HERITABILITIES AND CORRELATIONS FOR YIELD AND YIELD-RELATED CHARACTERS IN MUNGBEAN

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HERITABILITIES AND CORRELATIONS FOR YIELD AND YIELD-RELATED CHARACTERS IN MUNGBEAN

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INTRODUCTION

The two chapters of this dissertation are separate and complete manuscripts to be submitted to Crop Science for publication. The format of each manuscript conforms to the style of that journal.

CHAPTER I

Broad-Sense Heritabilities and Correlations for Yield and Yield-Related Characters in Mungbean

Broad-Sense Heritabilities and Correlations for Yield and Yield-Related Characters in Mungbean[1]

ABSTRACT

Previous genetic studies in mungbean [<u>Vigna radiata</u> (L.) Wilczek] have usually been based on relatively small, space-planted populations. The objectives of this research were to estimate broad-sense heritabilities and phenotypic and genotypic correlations for yield and yield-related characters in relatively large populations of mungbean under plantings approximating commercial spacing. Two small-seeded lines, M-1-77-OT-4 and EG-MG-16/ML-3, were crossed to each of two large-seeded lines, MG-50-10A(Y) and 3-1. The four resulting F_2 populations (each including approximately 700 individual plants) and their parents were planted under dryland conditions near Perkins, OK, in 1984 and 1985. Significant differences between years in heritability were observed in two F_2 populations for seed number/pod and pod number/plant and in one population apiece for 100-seed weight, vegetative weight, and harvest index. Potentially useful levels of genetic variability were identified for all characters examined, though not in all populations nor in all years. Those crosses containing M-1-77-OT-4 had higher

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heritability estimates for grain yield than those containing EG-MG-16/ML-3. However, they were more erratic for seed number/pod and pod number/plant. Seed number/pod, 100-seed weight, pod number/plant, vegetative weight, plant weight, and grain yield appear interdependent phenotypically, but for the most part not genotypically. One hundred-seed weight generally behaved independently from the other characters genotypically and only expressed low phenotypic correlations. Seed number/pod was significantly correlated genotypically with grain yield in most populations in most years.

Additional Index Words: *Vigna radiata* (L.) Wilczek, Phenotypic correlation, Genotypic correlation, Yield components.

INTRODUCTION

Mungbean [Vigna radiata (L.) Wilczek] is an important grain crop in India and Southeast Asia and has been for thousands of years. However, little research on cultivar improvement within the crop has been accomplished. Mungbean has been grown in the American Southwest, primarily in Oklahoma, since the 1930's. Until recently, importation of Asian mungbean kept production acreage relatively low in the USA. With change in evaluation of the dollar, interest has increased in growing mungbean in the domestically as an alternative crop both for domestic consumption as well as for export.

Previous studies have shown that the inheritance of yield components in mungbean is controlled predominantly by additive gene action. Dhaliwal and Singh (2) indicated that general combining ability (GCA) was significant for pod number/plant in F_1 and F_2 generations of the mungbean. Singh and Jain (10) found in F_1 mungbean populations that pod number/plant and grain yield were largely controlled by additive gene effects. They (11) also determined that seed size was largely controlled by additive gene effects, but observed some overdominance for the trait. Singh and Singh (13) obtained conflicting evidence in F_1, F_2, and F_3 mungbean populations. They found the nonadditive component of variance was significant for grain yield and pod number/plant, but the additive component was not significant in any generation. They also identified both additive and nonadditive components of variance for seed weight. Singh and Singh (16) also showed in the F_2 and F_3 of several mungbean populations that additive gene effects were more important than the nonadditive for pod number/plant and grain yield, but that nonadditive gene effects were still significant. They also demonstrated that for seed size additive gene effects were most important. Yohe and Poehlman (17) found components of grain yield were controlled by both additive and nonadditive gene effects in an F_1 population, but that additive effects were much larger than the nonadditive. Singh and Singh (14) found that GCA and specific combining ability (SCA) were significant for seed number/pod in F_1, F_2, and F_3 mungbean populations, but that GCA was significantly larger than SCA.

Because additive gene effects play the predominant role in expression of yield and yield components in mungbean, broad-sense heritabilities should provide fairly accurate estimates of potential response to selection. Empig et al. (3) in an F_2 population calculated that seed weight and grain yield had broad-sense heritabilities of 51.2 and 8.6%, respectively. Broad-sense heritabilities were also generated in the F_3, but those results were considered inconclusive due to extensive deviation from the F_2 estimates.

A strong correlation exists between a number of yield components and grain yield in mungbean. Gupta and Singh (6) demonstrated that grain yield was strongly and positively correlated phenotypically and genotypically with pod number/plant (0.71 and 0.69, respectively) and 50-seed weight (0.51 and 0.72, respectively). However, they were unable to show that seed number/pod was significantly correlated with yield. Singh and Malhotra (12) calculated that 100-seed weight was negatively associated with seed number/pod (-0.17) as well as pod number/plant (-0.16). Chandel et al. (1) noted positive correlations between the characters pod number/plant (0.82) and seed weight (0.54) vs. grain yield. Giriraj and Vijayakumar (5) observed a positive genotypic correlation between pod number/plant (0.70) and seed number/pod (0.09) vs. grain yield among 55 pure lines using path-coefficient analysis. They also calculated a negative correlation between 100-seed weight and grain yield (-0.41). Yohe and Poehlman (17) showed that yield components such as 1000-seed weight (0.76), seed number/pod (0.60), and pod number/plant (0.88) were positively correlated with grain yield in an F_1 5 X 5 diallel. Singh and Singh (15) obtained significant positive correlations between pod number/plant (0.81) and seed size (0.24) vs. grain yield in several F_2's. They concluded that selection for increased seed size would probably be effective in improving grain yield. Joshi and Kabaria (7) and Malhotra et al. (8) showed seed size (-0.21 and -0.65, respectively) and number of pods/plant (0.95 and 0.98, respectively) had large direct genotypic effects on yield. However, correlations between seed size and number of pods/plant were significant and negative (-0.73 and -0.79, respectively); thus, a compromise must likely be made between selection for those two traits if an increase in grain yield is to be realized. They concluded that number of pods/plant was the most important character contributing to yield.

