GENETIC ARCHITECTURE OF PROTEIN, LYSINE AND SUGAR CONTENTS IN GRAIN SORGHUM

K. A. NAYEEM

Marathwada Agricultural University
Parbhani 431 402

ABSTRACT

The high gca magnitude revealed the higher level of additive genetic variance compared to nonadditive variance is an indicative of direct selection for high protein and lysine content lines in the segregating population. The reciprocal effects for sugar content revealed careful choice for female parents. The ratio of dominant to recessive genes and that of $H_2/4H$, confirmed the equal distribution of dominant and recessive genes for protein content, while for lysine and sugar content there were some deviations.

Key words: *Sorghum bicolor*, protein, lysine, sugar contents, genetic architecture.

Intervarietal hybridization in sorghum is generally attempted to obtain superior recombinants or transgressive segregants, for evolving suitable varieties, restorers and male parents. For this purpose the breeder has to concentrate upon the conservation of additive and additive x additive components of genetic variance, which can be exploited for the improvement of a desirable trait. Therefore the present study was undertaken to reveal the genetic architecture of grain protein, lysine and sugar contents, with the help of graphical analysis, to understand the distribution of dominant and recessive genes in diallel set involving seven diverse, agronomically superior and local varieties in all possible combinations.

MATERIALS AND METHODS

The materials were same as reported earlier by Nayeem and Bapat [1]. Grains from 10 randomly selected panicles per entry were used to estimate protein lysine and total sugar contents using a modified procedure of Udy [2]. The graphic and component analysis of the diallel crosses were carried out by the methods of Jinks and Hayman [3, 4].

RESULTS AND DISCUSSION

The magnitude of gca was 18 and 15 times more than sca for protein and lysine contents. Higher level of additive genetic variance compared to nonadditive variance is indicative of usefulness of straight selection for high protein and lysine contents. Reciprocal differences were also significant for all the quality traits. Hence, this source of variation requires to be accounted for and high protein and lysine lines must be used as female parents in crossing programme for developing high protein and lysine content lines with other desirable agronomic character. However reciprocal effects were low for sugar content. Hence, there is a need for careful choice of female parent while planning hybridization programme.

Nayeem and Bapat [6] however indicated the better parents for quality traits on the basis of combining ability analysis in a line x tester mating system.

The estimates of the components of variation revealed all the characters under study were controlled by additive gene action. Nayeem and Bapat [1] found both additive and nonadditive gene action for inheritance of protein per cent, dominance based epistasis was mainly responsible for the inheritance of lysine content, while performing combining ability analysis in the same diallel set. However, nonadditivity for some genes controlling grain yield, protein per cent and protein yield per plant has also been reported [7].

In the present study, additive component (D) was highly significant for all the characters. Similar predominance of additive component was reported for protein content in sorghum [5]. Besides the additive component was larger in magnitude for all the character, additivity for grain yield and protein was also reported [7].

The H_1 and H_2 dominance components were highly significant for lysine content. In addition, H_1 exhibited significant differences for protein and total sugar contents. Wilson et al. [7] found relatively large volume for H_1, which indicated additivity for some genes controlling grain yield, protein content and protein yield per plant. They further stated that for protein content, H_1–H_2

Table 1. Analysis of variance and combining ability for grain quality characters in wheat

Source	d.f.	M.S.		
		protein content	lysine content (% of protein)	sugar content
Replications	2	0.24**	0.03**	0.004**
Genotypes	48	12.99**	0.83**	0.64**
Error	49	0.08	0.00	0.00
Combining ability				
Gca	6	27.73**	1.41**	1.15**
Sca	21	1.62**	0.07**	0.06**
Reciprocals	21	0.36**	0.16**	0.09**
Error	48	0.03	0.00	0.001

was much larger than its standard error, and hence for this character, the alleles with positive effects at the nonadditive loci and the alleles with negative effects were not equally frequent in the yield, the differences between H_1 and H_2 was much larger than its standard error, and hence for this character, the alleles with positive effects at the nonadditive loci and the alleles with negative effects were not equally frequent in the parents. In their studies, for grain yield, the differences between H_1 and H_2 were not much larger than its standard error. However, dominance components (H_1 and H_2) were reported to be almost equal to the additive component [5], but they were not significant for protein content being associated with high standard error.

On the basis of F component preponderance of dominant alleles for protein content was reported in sorghum [7], however, in the present investigation all the characters exhibited dominance of lower magnitude, while in the remaining character preponderance of dominant alleles existed. On the contrary, high number of dominant genes for controlling protein was found by other workers [5].

