes varied significantly for all measured traits except fibre fineness (FFN). Genotype x Environment interaction was also signinficant for plant height (PHT), number of sympodial branches (NOS), number of bolls (NOB), degree of pest attack (DPA), boll weight (BW) and seed cotton yield (SCY). This implies that environment is contributing to the expression of these traits. Replication was also significant, which indicates that the experimental design and/or blocking used was important and had captured the heterogeneity of the field. Agronomic traits such as the days to first flowering (DFF) varied from 54 – 68 days, yield components like the number of sympodial branches (NOS) ranged from 6.2-48.0 while the number of bolls per plant (NOB) ranged from 16.8-106.2 (Table 3). For boll weight (BW), it ranged from 1.9 - 5.8 g and seed cotton yield (SCY) from 108-1107 kg, however fibre quality traits like fineness (FFN) and length (FBL) ranged from 3.0 - 5.2 ug/inch, and 24-36 mm, respectively. The presence of wide variation among these genotypes could be exploited in breeding programmes to improve yield via selection and genetic recombination through crossing. Important parents can be identified for crossing with the local adapted varieties/landrace. These observations are contrary with some earlier research reports by Guang and Xiong-Ming, (2006), who stated that presence of low level of genetic variability in cotton and the cotton genotypes were obtained from few sources or closely related. The lower variability may be due to close relatedness of the cotton genotypes in their study. Materials used in the current study were a collection from USDA sourced from different cotton growing regions of the world that cut across four cultivated species.

Table 2: Mean squares of agronomic and fibre traits from cotton genotypes evaluated across two locations (Samaru and Malumfashi) in 2020.

Source of variation	DF	SCE	SCH	PHT	NOS	DFS	DFF	NOB	DPA	BW	SCY	FBL	FFN
Block (Env*Rep)	37	2.87**	2.16	14.60	3.63	0.98	0.91	13.51**	0.51*	1.05	4.05	0.09*	6.8*
Genotype	99	19.85**	31.39**	928.65**	271.56**	40.85**	16.30*	509.41**	0.47*	2.36**	1683.08**	0.11*	32.9
Environment	1	0.81	0.30	43077.00**	362.90**	0.00	0.00	2106.81**	0.00	161.29**	131232.31**	-	-
Replication	1	1.69	14.06**	99.20**	0.42	1.00	2.56	42.25*	0.72	6.76**	46.38**	0.05*	0.2*
Genotype*Envt	-	1.18	1.82	636.10**	4.06**	0.00	0.00	93.38**	0.49*	2.24**	1264.19**	-	-

DF= degree of freedom, SCE = stand count at emergence, SCH = stand count at harvest, PHT = plant height, NOS = number of sympodial branches DFS = days to first square, DFF = days to first flowering, NOB = number of bolls, DPA = degree of pest attack, BW = boll weight (g), SCY = seed cotton yield (kg/ha), FBL = fibre length, FFN = fibre fineness, * indicate significance (P< 0.05), ** indicate significance (P<0.01). Gen = Genotypes, Rep = Replication/s, Env = Environment/s

Table 3: Phenotypic distribution of the agronomic fibre traits of cotton evaluated across two environments (Samaru and Malumfashi) in 2020

GENOTYPES	SCE (count)	SCH (count)	PHT (cm)	NOS (count)	DFS (days)	DFF (days)	NOB (count)	DPA	BW (g)	SCY (kg)	FFN (ug/inch)	FBL (mm)	RSI
Best 10													
LONREN-1	7.3	8.8	115.8	25.1	54	65	37.0	2.4	4.1	533	4.2	25	243
VIR-7112-HG-69-15	6.3	5.9	98.7	14.3	51	62	27.2	2.1	3.2	356	4.7	29	270
VIR-7072	8.7	7.2	108.6	18.4	53	63	31.5	2.3	3.7	464	4.9	31	313
LA 213 SEA ISLAND LEAF	8.9	12.1	130.3	33.5	59	66	47.7	2.8	4.8	769	4.7	34	330
BULGARIA 996	8.6	10.5	126.2	29.3	56	65	41.7	2.6	4.4	655	3.9	29	332
30858	10.2	13.1	140.0	36.3	60	66	52.4	3.0	5.1	971	5.1	33	368
S-55	9.5	16.5	149.0	48.0	63	68	106.2	3.2	5.8	1107	4.8	32	371
BPA 68 C3 4030	9.7	7.6	110.2	20.5	53	64	32.7	2.3	3.8	494	4.3	30	380
HAR U 585-12	6.6	11.6	129.2	33.1	58	66	46.3	2.8	4.7	761	4.7	30	389
VAR-DIGVIJAY	7.6	8.5	113.5	24.1	54	64	34.4	2.4	4.0	523	4.4	31	390
Worse 10													
CH 252	6.3	5.4	92.7	13.6	51	61	24.6	1.9	3.1	303	4.3	30	638
AUB BR7	11.4	11.8	130.0	33.2	58	66	46.8	2.8	4.7	761	4.1	31	639
UKA B2(72)193	6.2	5.8	98.1	14.0	51	61	27.1	2.1	3.1	347	3.9	29	650
TADLA 1	7.0	10.9	128.2	31.1	57	66	44.4	2.7	4.6	713	4.5	27	664
AUB BR OK-7	6.7	9.2	117.8	26.2	55	65	38.7	2.4	4.2	567	4.5	29	667
SAMCOT 8	5.4	7.4	109.3	19.6	53	64	31.9	2.3	3.7	477	4.9	26	670
VIR 7116	6.3	14.1	142.0	38.1	61	66	53.4	3.1	5.4	1034	4.5	32	677

