

## Studies on Genetic Variability in Cultivated Sorghum (*Sorghum bicolor* L. Moench) Cultivars of Adamawa State Nigeria

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**Abstract:** Studies were carried out to estimate the extent of genetic variability in cultivated strains of sorghum (*Sorghum bicolor* L. Moench). Thirty landraces were evaluated for one year (2001) across two environments, to obtain information on genetic and morphological diversity. Significant mean squares were obtained for almost all characters in the individual analysis of variance as well as the combined analysis across environments, suggesting that, this sorghum population was highly variable for almost all the characters, therefore, would respond to selection. Mean performances for the combined analysis identified Whilawa, Jerma, Mbaburi, Jigarigir, Jigarimuv and Mboderi as the promising cultivars in terms of yield per hectare, flag leaf length, panicle length, panicle width, earliness and length of inter-node respectively. Individual and the combined analyses indicated that most characters had higher genotypic and phenotypic variance components than the environmental variance estimates, which is indicative that character expression in this sorghum population was genetic and can be exploited in breeding programs. The genotypes also exhibited varying degrees of heritability estimates. Characters such as plant height, days to 50 % flowering, number of nodes per plant, panicle length, number of leaves per plant and days to 95% maturity responded positively to selection because of high broad sense heritability estimates.

**Key words:** Sorghum · cultivars · yield components · variances and heritability

### INTRODUCTION

Progress in plant breeding depends on the extent of genetic variability present in a population. Therefore, the first step in any plant breeding program is the study of genetic variability, which cannot easily be measured. The phenotypic variability in a given environment can be measured easily, but it reflects non genetic as well as genetic influence on the phenotypic expression. The genetic facts are inferred from phenotypic observations, which are the results of interactions of genotype and the environment. Lukhele and Obilana [1], Abu-Gasim and Kambal [2], Aba *et al.* [3] studied their research materials under more than one environment to ascertain their stability across environments. Studies on variability in sorghum confined to one environment have been reported by several authors [4-6]. In the present study, therefore, the variability present in thirty (30) sorghum cultivars collected from Adamawa state, where sorghum is frequently cultivated [7], were studied with the objective

of estimating the amount of genetic variability present in this local cultivars across environments.

### MATERIALS AND METHODS

During the 2001 cropping season two locations were chosen as experimental environments for the evaluation of the collected germplasm in replicated trials. One of the locations was the Teaching and Research Farm F.U.T. Yola; (lat. 9° 14' N and long. 12° 32' E). Yola is at an altitude of 200 m above sea level and is located within the Sudan Savannah ecological zone. The soil type of the experimental site is sandy clay loam. The second location was at the College of Agriculture Research Farm Mubi, (lat. 10° 03' N and long. 13° 07' E) in the Sudan Savannah zone of Nigeria. Mubi is at an altitude of 286 m above sea level, the soil type is sandy loam [8].

At each environment 30 sorghum strains were laid out in a Randomized Complete Block Design (RCBD) with 3 replications. Each of the 30 plots consisted of 4 ridges,

each of which measured 5 m long and spaced 0.75 m apart. Three or four seeds per hill, spaced 30cm apart were sown on each ridge. Each stand was later thinned to 1 plant per hill, giving rise to a total of 66 plants per plot. Two and three hoe weeding were carried out in Yola and Mubi respectively. N.P.K. fertilizer was applied at the rate of 60 kg N ha<sup>-1</sup>, 30 kg ha<sup>-1</sup> of phosphorus (P<sub>2</sub>O<sub>5</sub>) and potassium (K<sub>2</sub>O) in two split dozes at 3 and 6 weeks after sowing. At maturity, the following characters were measured on ten plants sampled at random from each plot: number of leaves per plant, plant height, width of flag leaf, length of flag leaf, panicle length, panicle width, length of inter-node, number of nodes per plant, number of grains per panicle, 1000 grain weight, grain weight per panicle, days to 50% flowering, yield per hectare and days to 95% maturity.

