

Short Communication

Inheritance of Quality Traits in Forage Sorghum

R.S. Khatri, G.P. Lodhi and Ram Avtar

Department of Plant Breeding,

CCS Haryana Agricultural University, Hisar 125 004, India

Breeding for forage sorghum can be meaningful provided the new variety shows improvements in terms of quantity and quality. Breeding efforts in forage sorghum are required to concentrate on genetic improvement of its quality. The animal performance primarily depends upon forage quality, which is further dependent on intake, protein (%), digestibility and utilization by the animal system. Present study was, therefore, carried out to gather information on inheritance of quality traits such as protein content and *in vitro* dry matter digestibility in forage sorghum.

Six diverse parents, crossed in a diallel fashion (excluding reciprocals), with their 15 F₁s grown in two rows, each of 3 m length, in a randomized block design with three replications during *kharif* 1994, were selected. Protein content (MacKenzie and Wallace, 1954) and *in vitro* dry matter digestibility (Barnes *et al.*, 1971) were estimated in 5 randomly selected plants. Statistical analysis was carried out following Hyman (1954).

Genetic component analysis revealed that both additive (D) component of variance and the dominance component (H₁) were significant for protein, as well as for IVDMD

(Table 1). However, magnitude of dominance component was higher, implying that the inheritance of these traits was predominantly controlled by non-additive type of gene action. Similar trends have also been observed by Saini *et al.* (1977), Lodhi and Dangi (1981) for both protein and IVDMD per cent in forage sorghum. The overall summation of loci in heterozygous phase (h^2) was significant for protein content but non-significant for IVDMD, which revealed that dominance was unidirectional for protein, whereas it was not so for IVDMD. F value, which measures the distribution of dominant and recessive genes in the parents, was found to be significantly positive for IVDMD, indicating higher frequency of dominant alleles in the parent population, while non-significant F value for protein content depicted symmetrical distribution of dominant and recessive genes in the parents.

The mean degree of dominance, measured by the ratio $(H_1/D)^{1/2}$, indicated overdominance for both the quality traits studied. The proportion of positive and negative effects estimated by $H_2/4H_1$, where H₂ is the proportion of dominance variance due to positive and negative effects of genes, was fairly below its maximum value (uv

= 0.25) for both traits, indicating thereby an unequal distribution of positive and negative effects among parents. The ratio of total dominant and recessive alleles measured by $(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$ was observed to be above unity for both protein and IVDMD, which depicted that more number of dominant than recessive alleles was present in the parents for both these traits. The number of genes which control the character was worked out by the ratio (h^2/H_2) . It was observed that approximately two genes were responsible for the inheritance of protein content, while single

gene group was responsible for the inheritance of IVDMD, as indicated by the value of this ratio, 1.66 and 0.40, respectively.

Heritability (narrow sense) estimates were low to moderate for both protein and IVDMD, which might have been due to low contribution of additive genes and preponderance of non-additive genes.

Above results indicated that since both protein and IVDMD content are predominantly under the control of non-additive type of gene action, it would be fair to

Table 1. Estimates of genetic components of variance for quality traits studied in forage sorghum

Components of variation	Estimates	
	Protein (%)	IVDMD (%)
D	0.21* ± 0.09	15.41** ± 2.26
H ₁	0.75** ± 0.22	22.21** ± 5.74
H ₂	0.66** ± 0.22	17.04** ± 5.14
h ²	1.03** ± 0.13	6.72 ± 3.45
F	0.29 ± 0.21	10.83* ± 5.12
E	0.02 ± 0.03	0.00 ± 0.85
(H ₁ /D) ^{1/2}	1.88	1.20
H ₂ /4H ₁	0.21	0.19
$(4DH_1)^{1/2} + F$	2.15	1.83
$(4DH_1)^{1/2} - F$		
h ² /H ₂	1.66	0.40
t ²	0.79	0.52
Heritability (n.s.)	27.90	57.50

*, ** Significant at 5 and 1% levels, respectively.

Notation for Table 1:

D = Additive variance due to additive effect of the genes.

H₁ = Dominance variance due to dominant effect of the genes.

H₂ = Proportion of dominance variance due to positive and negative effects of genes.

h² = The overall summation of loci in heterozygous phase.

F = The mean of the covariance of additive and dominance effects over the array.

E = Expected environment component of variance.

m = Proportion of genes with positive effects in the parents.

v = Proportion of genes with negative effects in the parents.

exploit this portion of gene action through the production of hybrids on commercial scale, using existing cytoplasmic male sterility system.

References

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