



Research Article

Variability studies and genetic divergence in cotton (*Gossypium hirsutum* L.) germplasm using multivariate analysis

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Abstract

Two hundred germplasm lines of upland cotton (*Gossypium hirsutum* L.) were evaluated for genetic variability and divergence for seed cotton yield attributing traits and fibre quality traits at Regional Agricultural Research Station, ANGRAU, Lam, Guntur. The analysis of variance indicated significant genetic variability among the germplasm lines. The close symmetry between the phenotypic and genotypic coefficient of variances and lower values of environmental coefficient variance for all the studied attributes indicated that the traits were genetically controlled and under less influence of the environment. Higher broad sense heritability and genetic advance for all seed cotton yield attributing traits indicated that these attributes were governed by additive genes and early phenotypic selection for their improvement might be effective. Five principal components (PCs) were depicted as having Eigen value >1 and cumulative variability of 66.17%, out of which PC1 accounted for 26.81% and PC2 for 14.08% of variability. The attributes of significance depicted in PC1 were seed index, lint index, upper half mean length, uniformity index, and staple length. Bi-plot revealed that Lam GPC232, Lam GPC223, Lam GPC225, Lam GPC135, Lam GPC62, Lam GPC85, Lam GPC168, and Lam GPC203 were the most divergent germplasm. These genetically diverse genotypes with the absolute and significant association of attributes could be utilized in a future cotton breeding program.

Keywords: Genetic variability, Genetic advance, Heritability, PCA

INTRODUCTION

Cotton (*Gossypium hirsutum* L.) commonly known as “White Gold” is a fibre crop that is an immensely important crop for the sustainable economy of India and the livelihood of the Indian cotton farming community. It is cultivated in about 312 lakh hectares across the world and in around 117 lakh hectares in the country. India accounts for around 37.5% of the global cotton area and contributes to 26% (6.20 MT) of the global cotton production of 23.92 MT (<https://cotcorp.org.in/>). Plant breeding is an evolutionary process for the conservation of genetic stock in the best shape for superior cultivars,

breeding lines, and wild races (Latif *et al.*, 2015). The main objective of cotton breeding is continuous improvement in the genetics of the available plant germplasm for the creation of new genetic recombinants with objectives of seed cotton yield potential per unit area with acceptable fibre quality under varying agro-climatic conditions (Ali and Khan, 2007).

Genetic variability depends upon numerous agronomical and morphological attributes and their interaction with surrounding biotic and abiotic factors

(Liaqat *et al.*, 2015). The magnitude and nature of obtainable genetic variability among the germplasm have sufficient scope for utilization in successful breeding programs for the improvement of various attributes (Ahsan *et al.*, 2015).

The heritability estimated in the broad sense and expected genetic advance estimates reflects the preponderance of additive genetic effects controlling various attributes (Reddy and Reddy, 2016) and enable breeders in the execution of early generation phenotypic selection procedure for yield attributes which could result in better response to selection (Vineela *et al.*, 2013). Hence, the information regarding genetic variability, heritability and genetic advance existing in the material under study is significantly essential for any crop improvement program (Reddy and Reddy, 2016).

Seed cotton yield and fibre quality in cotton depends on sympodia and monopodia/plant, bolls/plant, seed index, boll weight, lint index and ginning out-turn and their association with yield is of utmost importance (Latif *et al.*, 2015). Principal component analysis has been used by many authors (Saeed *et al.*, 2014; Rehman *et al.*, 2015) to elucidate the variability among numerous germplasm for their utilization in future cotton improvement programs. Keeping in view the significance of genetic diversity, the present research was conducted to explore the genetic divergence and relationship among cotton germplasm for yield, yield-related traits, and fibre quality attributes.

