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Performance of S_1 and Half-sib Family Composites of IAP3BR(M) Random-mating Grain Sorghum Population[1]

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Performance of S_1 and half-sib (HS) family composites from the random-mating sorghum (*Sorghum bicolor* L. Moench) population IAP3BR(M) was evaluated in six environments in Iowa. Composites from C0 through C4 for both family types showed that mass selection for heavy 100-seed weight was effective for increasing seed size in the population. Grain yield also increased over cycles among HS bulks, but decreased in the S_1 bulks. Selection for large seed through four cycles resulted in fewer seeds/panicle in both family types, and in an increase in the means for days to midbloom and plant height.

Inbreeding effects determined from half-sib and S_1 family means were significant (P<0.05) only for grain yield, where a value of -29.6% was estimated. Inbreeding depression was estimated at -14.0% for 100-seed weight, -10.2% for seeds/panicle, and -22.7% for plant height, but none exceeded the 0.05 level of probability.

INDEX DESCRIPTORS: *Sorghum bicolor* L. Moench, seed size, recurrent selection, genetic male-sterility, mass selection.

Increasing the size of seed has received attention as a means for improvement of many crop species. Reasons for the interest in large seed differ among species, but usually they relate to traits such as emergence of seedlings, stand establishment, and biological yield, or to seed quality and processing characteristics. In sorghum (*Sorghum bicolor* L. Moench), the diversity in seed size available in world collections and in materials generated through the Sorghum Conversion Program (Stephens et al., 1967) has stimulated interest in increasing grain yield by improvement of this primary component. A wide range in 100-seed weight among exotic sorghums was reported by Miller (1968), and considerable breeding effort has been expended since then to incorporate large seed into genotypes adapted for production in the United States.

Cyclic recombination and recurrent selection have proved valuable for the improvement of quantitatively inherited characters in many crop species. Mass selection of individual plants has been proposed and used effectively in sorghum for characters that show high heritability (Doggett, 1968, 1972; Doggett and Eberhart, 1968; Jan-Orn et al., 1976; Lothrop et al., 1985b; Ross et al., 1971, 1976). The widespread use of genetic male sterility to develop random-mating populations of sorghum has served as a catalyst to the use of recurrent selection in sorghum breeding.

The random-mating sorghum population IAP3BR(M) was constituted by crossing a group of lines, chosen because of large seed (100-seed weight), onto a source of the genetic male-sterile ms_3. Advancement of the base population through four cycles of recurrent selection was made by choosing lines with heavy 100-seed weight for recombination in each cycle. Comparisons of the agronomic performance and genetic variability among individual S_1 families chosen randomly from C0 and C4 of the population have been reported previously (Kwolek, 1984). This paper presents the results from experiments conducted by using composite (or bulk) populations of S_1 (C0, C2, C3, C4) and half-sib families (C1, C2, C3, C4). Our objectives were to examine trends among the means for different cycles and to estimate inbreeding depression for several characters.

MATERIALS AND METHODS

The registration of IAP3BR(M) as germplasm (Atkins, 1982) describes the development of the population in detail. Thirty large-seeded B-lines (non restorer in A_1 cytoplasm) or R-lines (fertility restorer in A_1 cytoplasm) were crossed onto genetic male-sterile (ms_3) panicles of an existing population, IAP1R(M)C1 (Atkins, 1980). These lines were chosen from a collection of large-seeded entries obtained from sorghum breeders in 10 states. Weight of 100-seed for the 30 lines in observation rows at Ames, Iowa, in 1975 ranged from 3.50 to 5.03 g, with a mean of 4.11 g. All lines had short to medium height and displayed good agronomic type.

Seed from the 30 crosses was composited in equal amounts and an isolation planting of approximately 6000 plants of the base population (C0) was grown near Ames in 1977. Gridded mass selection for heavy 100-seed weight was practiced on an individual-plant basis in the isolation blocks of subsequent cycles. The heaviest 60% of the C0 plants harvested were advanced to C1, and the heaviest 15% of plants harvested from the preceding cycle were used in preparing seed composites for C2, C3, and C4.