Almost all experiments cited in this paper were space planted with 30 to 75 cm between plants both within and between rows. Also, the segregating populations have usually consisted of less than 300 plants/cross (e.g., 2, 3). The heritability study outlined herein was planted at high population densities and used large populations, the intent being to derive estimates of heritability and correlations that would probably correspond more closely to observed selection response than have those from studies previously reported.

The objectives of this research were to estimate broad-sense heritabilities and phenotypic and genotypic correlations for yield and yield-related characters in relatively large populations of mungbean under plantings approximating commercial spacing.

MATERIALS AND METHODS

Four parents were utilized in these experiments, i.e., M-1-77-OT-4, a high-yielding line with a small seed size (of about 5.7 g/100 seed); EG-MG-16/ML-3, another high-yielding line with small seed (of approximately 5.4 g/100 seed); 3-1, a large-seeded line (of about 7.8 g/100 seed); and MG-50-10-A(Y), another large-seeded line (of approximately 8.4 g/100 seed). The two small-seeded lines were crossed to each of the two large-seeded lines and advanced to the F_2 generation. Populations were designated as 1 for M-1-77-OT-4/3-1, 2 for M-1-77-OT-4/MG-50-10-A(Y), 3 for EG-MG-16/ML-3//3-1, and 4 for EG-MG-16/ML-3//MG-50-10-A(Y).

These experiments were grown in 1984 and 1985 under dry-land conditions on the Oklahoma State Univ. Agronomy Research Station near Perkins, OK. The soil was a Teller loam (fine-loamy, mixed, thermic Udic Argiustoll) with 1 to 3% slope, moderate permeability, and medium internal drainage. A soil test was conducted, and all nutrients tested were at adequate levels. Thus, fertilizers were not applied to the test area. Twelve rows of each F_2 were planted as a unit with four rows of a parent line for that cross planted on one side of the F_2 and four rows of the other parent on the other side.

The parents and their progeny were inoculated with Brady Rhizobium spp. [Vigna] and planted using a cone-type planter in rows 6.75 m long and 75 cm apart. Plants were spaced approximately 8 cm apart within the row. Mechanical and hand cultivation were used as required to maintain a weed-free environment during the growing season.

Just prior to harvest, the plants at the end of each row were removed to reduce border effects. If spaces without plants were evident within rows, the plants surrounding those spaces were also removed for the same reason. At harvest, 50 individual plants of those remaining were randomly harvested from each of the two center rows in the four-row plots containing parental lines. All individual plants of those remaining in the center 10 rows of the F_2 populations were harvested and labeled by row and cross. Number of mature pods/plant were counted in the field for each harvested plant. A pod had to contain at least one developed seed to be counted. Prior to threshing, each oven-dried plant was individually weighed in grams. Each plant was then threshed, and the seed from it were stored in individual coin envelopes. Grain yield/plant in grams and seed weight/100 seed in grams were then directly measured on each seed sample. With these characters and those previously measured, it was then possible to calculate several other important yield-related characters as follows:

Seed/pod = [(Grain yield/Seed weight)100]/Pod number;
Vegetative weight = Total weight - Grain yield; and
Harvest index = Grain yield/Total weight.

Broad-sense heritabilities (H_{BS}) were calculated for each character using the following formula (4):

$$H_{BS} = VX_G/VX_P$$

where VX_G denotes the variance of the F_2 minus the averaged variance of the parents for character "X", and VX_P is the F_2 variance estimated from the within mean square of a total-between-within analysis of variance. Confidence intervals were developed for each heritability estimate based on the F distribution with degrees of freedom for the F_2 and pooled parental populations. Differences ($P = 0.05$) in heritabilities between years were determined by the non-overlap of the confidence interval at ($P = 0.025$) in each year.

Phenotypic correlations between characters were estimated in the F_2 populations using the computer package devised by Nofziger et al. (9).

Genetic correlations (rg) between characters were calculated using the formula:

$$rg = \{CovXYF_2 - CovXYE\}/\{[VXF_2 - VXE]1/2[VYF_2 - VYE]1/2\}$$

Standard errors for rg's were calculated as:

$$\begin{aligned} SE(rg) = \{1/df_2\ [rg^2/G\ & (Cov^2XYF_2 + VXF_2 * VYF_2) \\ & - 2rg^4/G^3\ (CovXYF_2 * VXF_2 + CovXYF_2 * VYF_2) \\ & + rg^6/G^4\ (Cov^2XYF_2 + 1/2\ V^2XF_2 + 1/2\ V^2YF_2)] \\ & + 1/dfE\ [rg^2/G\ (Cov^2XYE + VXE * VYE) \\ & - 2rg^4/G^3\ (CovXYE * VXE + CovXYE * VYE) \\ & + rg^6/G^4\ (Cov^2XYE + 1/2V^2XE + 1/2V^2YE)]\}1/2 \end{aligned}$$

where $CovXYF_2$ and CovXYE denote the covariances between characters "X" and "Y" in the F_2 and in the environment, respectively. G = $CovXYF_2$ - CovXYE; dfE = the pooled degrees of freedom for P1 and P2; df_2 = the degrees for freedom of the F_2; VYF_2 = the variance of character "Y" in the F_2; and VXE and VYE = the environmental variances of characters "X" and "Y".

RESULTS AND DISCUSSION

Broad-sense heritabilities for all characters in both years are shown for the four populations in Table 1. Estimates in each year are provided because significant differences between years were detected in those estimates for at least one character in three of the four populations.

Heritabilities for seed number/pod exhibited significant inconsistency between years in populations 1 and 2, but not in 3 and 4. Selection would have been highly effective in either year in populations 3 and 4; however, in populations 1 and 2 it would have been considerably more effective in 1984 than in 1985. Though limited, these data suggest that EG-MG-16/ML-3 contributes to its progeny a stability over environments for this character that M-1-77-OT-4 does not. Heritabilities averaged being moderately high in populations 3 and 4 (0.41 - 0.63); whereas, in populations 1 and 2, they were high in 1984, but were low (population 1) or not different from zero (population 2) in 1985.