MATERIALS AND METHODS

The experiment was laid out at Regional Agricultural Research Station, Lam, Guntur, Andhra Pradesh (situated at 28.290 E longitude, 16.100N latitude, and 31.5m altitude) during *Kharif*, 2021-22. The experimental material comprised of 200 germplasm accessions, which were planted in an augmented block design (Federer, 1956), in four blocks. In each block, along with 48 test entries, two check entries (NDLH 1938 and LHDP cotton) were planted randomly. Each genotype was sown in two

rows with a row length of 6.0 m each with a spacing of 105 x 60 cm. Recommended package of practices were followed for better crop growth during the crop period. Data was collected in five randomly selected plants on various seed cotton yield contributing traits like plant height (cm), number of monopodia/plant, number of sympodia, number of bolls/plant, boll weight (g), lint index (g), seed index (g), ginning out turn (%) and fibre quality parameters like Upper Half Mean Length (UHML) (cm), uniformity index, micronaire ($\mu\text{g}/\text{inch}$), fibre strength (g/tex) and elongation (%). The analysis of variance was performed as per Johnson *et al.* (1955) and Falconer (1967). R software was used to study the factor analysis using the Pearson correlation matrix. Principal component analysis was assessed based on Kaiser criterion as per Kaiser (1960) using XL-STAT.

RESULTS AND DISCUSSION

ANOVA suggested existence of highly significant variation for the characters, plant height (cm), number of monopodia per plant, number of sympodia/plant, seed index, lint index, UHML, and strength (**Table 1**). The environmental coefficient of variation (ECV), genotypic coefficient of variation (GCV) and phenotypic coefficients of variation (PCV), heritability in the broad sense (h^2), genetic advance (GA) and expected genetic advance in the percentage of means (GAM) were determined for seed cotton yield and fibre quality traits. The results revealed higher heritability (h^2) (ranged from 75.09 to 99.50) coupled with high GA estimates (ranged from 0.77 to 63.46) for all the traits under study. The PCV estimates ranged from 1.04 to 47.48 while GCV estimates ranged from 0.92 to 47.16 and also showed a close affinity with each other for all traits under study (**Table 2**). The least PCV (1.04%) and GCV (0.92) values were observed for uniformity index. It was observed that there was a close similarity between phenotypic and genotypic variance for all the traits under study indicating less environmental influence for the expression of all the traits. Since the differences are inclined by the extent of the mechanisms of quantities of different traits, a

Table 1. Analysis of variance (ANOVA) for seed cotton yield attributes and fibre traits in cotton germplasm

Source	DF	Plant height (cm)	Number of Monopodia/plant	Number of Sympodia/plant	Number of bolls/Plant	Boll weight (g)	Seed Index (g)	Lint Index (g)	GOT (%)	UHML (mm)	UI (%)	MIC (μg)	Str (g/tex)	Elg (%)
Blocks	3	1672.50 **	0.12*	60.23**	1461567 **	0.45*	21.36**	1.52**	14.14	3.82*	0.35	1.40*	32.07**	2.02*
Treatment	193	955.11**	0.51**	13.84*	120.47	0.23	4.43*	0.46**	10.60	2.62*	0.81	0.29	2.65*	0.19
ERROR	3	4.83	0.01	1.08	17.33	0.05	0.41	0.01	2.65	0.14	0.17	0.07	0.27	0.04

**Significant at 1% level; *Significant at 5% level

GOT: Ginning Out Turn, UHML: Upper Half Mean Length, UI: Uniformity Index, MIC: Micronaire, Str: Strength, Elg: Elongation

Table 2. Estimation of environmental coefficient (ECV), genotypic coefficient (GCV), phenotypic coefficient (PCV) of variances, heritability (h^2) and expected genetic advance (GA) and genetic advance as per cent of mean in cotton germplasm

