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DIALLEL ANALYSIS OF FORAGE YIELD AND QUALITY CHARACTERS IN SORGHUM*

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SORGHUM, *Sorghum bicolor* (L) Moench, is a most important crop in Asia and Oceania owing to its great range of adaptation and productivity of both grain and fodder. Considerable interest has, therefore, been shown in the improvement of this crop in recent years, and rapid advances made, mainly due to the development of hybrids through the use of cytoplasmic male sterility. Such studies have, however, been mainly confined to the improvement of grain yield and its components. The presently cultivated forage sorghum varieties are generally high yielders but poor in nutritional quality characteristics like protein, energy value and dry-matter digestibility. To conceive a workable strategy for the improvement of these complex forage characters, an understanding of the genetic system controlling them is necessary. The present paper deals with the genetic analysis of forage yield and quality

characters and thus gives basic information necessary for formulating the most efficient breeding procedure for evolving forage sorghum varieties of high forage quality as well as yield.

MATERIALS AND METHODS

Eight diverse parents namely, I. S. 607-13, I. S. 607-40, I. S. 7149, I. S. 7237, I. S. 8007, I. S. 8345, I. S. 10719 and I. S. 12306, their 28 single crosses and F_2 's were tested in a randomized block design with four replications. Each plot was represented by two rows 3 m long each with 30 cm distance between the rows. Plant to plant distance was maintained at 10 cm. Twenty plants were selected at random in each plot for recording observations. The plants were used for the analysis of total soluble solids (hand refractometry) and for other characters, green forage yield per plant, dry-matter digestibility (following the nylon bag technique by

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Lawrey (1969), crude protein (macroKjeldahl) and dry-matter percentage, were studied on another ten plants. All the observations were recorded when the genotypes reached 50% blooming.

Since the quality characters were recorded in percentage, the data were transformed using angular transformation. The genetic parameters were estimated following Hayman (1954) and something like using the adaptation to the computer program suggested by J. Lee and P. G. Kaltsikes (Personal Communication). Heritability estimates were calculated by the method of Mather and Jinks (1971). Parents and F_1 's were included in the F_1 analysis and parents and F_2 's in the F_2 analysis.

RESULTS

The analysis of variance (Table 1) showed that there were significant differences among the treatments for all the characters under study.

The homogeneity of ($W_r - V_r$) variances over arrays confirmed the validity of the assumptions of diallel analysis for all the characters in both the sets of analyses (F_1 and F_2) except green forage yield per plant and crude protein in the F_2 analysis (Table 2).

A study of the estimates of the genetic components of variation (Table 2) indicated that additive component D was highly significant for all the characters except green forage yield per plant in both the analyses. Highly significant values of H_1 and h^2 in the F_1 analysis showed that the dominance type of gene action played a major role in the

determination of green forage yield per plant. Highly significant values of H_1 and H_2 in the F_2 analysis confirmed the findings of F_1 . The estimates of H_1 and H_2 were also highly significant for crude protein in the F_1 analysis. The dominance components were not significant for dry-matter digestibility, total soluble solids and dry-matter percentage in both the sets of data, indicating, thereby, the predominant role of an additive type of gene action controlling these characters.

The estimates of F were not significant for all the characters except crude protein. The results of both the sets of analyses indicated that the dominant and recessive genes were more or less the same in the parents. However for crude protein, the estimates of F were positive (both sets) and highly significant in the F_1 analysis, which indicated that there were more dominant alleles than recessives in the parents.