Pod number/plant heritabilities exhibited significant inconsistency between years in populations 1 and 2, but not in 3 and 4. Selection for this character in populations 1 and 2 would be more effective in certain environments than in others. In 1984, heritability was not significantly different from zero in population 1 and low in population 2.

In 1985, their respective heritabilities were moderately high to high. Population 3 exhibited significant and consistent, but very low, heritability estimates both years. Neither estimate for population 4 was significantly different from zero. As with seed number/pod, M-1-77-OT-4 appears to be inconsistent in the pod number/plant of its progeny from environment to environment; whereas, EG-MG-16/ML-3 appears more stable.

One hundred-seed weight exhibited significant heritability estimates both years in all four populations. Although a significant inconsistency between years was observed in population 1, the potential for improvement in that population through selection ranged from moderately high to very high. In populations 2, 3, and 4, average heritabilities were high, moderately high, and high, respectively.

Grain yield heritabilities exhibited consistency between years in all four populations; therefore, response to selection for this character would have been similar in both years. The heritability estimates for populations 1 and 2 (medium and moderately high, respectively) were substantially higher than were those for populations 3 and 4 (low and moderately low, respectively), suggesting that M-1-77-OT-4 was contributing more genetic variation to its offspring for yield than was EG-MG-16/ML-3.

Plant weight heritabilities exhibited consistency between years in all four populations, suggesting that response to selection for this character was independent of years. All estimates were significant and averaged moderately high.

Heritabilities for vegetative weight exhibited consistency between years in three of the four populations. Populations 1, 2, and 4 averaged medium, moderately high, and moderately high heritabilities, respectively. Population 3 was the exception, being high in 1984 and low in 1985. All estimates were significant, suggesting considerable genetic variability for vegetative weight. Thus, it should be feasible to develop a mungbean emphasizing forage rather than grain.

In populations 1, 3, and 4, heritability estimates for harvest index were consistent between years averaging medium, low, and medium, respectively. Only population 2 exhibited significant differences between years. Its estimates were moderately high in 1984 and not significantly different from zero in 1985.

Tables 2, 3, 4, and 5 present the phenotypic and genotypic correlations in both years for populations 1, 2, 3, and 4, respectively. When calculating genetic correlations from variance components, it is possible to derive estimates numerically greater than one. This occurred herein primarily between characters with high phenotypic correlations, but with low or insignificant heritabilities. For the most part, the phenotypic and genotypic correlations were very similar in magnitude. However, in a few instances they differed both in magnitude and direction. Because of the very large F2 population sizes, almost all phenotypic correlations were significantly different from zero. The distinction between statistical significance and practical value can be a problem with such large samples. Therefore, only phenotypic correlations of the larger magnitudes will be discussed. In each population, phenotypic correlations will be discussed first, then genotypic.

In population 1 (Table 2), seed number/pod was negatively correlated with 100-seed weight. Seed number/pod was positively correlated with grain yield, plant weight, vegetative weight, and harvest index. Pod number/plant was highly correlated with grain yield, plant weight, and vegetative weight in both years with a range of 0.78 to 0.94. Grain yield was correlated with plant weight and vegetative weight in both years, ranging from 0.78 to 0.96. Vegetative weight was highly correlated (0.96 and higher) to plant weight. Grain yield was moderately and positively correlated with harvest index. Because of large standard errors, few genotypic correlations were significant, even when approaching unity. Seed number/pod exhibited significant positive genotypic correlations with grain yield (0.24) in 1985 and vegetative weight (0.21) in 1984. The significant genotypic correlation between grain yield and plant weight (0.88) in 1985 is reasonable since grain yield is part of plant weight.

In population 2 (Table 3), seed number/pod was again negatively correlated with 100-seed weight, but positively correlated with grain yield, plant weight, vegetative weight, and harvest index. Large and significant correlations of pod number/plant with grain yield (0.91, 0.96), plant weight (0.89, 0.90), and vegetative weight (0.81, 0.79) were observed in 1984 and 1985, respectively. Grain yield was again highly and significantly correlated with plant weight (0.97, 0.93) and vegetative weight (0.87, 0.81) in 1984 and 1985, respectively. Limitations to vegetative growth are probably also important limiting factors in grain yield production in this and in the other populations examined. The correlation between vegetative weight and plant weight was also positive and highly significant in both years. Grain yield and pod number/plant were positively correlated with harvest index. Significant genotypic correlations were identified in seed number/pod vs. grain yield (0.33 and 0.53 in both years), plant weight (0.51 in 1985), and vegetative weight (0.49 in 1985). Significant genotypic correlations were also observed between plant weight and vegetative weight (0.97 and 0.96 in 1984 and 1985, respectively).

In population 3 (Table 4), seed number/pod was again negatively correlated with 100-seed weight. Seed number/pod was positively correlated with grain yield, plant weight, vegetative weight, and harvest index. Pod number/plant was highly correlated with grain yield (0.89, 0.93), plant weight (0.84, 0.90), vegetative weight (0.76, 0.83), and harvest index (0.46, 0.48) in 1984 and 1985, respectively. Grain yield was highly correlated with plant weight (0.94, 0.94), vegetative weight (0.84, 0.86), and harvest index (0.52, 0.53) in 1984 and 1985, respectively. Plant weight was highly correlated with vegetative weight (0.98) in both years. A positive genotypic correlation was observed between seed number/pod and grain yield (0.35, 0.29) in 1984 and 1985, respectively. Also, the genotypic correlation between seed number/pod and vegetative weight (0.37) in 1984 was significant. Grain yield was significantly correlated genotypically with vegetative weight (0.98, 1.26) in 1984 and 1985, respectively.

In population 4 (Table 5), seed number/pod was negatively correlated with 100-seed weight and positively correlated with grain yield, plant weight, vegetative weight, and harvest index. Pod number/plant again was highly correlated with grain yield (0.87, 0.93), plant weight (0.76, 0.90), and vegetative weight (0.62, 0.80), in 1984 and 1985, respectively. Pod number was less closely, though significantly, correlated with harvest index in both years.