Entries for the experiments reported here consisted of composites (bulks) of seed from fertile panicles (S_1 families) of C0, C2, C3, and C4 and composites from male-sterile panicles (half-sib families) of C1, C2, C3, and C4. Tests were conducted in Iowa near Ames (central), Beaconsfield (southern), and Sutherland (northwestern), during 1982 and 1983. Soil types were: Ames, Nicollet (fine-loamy, mixed, mesic Aquic Hapludolls); Beaconsfield, Grundy (fine, Montmorillonitic, mesic Aquic Argiudolls); and Sutherland, Primghar (fine-silty, mixed, mesic Aquic Hapludôlls).

All plantings were made between 23 May and 7 June, by using a randomized complete-block design with four replicates in each environment (i.e., year-location combination). Individual plots were single rows 4.27 m long with 1.02 m between rows. Seedlings were thinned to approximately 8 cm apart in the row in 1982 (129,000 plants/ha) and 10 cm in 1983 (97,000 plants/ha). Fewer plants at emergence in the 1983 experiments prompted us to thin to the wider spacing in order that stands would be comparable for all entries.

Data were obtained on a 3.05-m section of each plot for plants/plot, panicles/plot, weight of dry unthreshed panicles, and weight of 100 seed from a sample of five panicles/plot. Grain yield was estimated by using the procedure described by Robinson and Bernat (1963). Dried panicles from 12 plots/environment were threshed, and a regression equation was fitted to convert dry panicle weight per plot (x) to grain yield per unit area (y). Additional characters calculated from these data were panicles/plant and seeds/panicle. Days to midbloom and plant height were recorded only at Ames. In the combined analyses of variance, environments and replicates were considered random variables, whereas cycles and family types were considered fixed.

Estimates of inbreeding depression expressed in percentage based on the linear decline of the mean value of the trait as the inbreeding coefficient (F) increases, were computed for each character. Because

the half-sib families were derived from male-sterile panicles that were pollinated randomly, they were considered noninbred (F = 0). In contrast, S_1 families were descendant from fertile panicles that were predominately self-pollinated and thus inbred one generation, with F = ½. Because homozygosity will increase at the rate of 50% each selfed generation, the difference in means between S_1 and HS families for a given character should reflect one-half of the total inbreeding depression that would occur. Estimates of inbreeding depression (%) were calculated, therefore, by using the formula:

$$\frac{\bar{x}_{S_1} - \bar{x}_{HS}}{\bar{x}_{HS}} \times 200,$$

where $\bar{x}$ = character mean and S_1 and HS refer to S_1 and half-sib families, respectively.

RESULTS AND DISCUSSION

Climatic and production conditions were markedly different in the six environments. Excellent grain yields were obtained at Ames in both seasons (6.91 and 8.52 Mg ha^{-1} average in 1982 and 1983, respectively). At Beaconsfield, yields were moderate (5.08 and 4.86 Mg ha^{-1} average in 1982 and 1983). The average yield at Sutherland in 1982 was low, 3.26 Mg ha^{-1}, and yield data were not obtained in 1983. Extended hot, dry weather coupled with poor plant stands in many plots, made the Sutherland test not suitable for grain yield determination in 1983. Only data for 100-seed weight were obtained from that test.

Mean squares from the combined analysis of variance for the S_1 vs. HS bulks comparison were significant beyond P<0.05 for grain yield, but not for the other characters (Table 1). This comparison provides for an assessment of the effects of inbreeding on the different traits. S_1 family bulks were derived from fertile panicles, which are primarily self-pollinated (ca. 95%) (Doggett, 1970; Fehr and Hadley, 1980; Leonard and Martin, 1963) and have an inbreeding value, F, equal to 0.5. Half-sib (HS) family bulks were derived from male-sterile panicles, which are cross pollinated and have an inbreeding value, F, equal to 0. Significant (P<0.05) differences between HS and S_1 families occurred only for mean grain yield, where HS bulks yielded 6.08 Mg ha^{-1}, S_1 bulks yielded 5.18 Mg ha^{-1}, and total inbreeding depression was estimated at −29.6% (Table 2). Inbreeding depression also occurred for plant height (−22.7%), 100-seed weight (−14.0%), and seeds/panicle (−10.2%), but none of these reductions exceeded the 0.05 level of probability. HS bulks yielded more than S_1 bulks and had heavier 100-seed weights, more seeds/panicle, and taller plants.