Trait	ECV (%)	GCV (%)	PCV (%)	h^2 (bs)	GA	GAM (%)
Plant height (cm)	1.92	27.07	27.14	99.50	63.46	55.63
Number of monopodia/plant	5.49	47.16	47.48	98.66	1.43	96.50
Number of sympodia/plant	6.62	23.42	24.35	92.52	7.24	46.41
Number of bolls/plant	10.65	28.32	30.26	87.61	21.34	54.62
Boll weight (g)	6.48	12.82	14.37	79.66	0.77	23.58
Seed index (g)	5.18	15.69	16.53	90.17	3.79	30.70
Lint index (g)	1.57	15.18	15.27	98.93	1.33	31.12
GOT (%)	4.61	8.01	9.25	75.09	5.04	14.31
UHML (mm)	1.32	5.62	5.78	94.75	3.13	11.28
UI (%)	0.49	0.92	1.04	77.65	1.38	1.67
MIC (μ g/inch)	6.46	11.71	13.38	76.66	0.87	21.13
Strength (g/tex)	1.84	5.92	6.20	91.17	3.28	11.65
Elongation (%)	3.07	6.69	7.36	82.57	0.79	12.52

measure of coefficient of variation which is independent of the unit of measurement is more useful in comparing between populations. The traits plant height, number of monopodia per plant, number of sympodia per plant and number of bolls per plant exhibited higher PCV and GCV estimates signifying the existence of substantial genetic variability for these characters. Direct selection based on these traits will be useful to identify promising genotypes and to utilize them in further breeding programs. These results were in accordance with the reports of Dheva and Potdukhe (2002), Preetha and Raveendran (2007), Gnanasekaran *et al.* (2018) and Sri Subalakhshmi *et al.* (2022). The characters, boll weight per plant, seed index and lint index recorded moderate PCV and GCV estimates. Girase and Mehetre (2002) and Harshal (2010) have also reported similar results. These traits could be improved by rigorous selection. Low PCV and GCV estimates were recorded for the traits ginning out turn, UHML, uniformity index, micronaire value, fibre strength and elongation which in turn reflected that there was less divergence in the available germplasm. These results are in agreement with Venkatesan (2008). All the traits under study recorded high heritability estimates. The highest heritability estimates were recorded for ginning out turn percent (99.50%) while the lowest for plant height (75.09%). Selection of traits based on heritability in combination with genetic advance could be highly rewarding. The range for genetic advance as percent of mean for 13 traits varied from 1.67 to 96.50%. The number of monopodia per plant exhibited higher genetic advance as percent of mean (96.50%) followed by plant height (55.63%), number of bolls/plant (54.62), number of sympodia per plant (46.41 %), lint index (31.12%), seed index (30.70%), boll weight/plant (23.58%) and micronaire (21.13%), while the lowest value (1.67%) was exhibited by the trait uniformity index.

The traits plant height, number of monopodia per plant, number of sympodia per plant, number of bolls/plant, boll weight, seed index, and lint index recorded high heritability coupled with high genetic advance and hence, these traits are highly reliable during selection, whereas the traits, ginning out turn, UHML, strength and elongation exhibited high heritability combined with moderate genetic advance. These results are in agreement with Muhammad *et al.* (2004).

Lint index exhibited significant positive correlation at genotypic level with number of bolls/plant (0.223**), boll weight (0.156*), seed index (0.746**), UHML (0.235**), uniformity index (0.172*), strength (0.229**), elongation (0.150*) and ginning out (0.142*), while, seed index showed significant positive association with the plant height (0.140*), number of sympodia/plant (0.144*), number of bolls/plant (0.264**), boll weight (0.269**), lint index (0.746**), UHML (0.378**), uniformity index (0.356**), strength (0.340**) and elongation percent (0.172*) (Table 3). The characters with significant positive association can be exploited in the selection program leading to the improvement of cotton varieties. Plant height (cm) showed a significant positive association at the genotypic level with the number of sympodia (0.185**), number of bolls/plant (0.228**) and seed index (0.140*). These results agreed with the reports of Venkateswaralu *et al.* (2010) and Kaushik and Kapoor (2006). Fibre length (UHML) showed a significant positive association with the number of bolls/plant (0.184**), seed index (0.378**), lint index (0.235**), strength (0.496**) and elongation percent (0.245**). A non-significant negative correlation was observed between micronaire and UHML (-0.098) and ginning out turn (-0.122). Patil Malagouda *et al.* (2014) in their studies on cotton observed a negative association of UHML with micronaire.

