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Hybrid Performance of Sorghum Parental Lines Developed by Mass Selection and S_1 Yield Testing[1]

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Experiments were conducted to obtain information on the effects of two methods of developing parental lines from a random-mating population of sorghum (*Sorghum bicolor* L. Moench) on hybrid performance. Gridded mass selection for threshed panicle weight was used in developing IAP1R(M)C3, and a sister population, IAP4R(S1)C3, was advanced each cycle on the basis of grain yield of S_1 families in replicated yield trials. Hybrids with male parents developed by mass selection did not differ significantly for grain yield and panicles/plant from those with parents chosen on the basis of S_1 yield tests. The S_1-selection hybrids were significantly ($P \leq 0.01$ or $P \leq 0.05$) shorter and later to bloom, had smaller seed and more seeds/panicle, but the differences usually were small and of little practical consequence. Estimates of genetic variance, heritability, and expected gain from selection among hybrids developed with mass or S_1-selected male parents were similar for grain yield and most other characters. Collectively, the results of our experiments indicated that developing sorghum parental lines by using mass selection for panicle weight or replicated S_1 yield tests should be equally effective.
INDEX DESCRIPTORS: *Sorghum bicolor* L. Moench, recurrent selection, agronomic traits, random-mating population, quantitative inheritance, breeding methods.

Increasing yields and diversifying the germplasm base are primary goals of sorghum (*Sorghum bicolor* L. Moench) breeders. Both goals can be accomplished simultaneously through recurrent selection. Populations may be synthesized from parents that differ in genetic background and desirable agronomic traits. The population can then be steadily improved through various recurrent selection procedures. From advanced cycles of recombination, superior inbreds or varieties may be selected. Incorporation of genetic male sterility into sorghum populations makes the intermating of large numbers of plants feasible.

Iowa sorghum population IAP1R was constituted by using about 80% adapted germplasm and 20% converted exotic sorghums. Random mating was facilitated through infusion of the ms_3 genetic-male-sterility gene. IAP1R has been advanced through two different and independent methods of selection. IAP1R(M)C3 was developed by using three cycles of gridded mass selection for threshed panicle weight, which required one season per cycle (Atkins, 1980). IAP4R(S1)C3 was developed from the same base population by using three cycles of replicated S_1-family testing for grain yield, which required three seasons per cycle (Atkins, 1986). IAP4R(S1)C3 is later maturing than IAP1R(M)C3, most panicles are broader and more compact, and plants generally are shorter (Atkins, 1986).

Forty fertile plants from each of the C3 populations were chosen randomly and crossed to the inbred Al Redbine 58 to produce the hybrids grown in the experiments reported in this paper. The objective of our study was to examine diferences in agronomic performance and in estimates of genetic components of variance among hybrids with male parents developed by mass selection and by S_1-family yield testing.

MATERIALS AND METHODS

The random mating population IAP1R-CO was developed by crossing 10 lines that restore pollen fertility in A1 cytoplasm (R-lines) to male-sterile segregates of NP3R (Nordquist et al., 1973). The lines used were Tx 7078, Tx 7000 ('Caprock'), TX 2536, NB 9040, Iowa selections of IS2403C, IS3063C, IS12567C, and IS12608C temperate bulks, plus Iowa selections of 'Redbine 58' × AK 9-2, and 'Redlan' × OKY7. The mass- and S_1-selected families utilized in our experiments were derived from the base population IAP1R-CO. To advance the population by mass selection for panicle weight, 30 equal rectangular grids (5 rows, 6.08 m long) were superimposed in each cycle on an isolation planting of approximately 6,000 plants (30 rows, 30.4 m long, and 102 cm apart). All plants in the base population were male fertile (Ms_3 ms_3). Panicles born on the main culm were tagged at anthesis, and 15 to 25 tagged plants per grid were harvested. Selection was made for combine-height plants (100-150 cm), for medium to large panicles, and against extremely late maturity. Selected panicles were threshed individually, and the 10 panicles with the heaviest grain weight were chosen from each grid to provide seed for the next cycle of IAP1R(M). Equal amounts of seed by weight from the 300 selected panicles were composited and used to plant the second isolation block (C1). Male-sterile segregates (ms_3 ms_3) were tagged at anthesis in C1 and all following cycles. After three cycles of mass selection for panicle weight, the seed produced was designated IAP1R(M)C3.

