A genetic study of popping quality in Sorghum (Sorghum bicolor (L.) Moench)¹

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Received 30 September 1986; accepted 26 February 1987

Key words: Sorghum bicolor, sorghum, pop volume, popping quality, generation mean analyses, gene action

Summary

Two crosses of sorghum, *Sorghum bicolor* (L.) Moench (IS $1054 \times ICSV-1$, and IS $5604 \times IS 1054$) were evaluated in parental, F1, F2, and backcross generations for the variation in their popping quality as measured by pop volume (ml). Dominance was in the direction of low pop volume. Dominance and additive gene effects, in that order, governed most of the variation, while significant dominance \times dominance type of interaction effects could also be detected. There was no evidence for higher order gene interactions.

Introduction

Popped sorghum is a popular snack food in sorghum growing regions of India and Africa. Several land races of sorghum are recognized for their superior popping quality (Prasada Rao & Murty, 1982). Pop sorghum grains are characterized by small grain size, thick pericarp, hard endosperm, and a low germ/endosperm ratio (Murty et al., 1982). Preliminary studies on the inheritance of popping quality indicated that the character is under polygenic control (Murty et al., 1983). It was also noted that in reciprocal crosses of parents with good and poor popping quality, xenia effects were absent. The objective of this paper is to present the results of detailed genetic study of popping quality based on generation mean analysis.

Materials and methods

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Three sorghum cultivars (IS 5604, IS 1054 and ICSV-1) maintained by self pollination for several generations at ICRISAT Center, India were chosen as homozygous parents. IS 5604 and ICSV-1 exhibit excellent and moderate popping quality, respectively, while IS 1054 has poor popping quality. Two crosses, IS $1054 \times ICSV-1$ and IS $5604 \times ICSV-1$ IS 1054, were made during the post-rainy season 1982/83, followed by advancement of the F1 hybrids to the F2 and backcrossing of F1 to both the parents during 1983. The parents (P1 and P2), F1, F2, and backcross (B1 = F1 \times P1, B2 = F1 \times P2) generations of the two crosses (11 treatments) were grown under protective irrigation at ICRISAT Center in the post-rainy season 1983/84. The parental and F1 generation were allotted two rows each

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while the F2 and backcross generations were allotted ten and six rows respectively per replication. There were three replications (blocks). The individual row length was 4 meter and rows were spaced 75 cm apart. Seeds were machine sown in solid rows. Individual plants were thinned two weeks after planting to a spacing of 12 cm between plants. At maturity, ten randomly chosen plants were harvested individually from each replication in the parental and F1 generations while all the plants were individually harvested from the F2 and backcross generations.

Grain samples were dried to 10% moisture level and stored in plastic bottles until evaluation of popping quality. Popping quality was measured as pop volume (Murty et al., 1983). A sample of 5 g grain was placed on an open steel pan kept constantly at 300–325° C and the grains were stirred briskly. The popped material was collected after $1\frac{1}{2}$ min in a graduated glass cylinder and its volume was expressed in ml as pop volume.

The frequency distribution of pop volume (ml) computed from the original data showed significant level of skewness and kurtosis. Therefore logarithmic transformation of the data was carried out and was found to be suitable. Estimation of generation means was carried out using two alternative procedures as discussed by Singh (1982). Classical (simple) means as well as robust means (Tiku, 1980) were calculated for the various generations under study. Analysis of variance of the data showed a significant difference in response due to replicate positions for most of the generations. However, the individual plant variances for various treatments were nearly homogeneous over the blocks. The interaction of various genetic components with the blocks was therefore investigated by estimating genetic parameters from individual block means as well as from the pooled data.

The adequacy of a simple additive-dominance model to explain the inheritance of pop volume was tested by applying the joint scaling test (Cavalli, 1952). Since the joint scaling test was positive indicating the presence of interactions, attempts were made to test the digenic epistatic model of Hayman (1958) as outlined by Mather & Jinks (1977). Successive models starting with the simple mean effects [m] followed by one or more of the additive [d], dominance [h], additive \times additive [i], additive \times dominance [j] and dominance \times dominance [l] effects were fitted by the weighted least squares procedure and tested for goodness of fit. The model showing the least mean residual sum of squares from the observed generation means was chosen for genetic interpretation of the data.

Results and discussions

The distribution parameters (means, variances, skewness, kurtosis) of pop volume (ml) in the parental, F1, F2, and backcross populations (P1, P2, F1, F2, B1 and B2) derived from the two crosses, IS $1054 \times ICSV$ -1 and IS 5604 × IS 1054, are presented in Table 1. Significant levels of skewness were observed in the F2 population IS $1054 \times ICSV$ -1 and the backcross population (IS $5604 \times$ IS 1054) × IS 1054. The latter generation also exhibited significant kurtosis. Logarithmic transformation of the data reduced the skewness and kurtosis only to some extent. Since the variate under study involved the measurement of volume, and analysis of the generation means revealed that estimated genetic components exhibited a more satisfactory fit with the genetic model when logarithmic scale was applied, further analysis and interpretation of the data was carried out on the logarithmic scale.

The average performance of the F1 hybrids of both the crosses indicated larger dominance effects towards the low pop volume (Table 1). Average pop volume of the backcross generations was significantly skewed towards the recurrent parent and dominance of low pop volume was evident in both the crosses. In cross IS $5604 \times IS$ 1054, effects of dominance were larger than in the other cross, due to the wider range in pop volume of the parents.