Table 3. Genotypic correlation coefficients for seed cotton yield attributes and fibre traits in cotton germplasm

	Plant height (cm)	Number of Monopodia/plant	Number of Sympodia/plant	Number of bolls/Plant	Boll weight (g)	Seed Index (g)	Lint Index (g)	GOT (%)	UHML (mm)	UI (%)	MIC (µg)	Str (g/tex)
Number of Monopodia/plant	0.047											
Number of Sympodia/plant	0.185**	0.148*										
Number of bolls / Plant	0.228**	-0.035	0.381**									
Boll wt (g)	0.182*	-0.134	0.117	0.076								
Seed Index (g)	0.140*	-0.084	0.144*	0.264**	0.269**							
Lint Index (g)	0.101	-0.053	0.134	0.223**	0.156*	0.746**						
UHML (mm)	0.062	0.001	0.100	0.184**	0.070	0.378**	0.235**					
UI (%)	0.053	-0.056	0.058	0.174*	0.113	0.356**	0.172*	0.901**				
MIC (µg)	0.083	-0.102	-0.002	0.105	0.161*	0.005	0.034	-0.122	-0.098			
Str (g/tex)	0.018	0.004	0.096	0.307**	0.138	0.340**	0.229**	0.484**	0.496**	-0.151*		
Elg. (%)	0.114	0.001	-0.036	0.062	0.003	0.172*	0.150*	0.210**	0.245**	-0.043	0.106	
GOT (%)	0.026	-0.014	-0.010	-0.091	-0.106	-0.403**	0.142*	-0.272**	-0.292**	0.109	-0.147*	-0.088

GOT: Ginning Out Turn, UHML: Upper Half Mean Length, UI: Uniformity Index, MIC: Micronaire, Str: Strength, Elg: Elongation

Kaiser (1960) reported that the eigen value-one criterion is the effectively used criterion for the discovery of principal components. It is often called as the Kaiser criterion which is used to uphold and evaluate any component with an eigenvalue >1. To discover the substantial variation among 200 upland cotton germplasm, for seed cotton yield-related attributes and fibre quality traits, principal component analysis was carried out based on mean data of biometrical observations (Table 4). Out of the 14 principal components (PCs), five exhibited 66.61% of cumulative variability with Eigenvalue >1 for the characters under study. The PC I recorded eigenvalue of 3.754 with 26.814% variability. The accessions in PC I exhibited positive effects for the traits plant height (0.120), number of sympodia (0.126), number of bolls/plant (0.217), boll weight (0.231), seed index (0.438), lint index (0.392), UHML (0.364), uniformity index (0.352), fibre strength (0.319), elongation (0.156) while negative effects were observed for the number of monopodia per plant (-0.045), ginning out turn (-0.129) and micronaire value (-0.013). An eigenvalue of 1.972 with 14.085% the variability was recorded in PC II. The traits like the number of monopodia per plant (0.006), UHML (0.391), uniformity index (0.421), fibre strength (0.235) and fibre elongation (0.140) exhibited positive effects while negative effects were reported for plant height (-0.159), number of bolls/plant (-0.061), boll weight (-0.134), seed index (-0.163), lint index (-0.364), ginning out turn (-0.349) and micronaire value (-0.291). An eigenvalue of 1.455 with a variability

