

## GENETIC ANALYSIS OF HETEROSIS FOR TOTAL CRUDE PROTEIN AND DIGESTIBLE DRY MATTER IN GUINEA GRASS

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### ABSTRACT

Diallel cross analysis for tetraploid populations revealed that only nonadditive variance played a role in the inheritance of total crude protein (TCP) and digestible dry matter (DDM) per plant in guinea grass (*Panicum maximum* Jacq.) which indicated that crosses among sexual and apomictic clones should be attempted for improvement of these traits. Heterosis over the best parent P<sub>39</sub> ranged from -47.2 to 8.6% for TCP and from -46.5 to 20.7% for DDM, whereas heterosis over the commercial check, PGG19, varied from -18.9 to 66.9% for TCP and from -36.3 to 43.6% for DDM.

**Key words:** *Panicum maximum* Jacq., guinea grass, total crude protein, digestible dry matter, genetic analysis, heterosis.

Guinea grass (*Panicum maximum* Jacq.) is an important perennial grass, grown over tropics and subtropics. In Punjab, it is cultivated for stall feeding. It is highly nutritious as it contains sufficient amounts of crude protein, minerals and has high in vitro dry matter digestibility [1, 2]. It is mainly an apomict and hence there is paucity of information on its genetic architecture. However, in the recent past, some sexual strains have been identified by various workers [3-5]. The present investigation has been carried out to determine the magnitude and genetic architecture of heterosis for two quality traits, viz. total crude protein (TCP) and digestible dry matter (DDM) in guinea grass so as to devise a suitable breeding programme for the improvement of these traits.

### MATERIALS AND METHODS

The experimental material comprised eight clones (7 sexual and 1 apomictic) and their all possible one-way crosses. P<sub>1</sub>, P<sub>5</sub>, P<sub>6</sub>, P<sub>7</sub>, P<sub>20</sub>, P<sub>31</sub> and P<sub>39</sub> were sexual clones and

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P<sub>9</sub> (PGG 19) was apomictic clone. The sexual clones were used both as males as well as females and the apomictic clone was used only as a male. These clones were selected out of 183 clones maintained at Ludhiana. The parent strains and their crosses were grown in completely randomized block design with three replications. Each plot was a 5.5 m long single row having twelve plants. A distance of 50 cm was maintained from plant to plant and row to row. The recommended practices were followed to raise the crop. The nonexperimental rows were maintained to eliminate border effects. Ten plants from each row were harvested for estimation of total crude protein and digestible dry matter.

Total crude protein was estimated from a pooled sample of 10 plants, as suggested by [6]. Completely dried and finely ground forage sample weighing 1 g was taken for estimation of crude protein. Total crude protein per plant (TCP) was calculated as follows:

$$\text{TCP} = \text{Dry matter per plant (g)} \times \text{Crude protein/g}$$

In vitro dry matter digestibility (IVDMD) was estimated by using the method given by [7]. Digestible dry matter (DDM) per plant was calculated as follows:

$$\text{DDM} = \text{Dry matter per plant (g)} \times \text{IVDMD/g}$$

Forage samples from two cuttings, one each during 1988 and 1989, were used for the estimation of TCP and DDM.

Genetic analysis was done as suggested by [8, 9] for the tetraploid populations. The mixed effects model was used to calculate the components of genetic variance considering genotypes as random and environments as fixed.

## RESULTS AND DISCUSSIONS

### CHARACTER MEANS

Mean values of parents and their crosses for total crude protein and DDM are given in Table 1. The TCP varied from 5.87 – 13.28 g/plant in the parents and from 7.01 – 14.42 g/plant in the crosses. The DDM ranged from 36.24 – 90.51 g/plant in parents and from 48.43 – 109.22 g/plant in crosses. Expression of heterosis over the best parent, P<sub>39</sub>, ranged from –47.2 to 8.06% for TCP and from –46.5 to 20.7% for DDM. The superiority of the hybrids over the commercial check variety PGG 19 varied from –18.9 – 66.9% for TCP and from –15.8 – 89.9% for DDM. Two crosses, viz. P<sub>20</sub> × P<sub>9</sub> and P<sub>6</sub> × P<sub>20</sub>, had higher TCP and DDM, whereas four crosses, viz. P<sub>5</sub> × P<sub>9</sub>, P<sub>1</sub> × P<sub>6</sub>, P<sub>5</sub> × P<sub>39</sub> and P<sub>6</sub> × P<sub>7</sub>, had only higher DDM than the best parent P<sub>39</sub>.