Estimates of genetic parameters, obtained by choosing the best fitting digenic epistatic model through the weighted least squares procedure, are shown in Tables 2 and 3. The nonsignificant (at 1 and 5% probability) and small X^2 values of the goodness of fit test indicated that a digenic epistatic model could satisfactorily explain the inheritance of pop volume in both the crosses. The estimates of m, [d], [h], [i], [j] and [l] presented in Tables 2 and 3 were derived from classical generation means. Estimates of genetic components derived from robust generation means were similar to those derived from classical means and hence are not shown in the tables. Apparently, the variate pop volume did not exhibit large deviations from a normal distribution under logarithmic transformation and thus the robust estimates did not improve the precision of the analysis.

Analysis of variance of the generation means over replicates indicated highly significant response difference for 8 out of the 11 generations studied. Therefore, while considering the estimates derived from pooled means, it would be of interest to examine how the individual genetic components interacted with the blocks. In both

crosses, the [d] components were large and consistent indicating that a significant part of the variation in pop volume is governed by additive gene action. The magnitudes of dominance effects [h] were larger particularly in cross IS $5604 \times 1S 1054$. In cross IS $1054 \times ICSV-1$, the additive \times additive interaction effects [i] and the additive × dominance interaction effects [j] were small and were not consistent across the blocks. However, there were significant dominance × dominance [1] effects. In the cross 1S $5604 \times 1S 1054$, small but significant [i] effects were present, while the [i] effects were absent; dominance × dominance [1] effects were also significant. The dominance [h] and dominance × dominance [1] effects are consistently in opposite directions indicating duplicate type of interactions (Mather & Jinks, 1977).

Table 1. Mean, variance, skewness and kurtosis of distribution of pop volume (ml) in six generations of two crosses among three inbred lines of sorghum.

Cross	Gener- ation	No. of plants	Χ̈́	σ^2	SE	Skewness	Kurtosis	X Log scale	SE Log scale
IS 1054 × ICSV-1	P ₁	31	18.6	12.78	0.642	0.83	- 0.35	2.905	0.0329
	P_2	30	74.4	72.86	1.558	- 0.72	~ 0.65	4.302	0.0221
	\mathbf{F}_1	39	33.7	45.78	1.083	0.34	- 1.02	3.499	0.0320
	\mathbf{F}_2	319	41.6	313.47	0.991	0.62	-0.25	3.635	0.0246
	B	159	27.4	72.15	0.674	1.15	1.72	3.269	0.0230
	\mathbf{B}_2	185	61.2	274.62	1.218	- 0.15	- 0.21	4.072	0.0226
IS 5604 × IS 1054	P ₁	70	84.7	65.24	0.965	- 0.03	0.13	4.435	0.0116
	\mathbf{P}_2	31	18.6	12.78	0.642	0.83	- 0.35	2.905	0.0329
	\mathbf{F}_1	94	31.0	37.64	0.633	0.41	- 0.74	3.414	0.0202
	F_2	497	37.6	192.54	0.622	0.75	0.27	3.559	0.0165
	B ₁	186	48.3	283.95	1.236	0.17	- 0.35	3.808	0.0286
	\mathbf{B}_2	345	21.9	48.68	0.376	1.44	2.61	3.043	0.0155

Table 2. Estimates of components of generation means for pop volume in cross IS 1054 × ICSV-1 based on log transformed data.

Genetic component	Rep	Rep ₂	Rep ₃	Pooled data	
m	2.50 ± 0.196	4.47 ± 0.203	3.69 ± 0.030	3.60 ± 0.020	
[d]	0.73 ± 0.029	0.76 ± 0.021	0.63 ± 0.03	0.70 ± 0.020	
[h]	2.53 ± 0.498	-1.43 ± 0.476	0.24 ± 0.125	0.33 ± 0.086	
[i]	1.05 ± 0.194	-0.94 ± 0.201	-	-	
[j]	-	-	0.69 ± 0.107	0.21 ± 0.076	
[1]	-1.53 ± 0.322	0.28 ± 0.287	-0.30 ± 0.126	-0.43 ± 0.093	
X ²	3.64	1.02	0.46	1.50	

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Genetic component	Rep	Rep ₂	Rep ₃	Pooled data	
m	3.39 ± 0.066	4.88 ± 0.145	4.17 ± 0.56	4.21 ± 0.083	
[d]	0.70 ± 0.018	0.78 ± 0.025	0.71 ± 0.021	0.76 ± 0.015	
[h]	-0.02 ± 0.095	-3.26 ± 0.371	-1.67 ± 0.400	-1.80 ± 0.230	
[i]	0.22 ± 0.069	-1.31 ± 0.143	-0.39 ± 0.153	-0.54 ± 0.087	
[i]	0.09 ± 0.091	-	-	-	
[1]	-	1.76 ± 0.236	1.05 ± 0.258	1.00 ± 0.147	
X ²	0.75	0.34	0.56	0.0	

Table 3. Estimates of components of generation means for pop volume in cross IS 5604 × IS 1054 based on log transformed data.

Overall, these results show that the inheritance of pop volume is governed to a large extent by additive and dominance effects, in that order. The nonsignificant X² values indicated that higher order interactions were absent. In the presence of significant epistatic effects, the estimates of additive and dominance gene effects could be biased (Hayman, 1960). Since the genetic parameters are derived from the means, it is not possible to draw a direct inference on the absolute magnitudes of variation for additive and dominance effects. Cancellation of opposing gene effects also confound the interpretations. The generation mean analysis has thus indicated only the nature of gene action and the conclusions apply only to the populations under study. This study thus indicates the presence of significant dominance and dominance × dominance type of interactions in the inheritance of pop volume.

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