Grain yield was highly correlated with plant weight (0.92, 0.93) and vegetative weight (0.78, 0.80) in 1984 and 1985, respectively, as was plant weight vs. vegetative weight (0.96) in both years. Seed number/pod was correlated genotypically with grain yield (0.34 and 0.30 in 1984 and 1985, respectively) as well as with plant weight (0.49) and vegetative weight (0.51) in 1984. Pod number/plant was negatively correlated (-0.35, -0.41) with 100-seed weight in both years.

A general conclusion from these experiments is that significant levels of genetic variability are present for all characters examined, though not in all populations nor in all years. Environment from year to year played a large role in the expression of genetic variability in the characters seed number/pod and pod number/plant in populations 1 and 2 and for 100-seed weight in population 1, for harvest index in population 2, and for vegetative weight in population 3. Seed number/pod, 100-seed weight, pod number/plant, vegetative weight, plant weight, and grain yield appear interdependent phenotypically, but for the most part not genotypically, in mungbean. One hundred-seed weight generally behaved independently from the other characters genotypically and only expressed low phenotypic correlations. Seed number/pod was significantly correlated genotypically with grain yield both years in three of the four populations and in the other population 1 year, indicating a genetic relationship between the two characters. Selection studies should be conducted to confirm the degree of relationship between seed number/pod and grain yield.

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Table 1. Broad-sense heritabilities for yield and yield-related characters in four mungbean F_2 populations in 1984 and 1985.

Popn. no.+	Year	Seed no./pod	Pod no./plant	100-seed weight	Grain yield	Plant weight	Vegetative weight	Harvest index
1	1984	0.63**	0.18	0.51**	0.45**	0.57**	0.60**	0.47**
	1985	0.32**	0.54**	0.76**	0.53**	0.49**	0.38**	0.47**
	Diff.	*	*	*	NS	NS	NS	NS
2	1984	0.62**	0.28*	0.62**	0.48**	0.53**	0.52**	0.58**
	1985	0.19	0.64**	0.71**	0.63**	0.57**	0.56**	0.17
	Diff.	*	*	NS	NS	NS	NS	*
3	1984	0.53**	0.22*	0.46**	0.36**	0.54**	0.60**	0.44**
	1985	0.55**	0.21*	0.59**	0.34**	0.48**	0.30**	0.29**
	Diff.	NS	NS	NS	NS	NS	*	NS
4	1984	0.63**	0.17	0.54**	0.33**	0.57**	0.65**	0.45**
	1985	0.41**	0.19	0.69**	0.18	0.56**	0.46**	0.41**
	Diff.	NS	NS	NS	NS	NS	NS	NS

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.
+ Populations 1 through 4 are M-1-77-OT-4/3-1, M-1-77-OT-4/MG-50-10-A(Y), EG-MG-16/ML-3//3-1, and EG-MG-16/ML-3//MG-50-10-A(Y), respectively.

Table 2. Phenotypic and genotypic (in parentheses) correlations for mungbean population 1^{+} in 1984 and 1985.

Character	Pod no./plant	100-seed weight	Grain yield	Plant weight	Vegetative weight	Harvest index
Seed no./pod	-0.09*,‡	-0.24**	0.23**	0.23**	0.21**	0.10*
	0.13**	-0.34**	0.32**	0.26**	0.19**	0.22**
	(-0.40)	(-0.21)	(0.07)	(0.16)	(0.21)*	(-0.28)
	(0.22)	(-0.46)	(0.24)*	(0.22)	(0.21)	(-0.35)
Pod no./plant		-0.08	0.91**	0.87**	0.79**	0.38**
		0.00	0.94**	0.90**	0.78**	0.15**
		(-0.33)	(1.00)	(0.97)	(0.98)	(0.35)
		(-0.06)	(0.96)	(0.87)	(0.95)	(0.02)
100-seed weight			0.00	0.05	0.09*	-0.17**
			0.10*	0.11**	0.11**	0.05
			(-0.01)	(0.06)	(0.11)	(-0.28)
			(0.11)	(0.11)	(0.08)	(0.15)
Grain yield				0.96**	0.88**	0.38**
				0.93**	0.78**	0.22**
				(0.98)	(0.91)	(0.15)
				(0.88)*	(0.66)	(0.02)
Plant weight					0.98**	0.16**
					0.96**	-0.09
					(0.98)	(-0.06)
					(0.95)	(-0.46)
Vegetative weight						0.02
						-0.32**
						(-0.23)
						(-0.87)

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

$^{+}$Population 1 is M-1-77-OT-4/3-1.

‡ In each pair of correlations, the estimate on top was obtained in 1984; that on bottom in 1985.

Table 3. Phenotypic and genotypic (in parentheses) correlations for mungbean population 2^{+} in 1984 and 1985.

Character	Pod no./plant	100-seed weight	Grain yield	Plant weight	Vegetative weight	Harvest index
Seed no./pod	0.04‡ 0.17**	-0.25** -0.40**	0.33** 0.35**	0.29** 0.30**	0.24** 0.24**	0.22** 0.27**
	(0.09) (0.49)	(-0.23) (-0.76)	(0.33)* (0.53)*	(0.32) (0.51)*	(0.29) (0.49)*	(0.08) (-0.45)
Pod no./plant		-0.03 -0.03	0.91** 0.96**	0.89** 0.90**	0.81** 0.79**	0.38** 0.32**
		(-0.16) (-0.11)	(0.97) (0.98)	(0.93) (0.90)	(0.80) (0.74)	(0.39) (0.54)
100-seed weight			0.03 0.01	0.09* 0.06	0.15** 0.10*	-0.19** -0.15**
			(0.02) (-0.06)	(0.10) (-0.00)	(0.19) (0.04)	(-0.28) (-0.31)
Grain yield				0.97** 0.93**	0.87** 0.81**	0.41** 0.35**
				(0.97) (0.91)	(0.87) (0.76)	(0.31) (0.43)
Plant weight					0.97** 0.97**	0.22** 0.06
					(0.97)** (0.96)**	(0.12) (-0.18)
Vegetative weight						0.01 -0.16**
						(-0.09) (-0.52)

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

$^{+}$Population 2 is M-1-77-OT-4/MG-50-10-A(Y).