Mean square values for the S_1 and HS bulks were partitioned into component sources attributable to linear, quadratic, and cubic effects (Table 1). These effects characterize the nature of changes that occurred in trait means over cycles when selection was for 100-seed weight. Means for entries grouped by family-cycle (Table 3) show whether the changes were in a desirable direction.

For the HS bulks, highly significant (P<0.01) linear effects were shown for 100-seed weight and days to midbloom, and significant (P<0.05) linear effects were noted for grain yield. Grain yield also showed significant quadratic effects, and significant cubic effects were noted for 100-seed weight. The trend in HS means for 100-seed weight generally was upward, except for a small decrease from C2 to C3. The change observed in this trait from C1 to C4 was significant (P<0.05). Grain yield of the HS bulks increased over the first three cycles and then decreased in C4. The difference observed between C3 and C4 was significant, which would account for the significant quadratic effect. Days to midbloom of the HS bulks generally reflected the significant linear effect, means became larger in succeeding cycles, except between C3 and C4 cycles. The difference between these two cycles, however, was not significant.

There were no significant (P<0.05) linear, quadratic, or cubic effects for any character among cycles of the S_1 buks (Table 1). Cycle means (Table 3) lacked a definite pattern of change for most characters. These results suggest that the S_1 bulks do not serve as well as HS bulks for sampling and subsequent evaluation of the random-mating population. The unit of advancement of each cycle in IAP3BR(M) was a composite of seed from male-sterile panicles (half-sibs), and effects of inbreeding may influence the results when S_1 bulks are used as the unit of evaluation. Inbreeding would reduce heterozygosity in successive cycles and thereby may influence the range between S_1 bulk means.

A second consideration might be that size of the sample used to represent cycles of the population was not adequate. Each plot consisted of a 3-m row containing 30 to 40 plants and data from these units were used to estimate parameters for the entire population. However, the variation attributable to replications/environments was nonsignificant for all characters except plant height. This suggests that inbreeding effects more likely had an impact on the differential performance of the S_1 and HS bulks.

The significant inbreeding depression for grain yield, −29.6%, is more than twice the estimate of 13.6% reported by Lothrop et al. (1985a) for IAP1R(M) sorghum population. The sizable value determined from our experiments suggests that nonadditive gene action has an appreciable impact on the expression of yield in IAP3BR(M).

Table 1. Mean squares from the combined analysis of variance for agronomic characters measures on S_1 and half-sib (HS) bulks of IAP3BR(M) sorghum populations.

Source of variation	df	100-seed weight (x 10^{-1})	df	Grain[†] yield (x 10^{-1})	Seeds/ panicle[†] (x 100)	Panicles/ plant[†] (x 10^{-1})	df	Days to[‡] midbloom	Plant[‡] height (x 10)
S_1 vs. HS bulks	1	201.5	1	30.5*	17.4	28.4	1	6.3	65.2
Error (a)[¶]	5	31.6	4	2.5	9.7	13.9	1	0.6	1.5
HS linear	1	149.3**	1	3.7*	12.9	12.3	1	33.3**	8.9
HS quadratic	1	9.7	1	3.1*	0.3	7.4	1	9.0	1.4
HS cubic	1	53.9*	1	0.6	17.4	7.4	1	2.3	3.7
S_1 linear	1	30.1	1	0.0	10.9	3.4	1	7.4	9.5
S_1 quadratic	1	8.7	1	0.3	10.3	11.9	1	0.4	8.2
S_1 cubic	1	22.2	1	0.0	2.9	0.1	1	7.1	1.8
Error (b)[¶]	30	11.6	24	0.6	4.6	3.4	6	2.4	1.8
C.V. (%)		10.7		12.6	16.6	13.7		2.8	4.7

*, ** Significant beyond P<0.05, and P<0.01, respectively.
† Not determined at Sutherland in 1983.
‡ Record only at Ames.
¶ Error a = S_1 vs. HS bulks × Environments; Error b = Cycles in S_1 and HS bulks × Environments.