The proportion of the genetic components and heritability are presented in Table 3. The estimates of degree of dominance (H_1/D)^{0.5} were higher than unity for green forage yield per plant and crude protein which indicated over dominance. The proportion of genes having positive and negative effects ($H_2/4H_1$) was not close to 0.25 for all the five characters. This showed that such genes were not equally frequent in the parents. The proportion of dominant and recessive genes $[(4DH_1)^{0.5} + F] / [(4DH_1)^{0.5} + F]$ governing green forage yield per plant was 8.15 in the F_1 analysis, indicated that the proportion of dominant alleles was

TABLE 1. Analysis of variance

Source of variation	D. F.	Mean squares for				
		Green forage yield per plant (gm.)	Dry matter digestibility (angle)	Crude protein (angle)	Total soluble solids (angle)	Dry matter percentage (angle)
Replications	3	9889.3	246.7**	8.72**	15.27**	51.6**
Treatments	63	17367.0**	38.6**	2.28**	7.76**	27.3**
Generations	2	112750.0**	13.8	4.32*	12.95**	22.0*
Parents	7	3510.2	53.2**	4.99**	16.56**	59.3**
F ₁ 's	28	11628.5**	38.2**	2.03**	5.25**	25.9**
F ₂ 's	28	19634.1**	37.0**	1.67	7.62**	20.9**
Error	189	6483.1	11.0	1.16	1.59	5.9
C. V. %		25.4	8.1	7.2	6.1	8.2

*, P < 0.05

**, P < 0.01

TABLE 2. Estimates of genetic components of variation and test of significance of $W_R - V_R$ for five characters in sorghum.

Components	Green forage yield/plant	Dry matter digestibility	Crude protein	Total soluble solids	Dry matter percentage
<i>Parents and F₁'s</i>					
D	403.7	10.93**	0.85**	3.21**	11.04**
	± 1025.3	± 2.38	± 0.26	± 0.28	± 1.88
F	2914.7	- 9.04	0.71	0.56	- 2.32
	± 2422.6	± 5.63	± 0.61	± 0.67	± 4.45
H ₁	8613.2**	- 1.49	0.96	0.90	0.15
	± 2356.9	± 5.48	± 0.60	± 0.65	± 4.32
H ₂	3261.9	- 0.55	0.67	0.94	- 0.02
	± 2050.5	± 4.77	± 0.52	± 0.57	± 3.77
h ²	9567.0**	4.81	0.55	- 0.46	- 2.34
	± 1375.2	± 3.20	± 0.35	± 0.38	± 2.53
$W_R - V_R$ variance over arrays	16914.0	10.01	0.58	0.95	80.73
<i>Parents and F₂'s</i>					
D	403.7	10.93**	0.85**	3.21**	11.04**
	± 1212.8	± 2.88	± 0.29	± 0.38	± 1.69
F	- 1894.4	- 6.65	3.56**	- 0.42	1.01
	± 2665.7	± 6.81	± 0.69	± 0.89	± 4.00
H ₁	35725.3	- 14.07	7.30**	0.77	- 1.56
	± 2788.0	± 6.52	± 0.67	± 0.86	± 3.89
H ₂	27732.4**	- 16.41	3.41**	0.43	- 1.42
	± 2425.5	± 5.76	± 0.59	± 0.75	± 3.38
h ²	- 3058.7	6.63	0.97	0.93	0.88
	± 1626.6	± 3.86	± 0.39	± 0.50	± 2.27
$W_R - V_R$ variance over arrays	48003.2**	97.57	1.66**	1.89	15.73

** P < 0.01

TABLE 3. Proportions of genetic components and heritability estimates for five characters in sorghum.

Proportions/ heritability estimates	Green forage yield/ plant	Dry matter digestibility	Crude protein	Total soluble solids	Dry matter percentage
Parents and F_1 's					
$(H_1/D)^{0.5}$	4.62	0	1.07	0.53	0.12
$H_2/4H_1$	0.10	0.09	0.18	0.26	- 0.04
$(4DH_1)^{0.5} + F$	8.15	0	2.29	0.72	0.05
$(4DH_1)^{0.5} - F$					
Narrow sense heritability (%)	20.52	46.59	13.88	41.99	53.45
Broad sense heritability (%)	32.31	45.91	24.81	49.58	53.41
Parents and F_2 's					
$(H_1/D)^{0.5}$	9.41	0	2.93	0.49	0
$H_2/4H_1$	0.19	0.29	0.12	0.14	0.91
$(4DH_1)^{0.5} + F$	0.60	0	6.01	0.77	0
$(4DH_1)^{0.5} - F$					
Narrow sense heritability (%)	30.70	46.59	19.98	45.21	47.17
Broad sense heritability (%)	72.06	34.66	55.36	57.15	43.79

greater in the parents; however the reverse was found from the F_2 analysis. Both the sets of analyses indicated the higher proportion of dominant genes in parents governing crude protein.