To estimate the extent or magnitude of variation among these strains the data obtained was subjected to analysis of variance for each environment based on plot means followed by a combined analysis of the data across the two environments; these were done according to methods described by Singh and Chaudhary [9]. Mean separation was carried out according to Duncans multiple range test (DMRT) described by Duncans [10]. Components of variance ( $\delta^2p$ ,  $\delta^2e$ ,  $\delta^2g$ ) were used for the estimation of coefficients of variation (PCV, GCV) as described by Singh and Chaudhary [9] as follows:

$$PCV = \frac{(\sqrt{\delta^2g}) \times 100}{X}$$

$$GCV = \frac{(\sqrt{\delta^2g}) \times 100}{X}$$

but  $\delta^2g = P-(G \times E)-E$  and  $\delta^2p = \delta^2g + E$

Where;

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

X = Grand mean

GxE = Genotype x environment interaction effect

$\delta^2g$  = Genotypic variance

$\delta^2p$  = Phenotypic variance

## RESULTS AND DISCUSSION

The significant mean square values obtained from the analysis of variance for the individual location suggests that differences existed between the sorghum cultivars for most characters, indicating that they are highly variable (Table 1). The significant mean square values obtained for location (Table 2), for some of the characters indicated that the conditions in the two locations were not similar in many ramifications and that

Table 1: Mean square values for the fourteen traits measured at Mubi and Yola

Source of variation	DF	Number of leaves per plant	Plant height	Width of flag leaf	Length of flag leaf	Panicle length	Panicle width	Length of inter-node
MUBI								
Replication	2	1.28	484.9	0.17	0.62	47.2	2.35	0.34
Cultivar	29	68.8**	17754.0**	1.60**	60.8 <sup>ns</sup>	282.3**	1.67 <sup>ns</sup>	16.9**
Error	58	2.24	1420.0	0.23	29.39	21.3	1.08	6.53
YOLA								
Replication	2	5.24	702.0	0.32	28.8	2.78	0.41	5.2
Cultivar	29	35.60**	12074.0**	3.031**	69.4 <sup>ns</sup>	5.09.2**	10.48**	26.3**
Error	58	4.63	1871.0	0.77	35.3	26.3	1.98	5.13

Table 1: Continued

Source of variation	DF	Number of nodes per plant	Number of grains per panicle	1000 grain weight	Grain weight per panicle	Days to 50% flowering	Yield per plot (kg/ha)	Days to 95% maturity
MUBI								
Replication	2	5.16	715489.0	4.4	390.2	27.3	72.681	1.90
Cultivar	29	64.2**	574528.0 <sup>ns</sup>	43.8*	398.1 <sup>ns</sup>	709.5**	9604.000 <sup>ns</sup>	1758.30**
Error	58	3.3	385669.0	23.4	249.6	13.5	63218.000	1.12
YOLA								
Replication	2	5.42	617901.0	9.70	144.5	10.81	5014.6	0.63
Cultivar	29	35.80**	1139190.0**	60.30**	587.7**	504.30**	373.0**	1858.20**
Error	58	4.61	321566.3	15.72	179.7	14.70	99720.0	0.91

Table 2: Mean square values for the fourteen traits measured across two locations (Mubi and Yola)

Source of variation	DF	Number of leaves per plant	Plant height	Width of flag leaf	Length of flag leaf	Panicle length	Panicle width	Length of inter-node
Environment	1	28.48 <sup>ns</sup>	12632.00 <sup>ns</sup>	1.58 <sup>ns</sup>	50.88 <sup>ns</sup>	448.43 <sup>**</sup>	99.3 <sup>**</sup>	13.80 <sup>**</sup>
Rep.in environment	4	5.85	91.51	0.38	14.424	13.588	1.95	3.129
Cultivar	29	90.26 <sup>**</sup>	28187.00 <sup>**</sup>	2.48 <sup>**</sup>	92.93 <sup>**</sup>	747.78 <sup>**</sup>	7.9 <sup>**</sup>	33.71 <sup>**</sup>
Cultivar×environment	29	14.02 <sup>**</sup>	1642.40 <sup>ns</sup>	2.15 <sup>**</sup>	37.24 <sup>ns</sup>	43.75 <sup>ns</sup>	4.16 <sup>**</sup>	9.58 <sup>ns</sup>
Error	116	3.49	1681.80	0.50	32.61	24.39	1.55	5.89