of 10.394% was exhibited in PC III. In this group, positive effects were observed for plant height (0.396), number of monopodia (0.312), number of sympodia (0.586), number of bolls per plant (0.479), boll weight (0.099), micronaire (0.131) and fibre strength (0.033) while negative effects were recorded for seed index (-0.123), lint index (-0.186), ginning out turn (-0.104), UHML (-0.022), uniformity index (-0.031) and elongation (-0.116). The PC IV depicted 1.106 eigenvalues and 7.901% of variability. The germplasm lines in PC IV offered positive results for plant height (0.004), number of monopodia (0.543), number of sympodia (0.149), lint index (0.190), ginning out turn (0.412), UHML (0.087), uniformity index (0.013) and fibre strength (0.112) while negative results for the number of bolls per plant (-0.100), boll weight (-0.400), seed index (-0.061), micronaire (-0.514) and elongation (-0.015). An eigenvalue of 1.039 with 7.422 % of variability was observed for PCV. The germplasm in PCV presented positive effects for plant height (0.071), number of sympodia (0.002), number of bolls per plant (0.272), ginning out turn (0.602), UHML (0.124), uniformity index (0.138), micronaire (0.212), fibre strength (0.207) and elongation (0.344) while negative results for number of monopodia per plant (-0.396), seed index (-0.363) and lint index (-0.077).

In the principal component analysis, the scatter plot (Fig. 1) also known as polygon, differentiated the 200 germplasm lines based on the genetic nature. The