‡ In each pair of correlations, the estimate on top was obtained in 1984; that on bottom in 1985.

Table 4. Phenotypic and genotypic (in parentheses) correlations for mungbean population 3$^+$ in 1984 and 1985.

Character	Pod no./plant	100-seed weight	Grain yield	Plant weight	Vegetative weight	Harvest index
Seed no./pod	0.05‡	-0.25**	0.39**	0.36**	0.33**	0.30**
	0.09*	-0.16*	0.35**	0.31**	0.27**	0.30**
	(-0.01)	(-0.28)	(0.35)*	(0.30)	(0.37)*	(0.13)
	(0.14)	(-0.13)	(0.29)*	(0.27)	(0.29)	(0.26)
Pod no./plant		-0.09*	0.89**	0.84**	0.76**	0.46**
		-0.06	0.93**	0.90**	0.83**	0.48**
		(-0.34)	(0.93)	(1.04)§	(1.00)	(0.73)
		(-0.07)	(1.08)	(1.32)§	(1.62)§	(0.54)
100-seed weight			-0.03	-0.07	-0.10*	0.10*
			0.02	-0.05	-0.09*	0.17**
			(-0.14)	(-0.18)	(-0.20)	(0.21)
			(0.05)	(-0.14)	(-0.29)	(0.48)
Grain yield				0.94**	0.84**	0.52**
				0.94**	0.86**	0.53**
				(1.01)§	(0.98)*	(0.65)
				(1.09)§	(1.26)*§	(0.62)
Plant weight					0.98**	0.25**
					0.98**	0.29**
					(0.96)	(0.49)
					(1.07)§	(0.62)
Vegetative weight						0.08*
						0.13**
						(0.20)
						(0.82)

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

$^+$Population 3 is EG-MG-16/ML-3//3-1.

‡ In each pair of correlations, the estimate on top was obtained in 1984; that on bottom in 1985.

§ Correlation estimate greater than one (for which the most reasonable value is one).

Table 5. Phenotypic and genotypic (in parentheses) correlations for mungbean population 4^+ in 1984 and 1985.

Character	Pod no./plant	100-seed weight	Grain yield	Plant weight	Vegetative weight	Harvest index
Seed no./pod	-0.05‡	-0.18**	0.35**	0.40**	0.40**	0.09*
	0.09*	-0.31**	0.34**	0.25**	0.17**	0.33**
	(-0.27)	(-0.12)	(0.34)*	(0.49)*	(0.51)*	(-0.23)
	(0.28)	(-0.49)	(0.30)*	(0.17)	(0.03)	(0.21)
Pod no./plant		-0.10*	0.87**	0.76**	0.62**	0.43**
		-0.10*	0.93**	0.90**	0.80**	0.27**
		(-0.35)*	(0.79)	(0.76)	(0.68)	(0.87)
		(-0.41)**	(1.16)§	(1.21)§	(1.00)	(-0.26)
100-seed weight			-0.02	0.08*	0.13**	-0.23**
			-0.01	0.00	0.01	-0.01
			(-0.06)	(0.08)	(0.15)	(-0.33)
			(-0.22)	(-0.08)	(-0.07)	(-0.15)
Grain yield				0.92**	0.78**	0.42**
				0.93**	0.80**	0.36**
				(1.01)§	(0.86)	(0.54)
				(1.14)§	(0.82)	(0.40)
Plant weight					0.96**	0.10*
					0.96**	0.07
					(1.02)§	(0.19)
					(0.97)	(-0.25)
Vegetative weight						-0.13**
						-0.15**
						(-0.12)
						(-0.61)

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

$^+$Population 4 is EG-MG-16/ML-3//MG-50-10-A(Y).

§ Correlation estimate greater than one (for which the most reasonable value is one).

‡ In each pair of correlations, the estimate on top was obtained in 1984; that on the bottom in 1985.

CHAPTER II

Realized Heritabilities for Yield and Yield-Related Characters in Mungbean

Realized Heritabilities for Yield and Yield-Related Characters in Mungbean[1]

ABSTRACT

Genetic studies in mungbean [*Vigna radiata* (L.) Wilczek] have traditionally been conducted in relatively small, space-planted populations. Heritability estimates from such studies frequently do not correspond closely with the responses obtained in more densely planted breeder's plots. The objective of this research was to determine realized (i.e., narrow-sense) heritability estimates for yield and yield-related characters in more densely planted, large populations of mungbean. Two small-seeded, high yielding lines, M-1-77-OT-4 and EG-MG-16/ML-3, were each crossed to two large-seeded lines, MG-50-10A(Y) and 3-1. Individual F_2 plants were selected from each of the four populations based on high grain yield, seed weight, and/or pod number/plant. Selected plants and appropriate testers from the four populations were planted in progeny rows under dryland conditions near Perkins, OK, in 1986 and 1987. Each F_3 included approximately 190 progeny rows. At harvest grain yield and 100-seed weight were taken on each row. Results from these experiments indicate that the realized

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heritability for yield in thick plantings of mungbean is very low and is greatly influenced by environment. Thus, direct selection for yield in such plantings would likely not be very effective. Realized heritability of 100-seed weight was generally low to medium and relatively consistent between environments. Two of the populations in 1 year exhibited a moderate to strong positive indirect response for yield in selections made for increased seed weight. Indirectly, yield might be increased faster selecting for seed weight than through direct selection for yield itself. Further work under disease-free conditions is required to establish this hypothesis.

Additional index words: *Vigna radiata* (L.) Wilczek, Yield components, Narrow-sense heritability, Additive gene action, Progeny tests.