Table 2: Continued

Source of variation	DF	Nodes per plant	Number of grains per panicle	1000 grain weight	Grain weight per panicle	Days to 50% flowering	Yield per plot (kg/ha)	Days to 95% maturity
Environment	1	23.5 <sup>ns</sup>	321495.0 <sup>ns</sup>	398.50 <sup>**</sup>	2777.30 <sup>*</sup>	11.76 <sup>ns</sup>	1868157.0 <sup>**</sup>	9.800 <sup>ns</sup>
Rep.in environment	4	10.4	892728.0	0.86	52.28	3.51	34561.0	2.317
Cultivar	29	87.8 <sup>**</sup>	839986.0 <sup>**</sup>	65.15 <sup>**</sup>	291.44 <sup>ns</sup>	1028.80 <sup>**</sup>	280688.0 <sup>**</sup>	3596.000 <sup>**</sup>
Cultivar x environment	29	12.2 <sup>**</sup>	873732.0 <sup>*</sup>	38.94 <sup>ns</sup>	694.34 <sup>**</sup>	185.10 <sup>**</sup>	189637.0 <sup>ns</sup>	19.890 <sup>**</sup>
Error	116	3.9	361215.0	19.76	223.10	14.66	82213.0	1.023

ns = not significant, \* = Significant at (p=0.05), \*\* = Significant at (p=0.01)

Table 3: Estimate of phenotypic ( $\delta^2_p$ ), genotypic ( $\delta^2_g$ ), environmental ( $\delta^2_e$ ) variances and standard errors for the fourteen characters over two environments (Mubi and Yola) in 2001

Traits	$\delta^2_p$	$\delta^2_g$	$\delta^2_e$	SE
Flag leaf length (cm)	55.69	23.08	32.61	3.30
Flag leaf width (cm)	0.67	0.17	0.50	0.41
Panicle length (cm)	704.05	679.66	24.39	2.85
Panicle width (cm)	3.74	2.19	1.55	0.72
Number of leaves/plants	76.24	72.75	3.45	1.07
Plant height (cm)	26544.60	24862.80	1642.40	23.23
Number of nodes/plant	75.60	71.70	3.94	1.14
Length of inter node (cm)	24.13	18.24	5.88	1.40
Number of grains./panicle	33670.40	394961.00	361215.66	346.99
1000 grain weight	26.21	6.45	19.76	2.57
Grain weight/panicle (g)	34073.30	626.00	23.09	8.62
Days to 50% flowering	843.70	829.04	14.66	2.21
Days to 95% maturity	3576.11	3575.09	1.02	0.58
Yield/plot (Kg ha <sup>-1</sup> )	91051.00	8838.00	82213.20	165.54

is why the genotypes did not perform similarly in both environments. The significant effects of cultivar (genotype) x location, interaction mean squares that were observed (Table 2), in most characters also suggests that the environmental conditions in the two locations influenced the performance of the genotypes, thus suggesting the need to test genotypes over different environments across years to ascertain their stability for use as reliable genetic materials for crop improvement practice. Non-significant mean square values observed for some characters showed that the genotypes are genetically similar with regards to these characters. Selecting for these characters will therefore show no impact on genetic improvement.

The variance components for the two environments showed that most of the characters had higher phenotypic and genotypic variance estimates than the environmental variance estimates (Table 3). Therefore, expressions for most of the characters were genetic, which can be exploited in breeding programs. This finding is in agreement with the findings of Basu [4] and Abu-Gasim and Kambal [2] for several quantitative characters in sorghum genotypes. Zaveri *et al.* [11] also reported similar results in pearl millet. Lukhele [12] observed that high error or environmental variance estimate for some characters similar to what was obtained in this study could be attributable to sample size. To reduce error and consequently increase the precision and