The second method of population advancement was based on the results of replicated yield tests of S_1 families. In the first year, fertile panicles were selected from the CO isolation planting as described previously. In the second year, seed from each selected panicle was planted in a single 1.82-m row. Selection was made among these rows for desirable plant height (100-150 cm) and good agronomic type. Then, within each selected row, the best fertile panicle was chosen visually for inclusion in the yield trial. In the third year, a yield test of the S_1 families was conducted at the Agronomy and Agricultural Engineering Research Center near Ames, Iowa in single-row plots, 4.26 m long, spaced 102 cm apart, arranged in a simple-lattice design with two replicates. On the basis of grain yields from that test, remnant seed from the previous isolation block was composited to form the next cycle (C1).

Eighteen percent of the entries included in each yield trial were selected to make up each succeeding cycle. The male-sterility gene segregated in C1, and male-sterile panicles were chosen to constitute C2 and C3. After three cycles of S_1 yield testing, the seed produced was released as IAP4R(S1)C3. The progression of IAP4R(S1) C1 through C3 is described in Table 1.

Seed from 40 randomly chosen fertile plants from the isolation plantings of IAP1R(M)C3 and IAP4R(S1)C3 was planted at Ames in 1985, and crosses were made with each entry onto the inbred Al Redbine 58. The 80 hybrids were planted May 21, 1986, at the Agronomy and Agricultural Engineering Research Center near Ames. The experimental site was fertilized just before planting with 134 kg/

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Table 1. Procedure for advancing the sorghum population IAP4R through three cycles of selection.

No. of panicles planted from previous isolation	No. of panicles planted in yield test	No. of entries selected from yield test for next isolation planting	Cycle of next isolation planting
648 (fertile)	196	35	C1
540 (male-sterile)	169	30	C2
427 (male-sterile)	144	26	C3

ha of N. Applications of 67 kg/ha of P_2O_5 and K_2O were made the preceding autumn. A second planting of the experiment was made June 9, 1986, at the Burkey Research Farm near Ames. Applications of 67 kg/ha of P_2O_5v and K_0 were made the preceding autumn, but nitrogen fertilizer was not applied at that site.

The experimental unit in both tests was a 3.04-m section of a single-row plot 4.26 m long, with 102 cm between rows. Plots were thinned to 10 cm between plants, resulting in a population of about 96,800 plants/ha. At each location (environment) the experiment was arranged in a replicates-within-sets design, with four sets, and 20 entries replicated twice per set. Of the 20 entries per set, 10 were hybrids with male parents derived by mass selection and 10 were hybrids with male parents derived by S_1 yield testing. Data were recorded in each environment for grain yield, seeds/panicle, 100-seed weight, panicles/plant, plant height, and days to midbloom.

Variance components were estimated from the mean squares for genotypes, genotypes × environments, and error in the combined analysis of variance. Standard errors (SE) of the variance components were computed by using the formula presented by Searle (1971, p. 416). Heritabilities (h^2) and their standard errors were estimated by using formulae presented by Hallauer and Miranda (1981, p. 51, 90-91). Genotypic correlations were calculated by using mean products and estimates of genetic variance obtained from the combined analyses of variance. Gains obtainable by recombining selected entries (i.e., male-parents of the hybrids) were estimated by using the formula presented by Falconer (1981, p. 175).

RESULTS AND DISCUSSION

Cool, wet weather for about 10 days after planting at the Ames Research Center resulted in slow, uneven emergence of plants. Full

Table 2. Means, standard errors, low and high genotype values, and genotype LSD_{05} for traits measured on sorghum hybrids in the Ames and Burkey environments, 1986.

Trait	Method of selection	Genotype values			
		Mean	Low	High	Genotype LSD_{05}
Grain yield (Mg/ha)	Mass	6.85±0.08	5.17	7.98	1.06
	S_1	7.01±0.10	5.51	8.07	1.27
Seeds/panicle	Mass	1602±31	1202	2250	311
	S_1	1770±30	1308	2387	349
100-seed weight (g)	Mass	2.98±0.03	2.36	3.51	0.32
	S_1	2.85±0.03	2.26	3.45	0.35
Panicles/plant	Mass	1.65±0.03	1.41	1.99	0.30
	S_1	1.57±0.03	1.25	1.85	0.29
Plant height (cm)	Mass	144.9±1.17	122	177	13.7
	S_1	138.1±0.87	119	159	9.6
Days to midbloom	Mass	64.3±0.30	61.0	67.5	1.47
	S_1	66.1±0.29	63.0	70.0	2.10

Table 3. Estimates of variance components and their standard errors for traits measured on sorghum hybrids in the Ames and Burkey environments, 1986.