INTRODUCTION

Mungbean [Vigna radiata (L.) Wilczek] is an ancient grain crop in Southeast Asia and India. However, little research on cultivar improvement of the crop has been conducted. Recently, interest has arisen in the USA in growing mungbean as an alternative crop for domestic consumption and for export.

The inheritance of several yield components in mungbean are controlled largely by additive gene action. Dhaliwal and Singh (2) estimated general combining ability (GCA) was significant for pod number/plant in F_1 and F_2 generations of mungbean. Singh and Jain (9) showed in F_1 populations that pod number/plant and grain yield in mungbean were predominantly controlled by additive gene effects. They (10) likewise showed that seed weight was controlled primarily by additive gene effects, but observed some overdominance influencing the trait. Singh and Singh (12) found in F_1, F_2, and F_3 mungbean populations the nonadditive component of variance was significant for grain yield and pod number/pod, but the additive component was not in any generation. They detected additive and nonadditive variance components for seed weight. Singh and Singh (14) also found in the F_2 and F_3 of several mungbean populations that additive gene effects were more important than nonadditive for pod number/plant and grain yield, but significant nonadditive effects were also present. They showed for seed weight that additive effects were most important. Yohe and Poehlman (15) demonstrated that components of grain yield were controlled by both additive and nonadditive gene effects in an F_1 population, but that additive effects were much larger than nonadditive.

Empig et al. (3) in an F_2 population estimated that seed weight and grain yield had broad-sense heritabilities of 51.2 and 8.6%, respectively. Considerable genetic variability was noted for pod number/plant. Cupka (1988, personal observation) estimated broad-sense heritabilities for pod number/plant, seed weight, and grain yield in four F_2 populations ranging from 0.17 to 0.64, 0.46 to 0.76, and 0.18 to 0.63, respectively. Some of these heritability estimates for seed weight and grain yield were much higher than previously reported. However, that may have been for seed weight a consequence of the conscious selection of parents with extreme differences in seed size.

Strong correlations exist between selected yield components and grain yield in mungbean. Gupta and Singh (6) showed that grain yield was strongly and positively correlated with pod number/plant (0.69) and 50-seed weight (0.72). Singh and Malhotra (11) found 100-seed weight was negatively associated with pod number/plant (-0.17). Chandel et al. (1) noted positive correlations between pod number/plant (0.82) and seed weight (0.54) vs. grain yield, respectively. Giriraj and Vijayakumar (5) obtained positive genotypic correlations between pod number/plant and grain yield (0.70) among 55 pure lines using path-coefficient analysis. They also detected a negative correlation between 100-seed weight and grain yield (-0.41). Yohe and Poehlman (15) demonstrated that yield components such as 1000-seed weight (0.76) and pod number/plant (0.88) were positively correlated with grain yield in an F_1 5 X 5 diallel. Singh and Singh (13) found significant positive correlations between pod number/plant and grain yield (0.81) in several F_2 populations. Joshi and Kabaria (7) and Malhotra et al. (8) calculated that seed weight (-0.21 and -0.65, respectively) and pod number/plant (0.95 and 0.98, respectively) had large direct effects on yield. However, correlations between seed weight and pod number/plant were significant and negative (-0.73 and -0.79, respectively); thus, a compromise must likely be made between selection for those two traits if an increase in grain yield is to be realized. They considered pod number/plant was the most important yield contributing character. Cupka (1988, personal observation) observed significant phenotypic correlations between pod number/plant and grain yield ranging from 0.87 to 0.96 in four F_2 populations. He also obtained a moderate negative genotypic correlation (0.41) between 100-seed weight and pod number/plant in one of the four F_2 populations. One hundred-seed weight generally behaved independently of grain yield.

The objectives of this study were to determine realized (i.e., narrow-sense) heritabilities for 100-seed weight, pod number/plant, and grain yield in four large, closely spaced F_2 mungbean populations and to study indirect selection responses among those characters in the F_3 and F_4. Pod number/plant was abandoned after the first year because no significant estimates were obtained and because of time constraints at harvest.

MATERIALS AND METHODS

Four parents were used in these experiments, i.e., M-1-77-OT-4, a high-yielding line with a low seed weight of approximately 5.7 g/100 seed; EG-MG-16/ML-3, another high-yielding line with a low seed weight of about 5.4 g/100 seed; 3-1, a large-seeded line with seed weight of approximately 7.8 g/100 seed; and MG-50-10-A(Y), another large-seeded line with seed weight of about 8.4 g/100 seed. The two lines with small seed were crossed to each of the two large-seeded lines and advanced to the F_2 generation. Populations were designated as 1 for M-1-77-OT-4/3-1, 2 for M-1-77-OT-4/MG-50-10-A(Y), 3 for EG-MG-16/ML-3//3-1, and 4 for EG-MG-16/ML-3//MG-50-10-A(Y).

In 1984 each F_2 population was inoculated with Brady *Rhizobium* spp. [*Vigna*] and planted in 12 rows 6.75 m long and 75 cm apart using a cone type planter. Each row contained approximately 80 individual plants spaced about 8 cm apart. At harvest, each row and each plant within a row was harvested separately. A grid selection procedure (4) was used to select the top 10% of the plants from each of the F_2 populations for evaluation as progeny rows in the F_3 and F_4. Selections were practiced for high grain yield, weight/100 seed, and pod number/plant within each separate row. Thus, individual rows were used as grids in selection. The soil in this research was a Teller loam (Fine-loamy, mixed, thermic

Udic Argiustoll) with 0 to 1% slope, medium internal drainage, and moderate permeability. Soils were sampled to determine their fertility status, but no nutrients were required.

The F_3 progeny rows were also inoculated as before and grown under dryland conditions in 1986 on the OSU Agronomy Research Station near Perkins, OK. The F_4's were grown in 1987 in a similar manner. The selected progeny from each F_2 population were planted in single rows. However, several selections for large seed size had very low yield (less than 70 mature seed). Several such selections were bulked with similar F_2's, and the bulked seed were randomly planted in rows at the appropriate population density. Only some of the large-seeded selections were unable to produce adequate quantities of seed to plant an entire row. This procedure caused a bias in the large-seeded populations favoring those progeny which produced higher yields. Every fifth row planted was an F_3 or F_4 sample from the respective F_2 or F_3 unselected bulk of the appropriate population. A total of 768 rows were planted each year with population 1 including 192 rows; population 2, 192 rows; population 3, 184 rows; and population 4, 200 rows. Prior to harvest in 1986, pod number/plant was counted on two random plants in each row. That effort was not duplicated in 1987.