Table 4: Mean performances of the fourteen traits across the two environments

Cultivars (Genotypes)	Plant height (cm)	Flag Leaf width (cm)	Flag Leaf length (cm)	*Panicle length (cm)	*Panicle width (cm)	*No. of Leaves/plant	Length of internodes (cm)
Jerma	358.9AB	7.03BCDE	48.12A	41.25BC	6.8BCD	17.47DE	20.38AB
Mboderi Pelepeleri	298.9CDEF	6.30EFGHI	39.20DEFG	10.20M	5.3DE	18.40CD	17.04CDEFGH
Shakeli	343.6ABC	6.82CDEFG	46.46ABC	41.30BC	7.2BCD	20.78ABCD	17.49CDEF
Madiya hadawa	281.5EFG	6.67CDEFG	42.60ABCDE	14.65KLM	7.3BCD	18.01DE	12.68JKL
Ndani Pelepeleri	161.3JK	5.72HIJ	35.13H	16.37KLM	5.3DE	10.53H	14.06IJK
Jigarigir	179.0JK	7.72B	36.60FGH	21.06HIJKL	10.3A	15.11EF	12.26KL
Pelepelefara	198.5HIJ	8.72A	41.36CDEFGH	10.22M	5.3DE	15.17EF	10.86L
Farafara	211.4HIJ	6.85CDEFG	39.30DEFGH	16.38KLM	5.8CDE	13.52FG	15.03EFGHIJ
Sharalewa	131.8K	5.20J	36.13FGH	12.43LM	6.5BCDE	9.02H	14.50GHIJK
Germa	194.9HIJ	6.08FGHI	36.38FGH	18.03JKLM	6.7BCDE	11.22GH	17.74ECDE
Ngarwahi	379.9A	6.87CDEF	43.45ABCDE	23.08GHIJK	6.4CDE	21.53ABC	18.05ABC
Komguno	326.5ABCDE	6.60CDEFG	45.81ABC	10.04M	5.3DE	18.16DE	18.27ABC
Pelepele	321.6BCDE	6.57CDEFG	37.51EFGH	10.20M	5.3DE	18.20DE	17.89ABCD
Lamjare	298.4CDEF	6.05GHI	34.98H	41.05BC	7.0BCD	18.21DE	17.14CDEFG
Thirgawa	189.61J	6.62IJ	35.73GH	12.61LM	6.3CDE	13.83FG	13.88JK
Kwomchama	244.9FGH	6.86CDEFG	41.80ABCDEFG	12.09LM	4.3E	18.52CD	13.33JKL
Mbaburi	189.9JK	7.37BC	38.50DEFGH	17.33JKLM	7.8BC	9.17H	20.61A
Bachafurwe	340.5ABCD	6.47DEFGH	45.95ABC	52.38A	6.2CDE	18.55CD	18.56ABC
Whiwaham	319.9BCDE	6.82CDEFG	44.12ABCDE	33.43CDEF	7.9BC	19.03BCD	16.71CDEFGHI
Ngubur	283.3EFG	7.25BCD	47.63AB	19.77IJK	6.7BCDE	19.75ABCD	14.36HIJK
Jigaritu	345.7ABC	6.63CDEFG	40.60CDEFGH	34.68BCDE	6.7BCDE	20.70ABCD	16.84CDEFGH
Zumokunge	165.6JK	6.93BCDE	43.55ABCDE	15.74KLM	7.6BCD	10.95GH	15.16DEFGHIJ
Whijigga	236.9GHI	6.68CDEFG	41.11CDEFGH	25.55FGHIJ	9.9A	19.11ABCD	14.74GHIJK
Kaurari	311.4BCDE	7.08BCDE	46.46ABC	35.48BCDE	7.7BC	21.57ABC	14.53GHIJK
Chakala	285.0DEFG	6.47DEFGH	40.08CDEFGH	32.25DEF	6.9BCD	19.23ABCD	14.87EFGHIJK
Mubba Yare	286.0DEFG	6.63CDEFG	42.16ABCDEFG	15.10KLM	4.6E	19.53ABCD	14.79FGHIJK
Chikala	313.2BCDE	6.82CDEFG	41.96ABCDEFG	38.47BCD	5.9BCD	17.90DE	17.53CDEF
Jigaridzu	287.8DEFG	6.48DEFGH	46.17ABC	32.93CDEF	7.1BCD	20.25ABCD	18.48ABC
Whilawa	332.9ABCDE	6.38EFGHI	44.13ABCD	42.55B	8.8A	22.32A	16.82CDEFGH
Jigarimuv	297.5CDEF	6.37EFGHI	40.33CDEFGH	20.67IJKL	6.6BCDE	21.82AB	13.71JK