Trait	Method of selection	Variance component			
		σ^2	σ^2_{ge}	σ^2_g	σ^2_{ph}
Grain yield (Mg/ha)	Mass	0.32±0.05	0.12±0.07	0.28±0.10	0.43±0.10
	S_1	0.66±0.11	0.08±0.11	0.26±0.12	0.47±0.11
Seeds/panicle (× 100)	Mass	303±50	93±61	773±207	896±205
	S_1	448±74	83±80	552±166	706±162
100-seed weight (g)	Mass	0.04±0.01	0.01±0.01	0.08±0.02	0.09±0.02
	S_1	0.06±0.01	0.01±0.01	0.07±0.02	0.09±0.02
Panicles/plant (× 10)	Mass	0.04±0.01	0.01±0.01	0.01±0.01	0.02±0.01
	S_1	0.04±0.01	0.01±0.01	0.01±0.01	0.03±0.01
Plant height (cm)	Mass	68±11	13±12	135±37	159±36
	S_1	48±8	−1±7	66±18	78±18
Days to midbloom	Mass	0.95±0.16	0.07±0.15	1.38±0.38	1.66±0.38
	S_1	1.12±0.18	0.56±0.27	2.14±0.63	2.70±0.62

Table 4. Estimates of heritability for traits measured on sorghum hybrids in the Ames and Burkey environments, 1986.

Trait	Method of selection	Heritability	
		Progeny-mean basis	Plot basis
Grain yield	Mass	0.67±0.24	0.39±0.14
	S_1	0.56±0.25	0.26±0.12
Seeds/panicle	Mass	0.86±0.23	0.66±0.18
	S_1	0.78±0.24	0.51±0.15
100-seed weight	Mass	0.86±0.23	0.63±0.17
	S_1	0.82±0.23	0.54±0.15
Panicles/plant	Mass	0.40±0.27	0.15±0.10
	S_1	0.57±0.25	0.25±0.11
Plant height	Mass	0.85±0.23	0.62±0.17
	S_1	0.85±0.23	0.59±0.16
Days to midbloom	Mass	0.84±0.23	0.58±0.16
	S_1	0.79±0.23	0.56±0.17

plant stands were not established the entire length of some plots, thereby requiring adjustment of those data to the 3.04 m length. Rainfall soon after planting at the Burkey Farm, combined with warm soil temperatures, led to rapid emergence and excellent stands. Grain yields averaged 120.9 bu/a (7.59 Mg/ha) for the Ames test and 99.9 bu/a (6.27 Mg/ha) at the Burkey Farm. The genotypes/environments *sets mean square (analyses not shown) was significant only for seeds/panicle ($P \leq 0.05$) and days to midbloom ($P \leq 0.01$). All values presented in the tables were determined from data combined over the two environments.

Differences between the hybrids with male parents developed by mass selection and those with parents developed by S_1 yield testing were not significant, beyond $P \leq 0.05$, for grain yield and panicles/plant (analyses not shown). Hybrids with male parents developed by S_1 testing were shorter and had more seeds/panicle ($P \leq 0.01$), but the plants were later to bloom and seeds were smaller ($P \leq 0.05$) (Table 2). In total, the hybrids from S_1-selected lines had larger means for three characters, and the mass-selected hybrids were greater for the other three traits. Except for seeds/panicle, the advantage for either type did not exceed 5%. The advantage in mean grain yield for S_1-selection hybrids was only 2%. The high and low genotype values for each character, likewise, were similar for the mass- and S_1-selected hybrids. Collectively, there seemed not to be an advantage of practical consequence for the hybrids developed by either method of selection.

Progress from selection is dependent on the heritability of a trait and the extent of genetic variability in the population under selection. Genetic variances (σ^2_g) among the hybrids developed with mass- or S_1-selected male parents were similar for grain yield, 0.28 and 0.26, respectively (Table 3). In most instances, the values for other traits were nearly alike, or they were somewhat greater for the mass-selected group. Genotype × environment interaction variances were small relative to the estimates of error and genetic variance for all traits.

Heritability estimates on a progeny-mean basis most often were slightly higher for hybrids formed by using male parents that were developed by mass selection than for hybrids with male parents developed by S_1-select family selection (Table 4). Plot-basis heritabilities also were slightly higher for hybrids developed by using mass-selected male parents than those with S_1-selected male parents except for panicles/plant, although in no case was the difference greater than the standard error. Heritabilities on a plot basis were lowest over both selection methods for panicles/plant (0.15 and 0.25), followed by grain yield (0.26 and 0.39).