Prior to harvest, the rows were shortened to 6.15 m to eliminate border effects. At harvest, all rows were cut and threshed in the field. Seed from each row was bagged individually and placed in a dryer until the moisture level was reduced sufficiently to inhibit growth of pathogens. The seed were then processed in a seed cleaner to eliminate any leaf and/or insect debris left after threshing. The characters from each row then measured were grain yield in grams and 100-seed weight in grams.

The F_2 plant yields and the F_3 and F_4 row yields were both converted to g m-2 to convert them into the same units. Realized (i.e., narrow-sense) heritabilities (H_{NS}) for yield and 100-seed weight were then calculated using the following formula:

$H_{NS} = (\bar{x}\ F_3\ \text{sel.} - \bar{x}\ F_3\ \text{bulk})/(\bar{x}\ F_2\ \text{sel.} - \bar{x}\ F_2\ \text{popn.})$

with $\bar{x}\ F_3$ sel. and $\bar{x}$ F2 sel. being the means of the respective selected progeny and $\bar{x}\ F_3$ bulk and $\bar{x}\ F_2$ popn. being the respective means of the unselected bulk and original F_2 population.

A single F_2 plant could be selected for more than one character. A total of six different selection combinations in each population were tested in this study. They include grain yield, pod number/plant, and 100-seed weight, without regard to the other characters selected, grain yield plus pod number/plant, grain yield plus 100-seed weight, and grain yield plus 100-seed weight plus pod number/plant.

To test for significance of response to selection the selected progeny were compared with the nearest unselected bulk row in paired comparisons using t-tests. Because the selection combinations contained different numbers of progeny, each combination was evaluated individually.

RESULTS AND DISCUSSION

In population 1 in 1986 (Table 1), those progeny selected for 100-seed weight and yield plus 100-seed weight exhibited yields significantly greater than the unselected bulk. This suggests a positive relationship between seed weight and grain yield. Those progeny selected for increased grain yield or pod number/plant exhibited no significant difference from the tester. Those progeny selected for yield plus pod number/plant had significantly lower seed weights. The bulked 100-seed weight selections were compared to the unbulked 100-seed weight selections, and no significant differences were found for yield or seed weight in either year for any population. In population 1 in 1987 no selection combination exhibited a significant selection response for grain yield. The inconsistency between years for yield may be partially explained by a severe infestation of halo blight (Pseudomonas phaseolicola Burkh. Dows.) in 1987 which appeared to damage the relatively homogeneous selected progeny to a greater extent than the more heterogeneous tester rows. The 1986 yield results in population 1 do, however, suggest the importance of seed weight as a yield-component character and suggest that selection for increased 100-seed weight may have a significant and positive indirect effect on yield when direct selection for yield itself is ineffective. Selections for increased yield itself or for numbers of pods/plant were not effective in altering grain yield in either year. However, those progeny selected for 100-seed weight, yield plus 100-seed weight, and yield plus 100-seed weight plus pod number/plant all exhibited significantly larger seed weights than the tester.

In population 2 in 1986 (Table 2), the only selection which exhibited a significant positive response for grain yield was selection for increased 100-seed weight. However, in 1987 no group exhibited a significant response for yield. In population 2 those progeny selected for increased 100-seed weight, yield plus 100-seed weight, and yield plus 100-seed weight plus pod number/plant exhibited significantly larger seed weights than the tester in both years.

In population 3 (Table 3), none of the selected progeny exhibited significantly altered yield in either year. Those progeny selected for 100-seed weight, yield plus 100-seed weight, and yield plus 100-seed weight plus pod number/plant exhibited significantly larger seed than the tester in both years.

In population 4 in 1986 (Table 4) no progeny exhibited a significantly higher yield than the tester. Those progeny in population 4 selected for 100-seed weight and yield plus 100-seed weight exhibited significantly larger seed than the tester in both years. The selections for yield plus 100-seed weight plus pod number/plant exhibited significantly larger seed than the tester in 1987, but not in 1986.

Results from these experiments suggest that direct selection in mungbean for grain yield generally elicits little or no response when based on individual F_2 plant selections from dense plantings (Table 5) and, as such, is greatly influenced by environment. Genetic improvement through direct selection for yield in such plantings would likely not be very effective. Somewhat wider spacing than was used here may be necessary for yield differences to be clearly expressed. Results from populations 1 and 2 (Tables 1 and 2) in 1986 suggest that selection for increased 100-seed weight may be an effective way to indirectly increase yield in at least some populations. Results in the four populations over both years suggest that increased 100-seed weight can effectively be selected (Table 6) in such plantings and is less influenced by environmental conditions than is yield. Further work under disease-free conditions is required to establish whether selection for increased seed weight does positively affect yield.

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LIST OF TABLES

Table 1. Mean yield and 100-seed weight for all selection combinations tested in mungbean population 1+ compared with the unselected bulk for 2 years.

Selection combinations	1986 Grain yield	1986 100-seed weight	1987 Grain yield	1987 100-seed weight
	g m-2	g	g m-2	g
Unselected bulk	75.8	5.82	76.5	6.69
Grain yield	77.5	5.94	76.2	6.80
Pod no./plt.	75.5	5.72	78.3	6.61
100-seed wt.	81.7*	6.31**	74.9	7.10**
Yield + pod no./plt.	74.8	5.67*	79.1	6.55
Yield + 100-seed wt.	86.8*	6.06*	77.7	6.94*
Yield + 100-seed wt. + pod no./plt.	80.4	6.01	74.6	7.07*

*,** Significantly different than the tester at the 0.05 and 0.01 levels of probability, respectively.
+Population 1 is M-1-77-OT-4/3-1.