Table 1. Mean values and heterosis for TCP and DDM in guinea grass (pooled over 2 environments)

Genotype	TCP (g)	DDM (g)	Per cent heterosis for TCP		Per cent heterosis for DDM	
			BP	CH	BP	CH
P <sub>1</sub>	12.2	77.2	—	—	—	—
P <sub>1</sub> × P <sub>5</sub>	10.7	73.0	-19.3	24.1	-19.4	27.0
P <sub>1</sub> × P <sub>6</sub>	11.7	99.5	-12.1	35.1	10.0	73.0
P <sub>1</sub> × P <sub>7</sub>	10.6	74.7	-20.4	22.3	-17.5	29.9
P <sub>1</sub> × P <sub>20</sub>	11.9	76.7	-10.0	38.3	-15.2	33.4
P <sub>1</sub> × P <sub>31</sub>	11.3	74.1	-14.8	31.0	-18.1	28.9
P <sub>1</sub> × P <sub>39</sub>	10.9	78.2	-18.2	25.7	-13.6	36.0
P <sub>1</sub> × P <sub>9</sub>	7.0	51.7	-47.2	-18.9	-42.9	-10.1
P <sub>5</sub>	8.6	64.2	—	—	—	—
P <sub>5</sub> × P <sub>6</sub>	12.0	85.3	-9.9	38.5	-5.7	48.3
P <sub>5</sub> × P <sub>7</sub>	12.1	87.6	-9.0	39.9	-3.2	52.3
P <sub>5</sub> × P <sub>20</sub>	11.9	83.5	-10.2	38.0	-7.7	45.4
P <sub>5</sub> × P <sub>31</sub>	10.4	75.3	-21.5	20.7	-16.8	31.0
P <sub>5</sub> × P <sub>39</sub>	11.8	98.6	-10.8	37.2	8.9	71.5
P <sub>5</sub> × P <sub>9</sub>	12.3	109.2	-7.5	41.8	20.7	89.9
P <sub>6</sub>	8.6	62.5	—	—	—	—
P <sub>6</sub> × P <sub>7</sub>	13.3	94.0	0.0	53.9	3.9	63.5
P <sub>6</sub> × P <sub>20</sub>	14.2	99.1	7.1	64.6	9.5	72.3
P <sub>6</sub> × P <sub>31</sub>	10.4	71.2	-21.5	20.7	-21.3	23.8
P <sub>6</sub> × P <sub>39</sub>	10.2	70.7	-23.3	17.9	-21.9	23.0
P <sub>6</sub> × P <sub>9</sub>	12.8	88.2	-3.7	48.0	-2.5	53.4
P <sub>7</sub>	5.9	36.2	—	—	—	—
P <sub>7</sub> × P <sub>20</sub>	10.7	71.3	-19.4	24.0	-21.2	24.0
P <sub>7</sub> × P <sub>31</sub>	7.5	57.4	-43.2	-12.7	-36.5	0.0
P <sub>7</sub> × P <sub>39</sub>	8.6	60.9	-35.0	0.0	-32.7	5.9
P <sub>7</sub> × P <sub>9</sub>	11.5	79.1	-13.3	33.2	-12.6	37.6
P <sub>20</sub>	11.9	77.7	—	—	—	—
P <sub>20</sub> × P <sub>31</sub>	12.5	82.0	-5.8	44.8	-9.4	42.6
P <sub>20</sub> × P <sub>39</sub>	12.4	79.8	-6.6	43.5	-11.8	38.8
P <sub>20</sub> × P <sub>9</sub>	14.4	96.5	8.6	66.9	6.6	67.8
P <sub>31</sub>	9.2	57.7	—	—	—	—

(Contd.)