The estimates of heritability (narrow sense) varied from 13.9 (crude protein) to 53.4% (dry matter percentage). It was high in case of dry matter digestibility (46.6) and total soluble solids (42.0) in addition to dry matter percentage and low in green forage yield per plant and crude protein. The trend for heritability estimates was almost the same in the F_2 analysis.

DISCUSSION

Diallel analysis is based on the fulfilment of certain assumptions suggested by Hayman (1954). These assumptions are: no segregation, homozygosity of parents, no differences between reciprocal crosses, independence of action of non-allelic genes, no multiple alleles and independent distribution of genes among the parents. *Sorghum bicolor* (L.) Moench is a diploid. The parents included in the present study were maintained by selfing for several generations and thus were expected to be homozygous. The estimates of $W_r - V_r$ for all the characters were non-significant, which indicated the homogeneity of $W_r - V_r$ values and the validity of the various assumptions concerning diallel analysis.

Analysis of both sets of data suggested the importance of additive type of gene action for all the characters except green forage yield per plant. Dominance (H_1 and H_2) type of gene action was not signifi-

cant for dry-matter digestibility, total soluble solids and dry-matter percentage in both the sets of the data, which suggested that the additive type of gene action was playing a greater role for these traits. Dominance (H_1) component of variation was highly significant for green forage yield per plant, indicating non-additive type of gene action. The dominance (H_1 and H_2) component of variance was not significant in the F_1 analysis for crude protein. However, in the F_2 analysis these two components were highly significant. Disparity between F_1 and F_2 analysis may be due to certain linkages (Hayman, 1954, 1958) or due to sampling error.

Findings similar to these were reported for forage yield by Tarumoto (1970) in sorghum and Gupta and Sidhu (1970) in pearl millet. However, Blum (1968) and Tarumoto (1969) in sorghum reported a predominant role of the additive type of gene action for forage yield. This could be due to having used a different material in their studies. Studies on the inheritance of forage quality characters in sorghum are very scanty. However, Ross et al. (1970) reported a predominant role of the additive type of gene action for dry-matter digestibility in smooth brome grass. This is similar to our finding.

Narrow sense heritability estimates were high for dry-matter digestibility, total soluble solids and dry-matter percentage. It ranged from 41.0 to 54.0% for these characters. Improvement of these characters through selection is expected to be rapid. Heritability estimates were

low for green forage yield per plant and crude protein. This is mainly due to non-additive type of gene action. The selection gains through usual selection procedures may not be substantial for these characters. Under such a situation where both additive and non-additive gene effects are important, some form of recurrent selection programme is suggested for greater amelioration. After two cycles of recurrent selection, the selected elite lines should be subjected to multilocation tests for further evaluation.

SUMMARY

Two 8×8 diallel cross analysis (eight parents plus their 28 non reciprocal crosses and eight parents plus 28 F_2 's) involving diverse parents, I. S. 607-13, I. S. 607-40, I. S. 7149, I. S. 7237, I. S. 8007, I. S. 8345, I. S. 10719 and I. S. 12306 was conducted for estimating the gene effects, through component analysis for five forage characters namely green forage yield per plant, dry-matter digestibility, crude protein, total soluble solids and dry-matter percentage in sorghum (*Sorghum bicolor* (L.) Moench). Dry-matter digestibility, total soluble solids and dry-matter percentage were predominantly governed by additive type of gene action, whereas, dominance variance were more important in expressing green forage yield per plant and crude protein. Recurrent selection procedure for maximum exploitation of the prevalent gene actions is suggested for evolving high yielding and better quality forage sorghum varieties.

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