Table 2. Mean yield and 100-seed weight for all selection combinations tested in mungbean population 2[+] compared with the unselected bulk for 2 years.

Selection combinations	1986 Grain yield	1986 100-seed weight	1987 Grain yield	1987 100-seed weight
	g m-2	g	g m-2	g
Unselected bulk	74.1	5.93	65.5	6.77
Grain yield	79.7	6.18	65.7	7.02
Pod no./plt.	77.9	6.01	66.3	6.89
100-seed wt.	82.6**	6.54**	63.2	7.21**
Yield + pod no./plt.	78.8	6.05	65.9	6.92
Yield + 100 seed wt.	82.0	6.99**	61.0	7.46*
Yield + 100-seed wt. + pod no./plt.	67.3	7.03*	47.3	7.64*

*,** Significantly different than the tester at the 0.05 and 0.01 levels of probability, respectively.

[+] Population 2 is M-1-77-OT-4/MG-50-10-A(Y).

Table 3. Mean yield and 100-seed weight for all selection combinations tested in mungbean population 3[+] compared with the unselected bulk for 2 years.

Selection combinations	1986 Grain yield	1986 100-seed weight	1987 Grain yield	1987 100-seed weight
	g m-2	g	g m-2	g
Unselected bulk	38.7	5.52	54.7	6.01
Grain yield	41.1	5.70	53.9	6.30
Pod no./plt.	41.7	5.45	52.7	6.12
100-seed wt.	40.4	6.13**	51.6	6.70**
Yield + Pod no./plt.	40.8	5.60	53.2	6.16
Yield + 100-seed wt.	37.3	6.14**	57.4	6.61**
Yield + 100-seed wt. + pod no./plt.	34.7	6.03*	55.1	6.56*

*,** Significantly different than the tester at the 0.05 and 0.01 levels of probability, respectively.

[+] Population 3 is EG-MG-16/ML-3//3-1.

Table 4. Mean yield and 100-seed weight for all selection combinations tested in mungbean population 4[+] compared with the unselected bulk for 2 years.

	1986		1987	
Selection combinations	Grain yield	100-seed weight	Grain yield	100-seed weight
	g m-2	g	g m-2	g
Unselected bulk	45.2	6.64	65.1	7.17
Grain yield	45.0	6.81	60.1	7.37
Pod no./plt.	45.0	6.64	61.1	7.28
100-seed wt.	43.7	7.13**	60.0	7.59**
Yield + Pod no./plt.	45.6	6.64	62.9	7.35
Yield + 100-seed wt.	48.3	7.14**	65.9	7.83**
Yield + 100-seed wt. + pod no./plt.	52.7	7.20	77.1	7.63*

*,** Significantly different than the tester at the 0.05 and 0.01 levels of probability, respectively.

[+] Population 4 is EG-MG-16/ML-3//MG-50-10-A(Y).

Table 5. Realized heritability for mungbean yield in all selection combinations including that trait for 2 years.

Selection combinations	1986	1987
Population 1[+]		
Grain yield	0.01	0.00
Yield + pod no./plt.	-0.01‡	0.02
Yield + 100-seed wt.	0.04*	-0.00‡
Yield + 100 seed wt. + pod no./plt.	0.02	-0.01‡
Population 2[+]		
Grain yield	0.03	0.00
Yield + pod no./plt.	0.03	0.00‡
Yield + 100-seed wt.	0.06	-0.03‡
Yield + 100 seed wt. + pod no./plt.	-0.01‡	-0.08‡
Population 3[+]		
Grain yield	0.02	-0.01‡
Yield + pod no./plt.	0.01	-0.01‡
Yield + 100-seed wt.	0.02	0.02
Yield + 100 seed wt. + pod no./plt.	0.00	0.01
Population 4[+]		
Grain yield	0.00	-0.04‡
Yield + pod no./plt.	0.00	-0.02‡
Yield + 100-seed wt.	0.05	0.00
Yield + 100 seed wt. + pod no./plt.	0.06	0.05

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

[+] Populations 1 through 4 are M-1-77-OT-4/3-1, M-1-77-OT-4/MG-50-10-A(Y), EG-MG-16/ML-3//3-1, and EG-MG-16/ML-3//MG-50-10-A(Y), respectively.

‡ Negative estimate (for which the most reasonable value is zero).

Table 6. Realized heritability for mungbean 100-seed weight in all selection combinations including that trait for 2 years.

Selection combinations	1986	1987
Population 1 +		
100-seed wt.	0.30**	0.25**
Yield + 100-seed wt.	0.20*	0.19*
Yield + 100 seed wt. + pod no./plt.	0.19	0.22*
Population 2 +		
100-seed wt.	0.32**	0.23**
Yield + 100-seed wt.	0.45**	0.21*
Yield + 100 seed wt. + pod no./plt.	0.49*	0.63*
Population 3 +		
100-seed wt.	0.38**	0.43**
Yield + 100-seed wt.	0.38**	0.37**
Yield + 100 seed wt. + pod no./plt.	0.23*	0.35*
Population 4 +		
100-seed wt.	0.27**	0.23**
Yield + 100-seed wt.	0.35*	0.46**
Yield + 100 seed wt. + pod no./plt.	0.23	0.41*

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

+ Populations 1 through 4 are M-1-77-OT-4/3-1, M-1-77-OT-4/MG-50-10-A(Y), EG-MG-16/ML-3//3-1, and EG-MG-16/ML-3//MG-50-10-A(Y), respectively.

VITA

Timothy Brian Cupka

Candidate for the Degree of

Doctor of Philosophy

Thesis: HERITABILITIES, AND CORRELATIONS FOR YIELD AND YIELD-RELATED CHARACTERS IN MUNGBEAN

Major Field: Crop Science

Biographical:

Personal Data: Born December 8, 1959, in Lafayette, Indiana, the son of Richard D. and Delores J. Cupka; married Nancy Jo Cook on July 7, 1980; daughters Susan Ann born July 19, 1985, and Dorothy Lynn born January 14, 1988.

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