Table 1. (contd.)

Genotype	TCP (g)	DDM (g)	Per cent heterosis for TCP		Per cent heterosis for DDM	
			BP	CH	BP	CH
P <sub>31</sub> x P <sub>39</sub>	7.2	48.4	-45.6	-16.4	-46.5	-15.8
P <sub>31</sub> x P <sub>9</sub>	11.1	63.0	-16.5	28.4	-30.4	9.6
P <sub>39</sub>	13.3	90.5	-	-	-	-
P <sub>39</sub> x P <sub>9</sub>	12.2	85.6	8.4	40.7	-5.4	49.0
P <sub>9</sub>	8.6	57.4	-	-	-	-
Mean	10.9	76.1	-	-	-	-
C.D. (5%)	5.1	28.7	-	-	-	-

BP — best parent (P<sub>39</sub>), CH — commercial heterosis over check variety PGG 19 (P<sub>9</sub>).

#### COMPONENTS OF GENETIC VARIANCE

Mean squares due to general combining ability (gca), specific combining ability (sca) and parental clones as well as their interactions with environment are presented in Table 2. The parent-offspring covariances are given in Table 3.

Mean squares due to sca and parents were significant but nonsignificant for gca. Similarly, the parent-offspring covariances were nonsignificant. This suggested that only nonadditive variance played a role in the inheritance of these traits. The parent x environment interaction variance was significant only for total TCP, the other interactions were nonsignificant for both traits. It indicates that the parental clones showed differential response over the environments only for TCP. Gca and sca showed nondifferential response over the environments for both traits.

Table 2. Analysis of variance for gca, sca and parents for quality traits in guinea grass

Source of variation	d.f.	Mean squares	
		TCP	DDM
Gca	7	12.472	760.7
Sca	28	7.306**	453.4**
Parents	7	12.034**	544.3**
Gca x env.	7	2.168	107.1
Sca x env.	28	3.489	106.9
Parents x env.	7	8.205*	136.8
Pooled error	140	3.366	106.9

\*, \*\* Significant at 5% and 1% level, respectively.

The components of genetic variance, i.e.  $\sigma_A^2$  (additive variance),  $\sigma_D^2$  (dominance variance),  $\sigma_I^2$  (interlocus trigenic interaction variance), and  $\sigma_F^2$  (interlocus quadrigenic variance) are presented in Table 4.  $\sigma_A^2$  and  $\sigma_I^2$  were positive and the magnitude of  $\sigma_I^2$  was higher than

that of  $\sigma_A^2$ ,  $\sigma_D^2$  and  $\sigma_F^2$  were negative either due to epistasis or sampling error. Though  $\sigma_T^2$  might be biased due to epistasis, yet its magnitude was much higher than that of  $\sigma_A^2$ . This may be due to the fact that guinea grass evolved in nature as a polyploid apomict [10, 11]. The polyploid apomicts have the mechanism to fix heterosis which may otherwise disappear due to inbreeding and sterility. In the autopolyploids, sterility may arise due to irregular meiosis. Hence in nature, autopolyploids can survive through apomixis which improves seed setting. The emphasis should be laid on development of new apomictic hybrids through hybridization among sexual and apomictic parents.

Table 3. Parent-offspring covariances for TCP and DDM in guinea grass (pooled over 2 environments)

Generation pair	D.F.	Covariance	
		TCP	DDM
Parents-offsprings	7	0.03	11.3
Parents-offsprings x Env.	7	-0.69	-17.9
Error	28	0.41	16.4

Table 4. Estimates of components of genetic variance for quality traits in guinea grass

Components of genetic variance	TCP (g)	DDM (g)
$\sigma_A^2$	1.56	92.2
$\sigma_D^2$	-4.65	-276.5
$\sigma_T^2$	45.70	3746.6
$\sigma_F^2$	-38.26	-3343.6

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