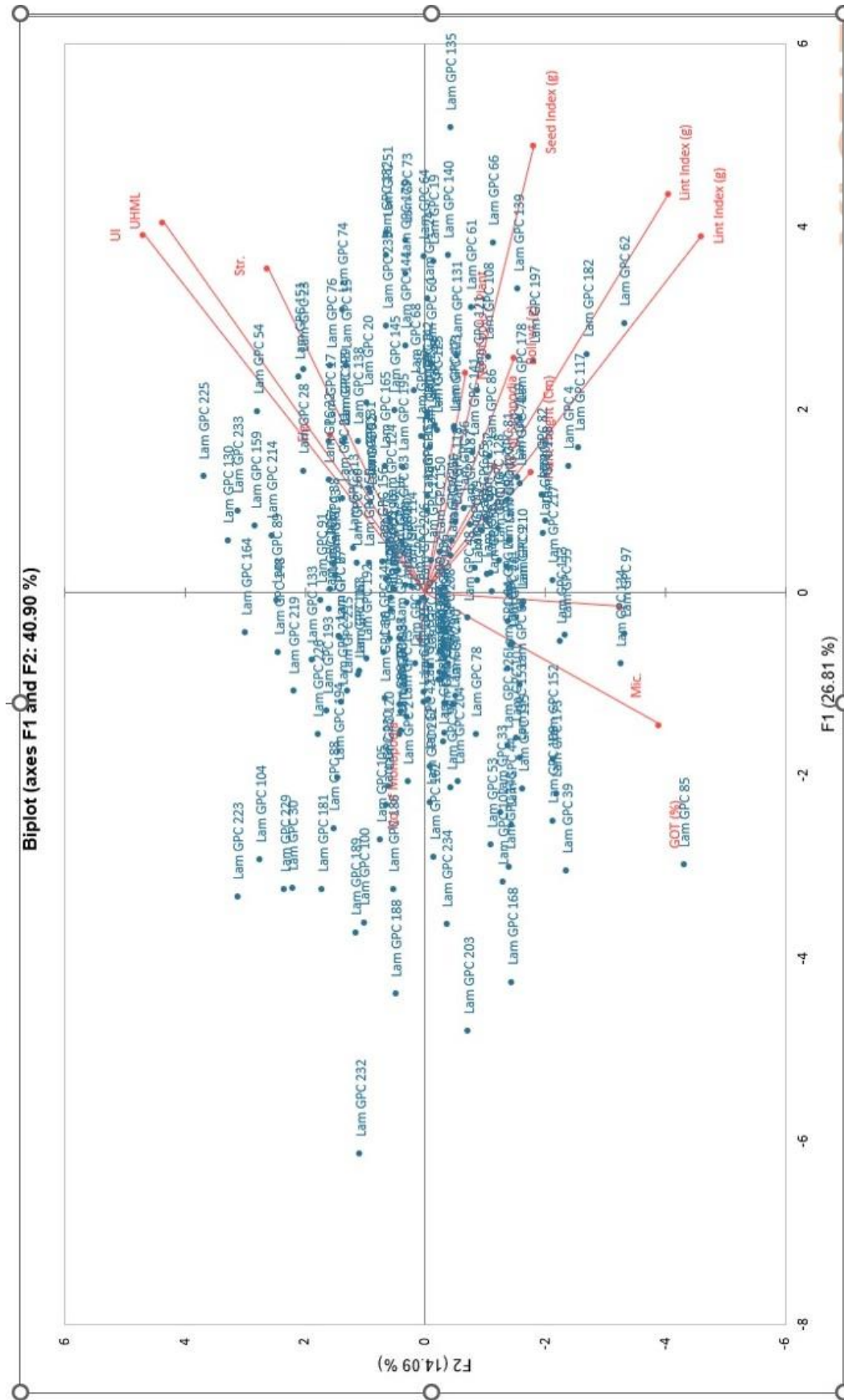


Fig. 1. Scatter biplot for cotton germplasm lines

Table 4. Principal component analysis

Eigen values, percentage of variability, cumulative variability, and attributes that contributed towards principal components					
Statistical variable	PC1	PC2	PC3	PC4	PC5
Eigenvalue	3.754	1.972	1.455	1.106	1.039
Variability (%)	26.814	14.085	10.394	7.901	7.422
Cumulative %	26.814	40.899	51.293	59.194	66.617
Traits	PC1	PC2	PC3	PC4	PC5
Plant Height (Cm)	0.120	-0.159	0.396	0.004	0.071
Number of Monopodia	-0.045	0.006	0.312	0.543	-0.396
Number of Sympodia	0.126	-0.105	0.586	0.149	0.002
Number of bolls / Plant	0.217	-0.061	0.479	-0.100	0.272
Boll wt (g)	0.231	-0.134	0.099	-0.400	-0.152
Seed Index (g)	0.438	-0.163	-0.123	-0.061	-0.363
Lint Index (g)	0.392	-0.364	-0.186	0.190	-0.077
GOT (%)	-0.129	-0.349	-0.104	0.412	0.602
UHML (mm)	0.364	0.391	-0.022	0.087	0.124
UI (%)	0.352	0.421	-0.031	0.013	0.138
MIC (µg)	-0.013	-0.291	0.131	-0.514	0.212
Str (g/tex)	0.319	0.235	0.033	0.112	0.207
Elg. (%)	0.156	0.140	-0.116	-0.015	0.344

germplasm lines Lam GPC232, Lam GPC223, Lam GPC225, Lam GPC135, Lam GPC62, Lam GPC85, Lam GPC168 and Lam GPC203 were identified as the most divergent germplasm as they were located at the apex of polygon. These genotypes could be effectively used in crop improvement. The germplasm accessions, Lam GPC 114, Lam GPC 206, Lam GPC 99, Lam GPC 1, Lam GPC 87, Lam GPC 209 and Lam GPC 136 were located very near to the origin of the polygon. It could be because of low genetic diversity among the accession, which could be attributed to their narrow genetic base.

Five principal components out of the fourteen exhibited eigenvalue >1 and cumulative variability of 66.61% for all the attributes under study. Among these groups, PC I and PCII contributed cumulative variability of about 40.9%. In PC I and PC II, the traits, UHML, uniformity index, and fibre strength were found to exhibit great influence towards cumulative variability. Hence, special importance should be given to these traits in cotton breeding programs. Similar findings were reported by Kaleri *et al.* (2015).

Based on the study it could be concluded that the traits plant height, number of monopodia per plant, number of sympodia per plant, number of bolls/plant, boll weight, seed index, and lint index which recorded high heritability coupled with high genetic advance could be reliable selection indices in cotton. The traits, UHML, uniformity index, and fibre strength were observed to exert great influence towards cumulative variability.

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