Table 3 continuation

GENOTYPES	SCE (count)	SCH (count)	PHT (cm)	NOS (count)	DFS (days)	DFF (days)	NOB (count)	DPA	BW (g)	SCY (kg)	FFN (ug/inch)	FBL (mm)	RSI
VIR-7114 1780/N	7.7	7.1	107.0	17.8	53	63	31.4	2.2	3.6	447	3.8	28	694
S918-12302 RESEL	10.6	7.5	109.7	19.9	53	64	32.5	2.3	3.7	486	3.5	29	708
LINIA 7010	4.7	6.1	99.1	14.6	51	62	27.7	2.1	3.2	369	4.6	31	712
CV	15.17	14.79	2.87	6.69	1.99	1.41	6.85	24.76	22.59	30.4	4.38	29.4	??
LSD	1.73	1.80	4.58	2.25	1.51	1.26	3.54	0.83	1.25	239	13.75	10.70	??
MEAN	8.15	8.72	114.40	24.02	54.56	63.94	37.05	2.39	3.96	562.4	1.20	0.63	??
RANGE	3.53-14.44	1.7-16.5	72.41-148.9	6.23-48.02	48.8-62.9	53.7-67.6	16.8-106.2	1.4-3.21	1.9-5.8	108-1107	3.00-5.19	24-36	??

SCE = stand count at emergence, SCH = stand count at harvest, PHT = plant height, NOS = number of sympodial branches DFS = days to first square, DFF = days to first flowering, NOB = number of bolls, DPA = degree of pest attack, BW = boll weight (g), SCY = seed cotton yield (kg/ha), FBL = fibre length, FFN = fibre fineness, RSI= rank summation index, CV = coefficient of variation, LSD = least significant different

Table 4 presents the level of variability as determined by phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). The highest coefficient of variability for both phenotype and genotype (36.5 and18.2) were realised in seed cotton yield, number of sympodial branches (34.30 and 34.04) and number of bolls (30.45 and 27.53), however these explained their potential use for improvement through hybridization and selection. Similar findings reported that there is a wide range of variation for almost all the characters that showed very small difference between their GCV and respective PCV (Sumathi and Nadarajan, 1996; Jagtap and Mehetre, 1998; Rao and Reddy, 2001; Erande *et al*. 2014). This implies that they were least affected by environment. The equal magnitudes of PCV and GCV for fibre length and fibre fineness depict ample scope for improvement through selection. The traits with high differences between PCV and GCV indicated influence of environment on the expression of the traits thereby restricting the scope for their improvement through early selection. Low values of GCV and PCV for plant height, days to first square formation, days to first flower, degree of pest attack and fibre length indicated narrow range of variability for these traits also hence restricts the scope for selection. Lowest GCV and PCV for DFF, PHT and uniformity ratio were previously reported (Sumathi and Nadarajan, 1996; Jagtap and Mehetre, 1998; Rao and Reddy, 2001; Erande *et al*. 2014). Moderate variability among the genotypes was observed based on the range in all the means recorded in the morphological and fibre quality traits. Therefore, the best genotypes for each trait could be selected. No single genotype was found to possess all the desirable traits, thereby indicating the need for hybridization for improvement of desirable trait in a variety. Thus, as a strategy for obtaining superior cotton genotypes possessing traits of interest and selection on the basis of the desirable traits followed by hybridization will be very effective.

Table 4: Estimates of variances and coefficient of variations for morphological and fibre quality traits in cotton genotypes evaluated under two environments (Samaru and Malumfashi) in 2020

Traits	$\partial^2 e$	$\partial^2 g$	$\partial^2 p$	GCV	PCV	H (%)
SCE	1.5	4.7	5.1	0.3	27.8	90.9
SCH	1.7	7.4	7.8	0.3	32.1	94.2
PHT	10.8	73.1	232.2	7.5	13.3	31.5
NOS	2.6	66.9	67.9	34.0	34.3	98.5
DFS	1.2	10.2	10.8	5.9	6.0	94.5
DFF	0.8	4.1	10.6	3.4	5.1	38.4
NOB	6.4	104.0	127.4	27.5	30.5	81.7
DPA	0.4	0.0	0.1	3.0	14.3	4.3
BW	0.8	0.0	0.6	4.4	19.4	5.1
SCY	2.9	104.7	420.8	18.2	36.5	24.9
FFN	0.4	16.3	16.5	92.0	92.6	98.8
FBL	0.1	0.0	0.1	2.4	7.9	9.3

SCE = stand count at emergence, SCH = stand count at harvest, PHT = plant height, NOS = number of sympodial branches DFS = days to first square, DFF = days to first flowering, NOB = number of bolls, DPA = degree of pest attack, BW = boll weight (g), SCY = seed cotton yield (kg/ha), FBL = fibre length, FFN = fibre fineness. , $\partial^2 e$ = error variance,$\partial^2 g$ =genotypic variance, $\partial^2 p$ = phenotypic variance, GCV = genotypic coefficient of variation PCV = Phenotypic coefficient of variation, H= heritability

The genotypes used in this study varied significantly for important agronomic, seed cotton yield and its, components and fibre quality traits which may have agronomic impact in further selection for genetic improvement. The genotypes LONREN-1, VIR-7112-HG-69-15, VIR 7015, VIR 7072, LA 213 SEA ISLAND LEAF, BULGARIA 996, 30858 and S – 55 based on the rank summation index which were the best genotypes in respect of all the traits studied. It is therefore recommended that these genotypes be used in breeding programmes for yield improvement of seed cotton in Nigeria.

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