Table 2. Means by family type, L.S.D. 0.05, and estimates of total inbreeding depression from S_0 to S_∞ for characters measured on S_1 and half-sib (HS) bulks of IAP3BR(M) sorghum population.

Character	Mean HS	Mean S_1	L.S.D. (0.05)	Inbreeding depression (%)
100-seed weight (g)	2.99	2.78	0.21	− 14.0
Grain yield (Mg ha^{-1})[†]	6.08	5.18	0.70	− 29.6*
Seeds/panicle[†]	1278	1213	137	− 10.2
Panicles/plant[†]	1.4	1.4	0.16	0.0
Days to midbloom[‡]	67	68	2.4	3.0
Plant height (cm)[‡]	176	156	39	− 22.7

*Significant beyond P 0.05.
[†]Not determined at Sutherland in 1983.
[‡] Recorded only at Ames.

The estimate of inbreeding depression for 100-seed weight in our experiments was 14%, again much higher than the 4.9% determined by Lothrop et al. (1985a) for IAP1R(M). Malm (1968) and Laosuwan and Atkins (1977, 1978) evaluated the performance of hybrid sorghums that involved either unadapted or exotic parents and found that additive gene effects were of major importance in the inheritance of seed size. Investigations that involved parents better adapted in the area of evaluation, however, indicated that nonadditive gene action also contributed appreciably to the expression of seed size (Niehaus and Pickett, 1966; Beil and Atkins, 1967; Liang and Walter, 1968). The greater inbreeding depression for IAP3BR(M) in comparison with IAP1R(M) may reflect greater adaptability of the parental materials as well as the markedly larger seed of most parents. Even with an inbreeding depression of 14%, our results indicate that 100-seed weight is controlled primarily by additive gene effects, and they support the findings of Lothrop et al. (1985a) and Jan-Orn et al. (1976) with other random-mating sorghum populations.

Our results with S_1 and HS family composites showed that mass selection for heavy 100-seed weight through four cycles was effective for increasing seed size of IAP3BR(M), more so among HS bulks. Cycle means for grain yield did not reflect a definitive pattern of change. The trend over cycles was upward among HS bulks, but mean yields decreased among the S_1 bulks. Selection for large seed through four cycles resulted in fewer seeds/panicle in both the S_1 and HS family bulks, and the means for days to midbloom and plant height increased.

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Table 3. Means for entries grouped by family-cycle for agronomic characters measured on S_1 and half-sib (HS) bulks of IAP3BR(M) sorghum population.

Family-cycle	100-seed weight	Grain yield[†]	Seeds/panicle[†]	Panicles/plant[†]	Days to midbloom[‡]	Plant height[‡]
	--- g ---	---Mg ha^{-1}---	--------------- no. ---------------			--- cm---
HS-C1	2.76	5.72	1352	1.4	65	168
HS-C2	3.06	6.00	1234	1.4	67	171
HS-C3	2.97	6.58	1333	1.5	69	185
HS-C4	3.15	6.08	1192	1.4	68	180
S_1-C0	2.66	5.26	1305	1.4	67	143
S_1-C2	2.87	5.37	1151	1.4	68	164
S_1-C3	2.76	5.16	1198	1.4	67	158
S_1-C4	2.84	4.91	1194	1.3	69	158
L.S.D. 0.05 Among S_1 or HS cycles	0.20	0.49	140	0.1	2	16

[†] Not determined at Sutherland in 1983.
[‡] Recorded only at Ames.

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