The phenotypic correlation between grain yield and seeds/panicle (Table 5) was moderately strong, $r = 0.59$ ($P \leq 0.01$), among the hybrids developed from mass-selected male parents, reflecting the influence of visual selection for large panicles. In contrast, 100-seed weight showed a smaller negative correlation, $r = -0.36$ ($P \leq 0.05$), with grain yield. Also, among the mass-selected group, plant height was correlated positively with 100-seed weight and panicles/plant. Among the hybrids developed from S_1 yield-tested lines, phenotypic correlations were significant for grain yield with panicles/plant, $r = 0.54$ ($P \leq 0.01$) and plant height, $r = 0.38$ ($P \leq 0.05$). Strong

Table 5. Phenotypic (above diagonal) and genotypic (below diagonal) correlations among traits measured on sorghum hybrids in the Ames and Burkey environments, 1986.

Trait and method of selection	Grain yield	Seeds/ panicle	100-seed weight	Panicles/ plant	Plant height	Days to midbloom
Grain yield						
Mass		0.59**	−0.36*	0.02	−0.02	0.22
S_1		0.21	−0.02	0.54**	0.38*	−0.31
Seeds/panicle						
Mass	0.71		−0.82**	−0.59**	−0.53**	0.18
S_1	0.08		−0.88**	−0.31	−0.15	0.05
100-seed weight						
Mass	−0.50	−0.85		0.32	0.61**	−0.09
S_1	−0.02	−0.95		0.16	0.28	−0.18
Panicles/plant						
Mass	−0.43	−0.94	0.54		0.47**	0.07
S_1	0.65	−0.45	0.28		0.37*	−0.02
Plant height						
Mass	−0.11	−0.63	0.71	0.55		0.06
S_1	0.40	−0.21	0.32	0.43		−0.09
Days to midbloom						
Mass	0.27	0.20	−0.12	0.17	0.04	
S_1	−0.54	0.04	−0.20	−0.22	−0.12	

*,**Significant beyond the 0.05 and 0.01 probability levels, respectively.

Table 6. Estimated gains per cycle from mass and S_1 selection with 20% selection intensity for traits measured on sorghum hybrids in the Ames and Burkey environments, 1986.

Type of selection	Grain yield (Mg/ha)	Seeds/ panicle	100-seed weight (g)	Panicles/ plant	Plant height (cm)	Days to midbloom
Mass†	0.47	317	0.31	0.05	12.9	1.25
S_1 yield testing‡	0.54	291	0.34	0.13	10.5	1.82

†Estimated gain calculated by using plot-basis heritability estimate
‡Estimated gain calculated by using progeny-mean heritability estimate

negative correlations ($P<0.01$) between seeds/panicle and 100-seed weight were exhibited for both mass- and S_1-selection, $r=-0.82$ and -0.88, respectively. Most of the phenotypic correlation coefficients were larger for the mass-selected group. The genotypic correlations (Table 5) also reflected that pattern, and most often they were slightly larger than the corresponding phenotypic correlation.

Estimated gains from selection relative to hybrid performance (Table 6) indicated that the gain for yield should be slightly greater with male parents developed by S_1 testing than with male parents developed by mass selection, 0.54 vs. 0.47 Mg/ha/cycle, respectively. When the expected gain for yield with mass selection was calculated by using an individual-plant heritability estimate, the expected gain was considerably lower, 0.29 Mg/ha/cycle. For three of the other traits measured, a small advantage was shown for S_1-yield testing, wheras the estimated gains for two traits were larger for the hybrids with male parents developed by mass selection.

Collectively, the results of our experiments did not provide strong support in favor of either mass selection for panicle weight or S_1 yield testing as a procedure for developing parental lines for use in sorghum hybrids. The population means, genetic variances, heritability of plant characters, and other parameters estimated were not consistently greater for either selection procedure. Usually, when a character difference for hybrids with mass- vs. S_1-selected male parents met the common standards for statistical significance, the magnitude of the difference seemed of little consequence practically.

Advancing a population through successive cycles on the basis of performance of S_1 families in replicated yield trials requires an appreciable commitment of time and resources. Some sorghum breeders may deem those expenditures acceptable within total project goals and resources. Mass selection for panicle weight is much less consuming of project resources. The results of our experiments indicated that developing sorghum parental lines by using mass selection for panicle weight or replicated S_1 yield tests should be equally effective. When project resources are limited, the use of mass selection for panicle weight seems an attractive alternative for advancing breeding populations.

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