In the present study, protein and sugar contents exhibited partial dominance, while lysine content exhibited to dominance. A rough estimate for the minimum number of genes exhibiting some degree of dominance is given by $4h^2/H_2$. These estimates suggest that the quality characters had very little dominance component. At least three genes for yield and two or three for protein content have been reported [7].

For protein content, the value of H_2/H_1 was nearly at the expected level of 0.25; indicating that negative and positive homozygotes were in equal proportion among the seven parents. Vasudeva Rao and Goud [5] also indicated unequal distribution of positive and negative alleles. In another study also, [7], the frequencies of positive and negative alleles were in the

Table 2. Estimates of genetic and environmental components of quality traits in wheat

Component	Protein content	Lycine content (% of protein)	Sugar content
D	6.561[**] (±0.308)	0.596 (±0.0162)	0.539[*] (±0.019)
H_1	3.542[**] (±0.749)	0.207[**] (±0.039)	0.189[**] (±0.046)
H_2	3.177[*] (±0.653)	0.132[**] (±0.034)	0.121[*] (±0.041)
F	0.787 (±9.739)	0.268[**] (±0.038)	0.278[**] (±0.046)
E	0.20 (±1.09)	0.000 (±0.005)	0.001 (±0.006)
E_1	0.014 (±0.054)	0.000 (±0.002)	0.000 (±0.000)
H_1-H_2	0.365	0.075	0.068
H_2-4H_1	0.224	0.159	0.160
h^2/H_2	0.049	0.000	0.002
$4h^2/H_2$	0.199	0.000	0.009
$\dfrac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F} + F$	0.925	2.210	2.545
h^2	60.332	99.531	99.451

Figures in parentheses are standard errors.

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

neighbourhood of 0.3 and 0.7 for protein content. Lysine and sugar contents exhibited partial imbalance of homozygous loci because of lower estimated value of $H_2/4H_1$.

The relationship of $(4DH_1)^{1/2} + F$ $(4DH_1)^+ - F$ provides the ratio of the total number of dominant to the total number of recessive genes governing a given character. In the present study, the estimates of this quantity was nearly unity in case of protein contents, indicating that recessive and dominant genes distributed in equal proportion. The estimates of this ratio, however, was more than unity for the lysine and sugar contents. This indicated assymetry of gene distribution amongst the parents chosen for study for these characters.

The estimates of this unity, and that of $H_2/4H_1$ confirmed the equal distribution of dominant and recessive genes for protein content, while for lysine and sugar content there were some deviations.

Asymmetry of gene distribution was also borne out by the fact that the estimates of H_1 and H_2 were unequal in magnitude, H_1-H_2 being not equal to zero, for all the quality characters, which indicated high undirectionality of gene distribution.

The ratio $4h^2/H_2$ denotes the number of groups of genes, or simply genes, that exhibit dominance, to some extent. On an average, the value was more than one, indicating that at least one group of genes exhibited dominance in the determination of the above characters. It is interesting to note that grain quality characters like protein content, lysine and sugar have shown very low values, indicating absence of dominance gene action for these traits. A low value of $4h^2/H_2$ would not necessarily suggest the absence of dominance genes. It would also results when the negative and positive effects of dominance genes nullify the effects of each other.

To improve protein, lysine and total sugar contents by breeding within the genetic material available, both parents of a desirable hybrid derivative must have high protein content.

Efforts to bring together the recessive characters (e.g. protein %) with dominant genes for high lysine content in homozygous condition through recombination would present difficulties and appear to be the main cause of limited success in protein improvement.

REFERENCES

1. K. A. Nayeem and D. R. Bapat. 1988. Inheritance of protein and lysine content in sorghum, *Sorghum bicolor* Moench. Indian J. Genet., **48**(3): 368–370.

2. C. Dayle Udy. 1956. Estimation of protein in wheat and flour by dye-binding. Cereal Chem., **33**: 190–197.

3. J. L. Jinks and B. J. Hayman. 1953. The analysis of diallel crosses. Maize Genetics Newsl., **27**: 48–54.

4. B. I. Hayman. 1954. The theory and analysis of diallel crosses. Genetics, **39**: 759–808.

5. J. L. Jinks. 1955. The analysis of continuous variation in a diallel cross of *Nicotiana nutica* varieties. Genetics, **39**: 767–788.

6. K. A. Nayeem and D. R. Bapat. 1986. Combining ability of grain sorghum. Indian J. Genet., **44**(1): 353–357.

7. N. D. Wilson, D. E. Weibel and R. W. McNew. 1978. Diallel analysis of grain yield, per cent protein and protein yield in grain sorghum. Crop. Sci., **18**(3): 491–495.