Table 4: Continued

Cultivars (Genotypes)	*No. of nodes (cm)	*No. of grains/ panicle	*1000 grain weight (g)	Grain weight per panicle (g)	Days to 50% flowering	*Days to 95% Maturity	*Grain yield plot (Kg/ha)
Jerma	17.47DE	2296.0ABC	25.28ABCDE	56.44ABC	122.50EFG	180.0BC	701.0BCD
Mboderi Pelepeleri	18.40CD	1560.0C	21.47ABCDE	43.44ABCDE	122.83DEFG	178.0DEF	639.0BCD
Shakeli	20.78BCD	1665.0C	24.16ABCDE	46.03ABCDE	127.17ABCD	177.0DE	451.0CD
Madiya hadawa	22.32A	2841.0AB	18.03EF	50.51ABCDE	125.17BCDE	182.0B	608.0BCD
Ndani Pelepeleri	10.53H	1895.0B	23.94ABCDE	48.46ABCDE	107.83H	128.0O	591.0BCD
Jigarigir	15.11EF	2327.0ABC	25.12ABCDE	59.31AB	105.33H	129.0NO	471.0CD
Pelepelefara	15.17EF	1572.0C	19.48DEF	36.18E	96.83JK	118.0Q	320.0D
Farafara	13.52FG	1828.0BC	24.13ABCDE	46.91ABCDE	100.83IJ	119.0PQ	507.0CD
Sharalewa	9.02H	1632.0C	24.64ABCDE	41.25CDE	86.33L	120.0P	643.0BCD
Germa	11.22GH	1811.0BC	27.10ABCDE	45.81ABCDE	100.17IJ	128.0O	476.0CD
Ngarwahi	21.53ABC	2155.0BC	20.7BCDEF	41.19CDE	122.66EFG	175.0HI	469.0CD
Komguno	18.16DE	1681.0C	19.05DEF	32.70E	105.67H	176.0GH	349.0D
Pelepele	18.20DE	1637.0C	28.25AB	38.05DE	124.50CDE	178.0DEF	329.0D
Lamjare	18.21DE	2088.0BC	21.42ABCDE	46.98ABCDE	123.50DEFG	179.0CD	555.0BCD
Thirgawa	13.83FG	1685.0C	23.62ABCDE	38.92DE	106.00H	130.0N	717.0BCD
Kwomchama	18.52CD	1683.0C	21.25ABCDE	46.71ABCDE	122.50EFG	181.0B	301.0D
Mbaburi	9.17H	2269.0ABC	22.77ABCDE	56.73ABC	93.33K	132.0M	475.0CD
Bachafurwe	18.55CD	2286.0ABC	21.58ABCDE	49.19ABCDE	120.00FG	178.0DEFG	1010.0AB
Whiwaham	19.03BCD	2114.0BC	27.78ABC	42.52BCDE	121.83EFG	177.0FG	698.0BCD
Ngubur	19.75ABCD	2225.0BC	22.87ABCDE	45.94ABCDE	104.17HI	182.0B	403.0D
Jigaritu	20.70ABCD	1836.0BC	27.03ABCD	49.87ABCDE	123.33DEFG	164.0K	945.0ABCD
Zumokunge	10.95GH	1723.0C	24.44ABCDE	44.35ABCDE	96.66JK	136.0L	416.0D
Whijigga	19.11ABCD	3267.0A	14.47F	46.24ABCDE	93.33K	173.0J	611.0BCD
Kaurari	21.57ABC	1983.0BC	25.51ABCDE	56.53ABC	129.50AB	174.0IJ	413.0D
Chakala	19.23ABCD	1929.0BC	29.24A	59.58A	121.50EFG	181.0B	677.0BCD
Mubba Yare	19.53ABCD	1557.0C	23.19ABCDE	38.18DE	119.50G	181.0B	472.0CD
Chikala	17.90DE	2315.0ABC	14.47F	37.77DE	130.33A	175.0HI	671.0BCD
Jigaridzu	20.25ABCD	2189.0BC	23.88ABCDE	53.91ABCD	100.67IJ	177.0EFG	708.0BCD
Whilawa	18.01DE	2053.0BC	26.54ABCD	57.05ABC	124.17CDEF	179.0DE	1302.0A
Jigarimuv	21.82AB	2232.0BC	19.77CDEF	49.35ABCDE	128.17ABC	189.0A	443.0CD

Means in the same column with the same letters are not significantly (p=0.05)

Table 5: Estimates of means, ranges, genotypic, phenotypic coefficients of variation and heritability for yield and yield components combined across the two locations

Traits	Means	Range	GCV (%)	PCV (%)	Heritability (%)
Flag leaf length (cm)	41.40	34.98-48.12	81.8	81.1	41
Flag leaf width (cm)	6.70	5.20-8.72	31.4	41.0	25
Panicle length (cm)	26.40	10.04-52.38	302.4	317.3	96
Panicle width	7.00	4.3-10.30	55.5	72.8	58
Number of leaves per plant	17.30	9.02-22.32	129.5	137.0	95
Plant height (cm)	270.20	131.80-379.90	34.9	37.9	93
Number of nodes per plant	17.30	9.02-22.32	127.2	135.8	94
Length of inter-node	15.90	10.86-20.61	78.2	97.5	75
Number of grains per panicle	2040.10	<b>15.57-32.67</b>	884.4	1597.8	11
1000 grain weight (g)	23.40	14.72-29.24	80.4	122.0	24
Grain weight/panicle (g)	47.00	32.70-59.58	69.6	228.7	10
Days to 50% flowering	113.50	88.33-130.33	172.5	176.3	95
Days to 95% maturity	581.50	118.00-189.00	271.3	271.4	99
Yield/plot (kg/ha <sup>-1</sup> )	162.80	301.00-1302.00	1066.6	1597.3	10

reliability of estimates Allard and Bradshaw [13] suggested increasing sample size and number of environments or years during trials. However the disadvantage of this suggestion would be delay in the release of results.

Comparative performances of the 30 sorghum cultivars across the two locations for the fourteen characters studied (Table 4) provide a clear indication of the superiority of some of the cultivars over others. Good breeding potential therefore exists for cultivars such as Jerma, Madiyahadawa, Pelepelefara, Mbaburi, Jigarigir, Chikala, Whilawa, Bachafurwe, Jigarimuv, Whijigga and Ngarwahai, which performed very well for both yield and yield components at both locations. Depending on the breeding objectives, there was a wide range of cultivars to choose from. For instance if the breeding objective is to produce high yielding and early maturing variety, then hybridization between Whilawa x Pelepelefara, which are, the highest yielding cultivar per hectare and the earliest maturing cultivar respectively will be promising.

The means, ranges and coefficient of variations namely; genotypic coefficient of variation (gcv) and phenotypic coefficient of variation (pcv) and heritability estimates across the two locations are presented in Table 5. Generally, the gcv are lower in magnitude than the pcv. High gcv and pcv were also observed for some characters, this reveals that the genotypes have a broad base genetic background as well as good potential that will respond positively to selection. Similar results were obtained by William *et al.* [14] while studying effect of environment on yield components of sorghum. High heritability estimates were observed in some characters such as panicle length, number of leaves per plant, plant height, number of nodes per plant, days to 95 % maturity and days to 50 % flowering (Table 5). These characters therefore, could respond to selection pressure [15, 16].

The success of any breeding program depends upon the genetic variation in the materials at hand. The greater the genetic variability the higher would be the heritability, hence the better the chances of success to be achieved through selection. In this study most characters showed high broad sense heritability (Table 5), indicating the possibility of a positive response to selection. This is because there is likelihood of transferring the heritable components from parents to offspring during breeding. The high heritability obtained for most of the characters agreed with the findings of Ekebil *et al.* [17], Totok [18], Aba *et al.* [3] and Biswas *et al.* [19]. Also the moderate heritability obtained for flag leaf length (Table 5) agreed with the findings of Biswas *et al.* [19]. From this study, characters such as number of nodes per plant, panicle length, number of leaves per plant, plant height, days to 50% flowering and days to 95% maturity would respond positively to selection when selected for because of their high broad sense heritability. On the other hand grain weight per panicle, number of grains per panicle and yield per panicle would not respond to selection because of their low heritability estimates in this sorghum population. However, similar results were observed by Bello *et al.* [20], they reported that the low heritability estimate of grain yield is due to the direct or indirect multiplicative effects of several yield components on grain yield. There is need also to understand which portion of heritability is genetic and which is environmental, since the heritability obtained in this study was broad sense, Obilana and Fakorede [21] opined that, if a character is influenced by environment, its heritability would be low in a population in which environments vary widely. On the other hand, in another population in which the environment is rigidly controlled so that those variations do not occur, the same character would tend to have high heritability.

## CONCLUSIONS

Fourteen characters involving Leaf, Stem, Seed and other parameters were used; there was considerable variability present in the materials analyzed. These results would be useful in choosing populations to use in a breeding program to improve productivity. The variation could be effectively manipulated with appropriate breeding methods to develop improved varieties, synthetics and hybrids for use by farmers and the industries.

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