Change in heritability estimates due to half-sib family selection in the maize variety Pahari

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ABSTRACT. This research was carried out at the Agriculture Research Farm, Khyber Pakhtunkhwa Agricultural University, Peshawar, and the Cereal Crops Research Institute, Pirsabak, Nowshera, during 2009 and 2010. Half-sib families (HS) derived from the maize variety Pahari in spring crop seasons 2009 and 2010 were developed at the Cereal Crops Research Institute. All HS families were detasseled well before pollen shedding. At maturity, each family was harvested and shelled separately. During the summer crop of seasons 2009 and 2010, these HS families were evaluated in 12 x 12 and 11 x 11 partially balanced lattice square arrangements at the Khyber Pakhtunkhwa Agricultural University, Peshawar, for various flowering and yield traits, respectively. The data on days to mid-silking, anthesis, anthesis-silking interval, 100-grain weight,

and grain yield were recorded. The results revealed significant differences among families for all traits in both cycles. High heritability (0.88) was observed for days to mid-silking in cycle 0 (C_0), while moderate heritability (0.42) was recorded for 100-grain weight in C_1. The selection differential was quite reasonable and varied according to the traits of interest. The observed response for grain yield in C_0 (815.74 kg/ha) was greater than the expected response (681.76 kg/ha).

Key words: Maize; Half-sib; Recurrent selection; Pahari; Heritability; Khyber Pakhtunkhwa

INTRODUCTION

Maize is a multipurpose crop. In Asia, maize is grown in Pakistan, India, and Nepal as a food, feed, and fodder crop. It is also produced in Indonesia and Thailand, but is not a preferred human food in these countries. It is the major staple food in many countries in Latin America and Africa. Approximately two-thirds of the total world production of maize is used for livestock feed or for commercial starch and oil production (Khalil and Jan, 2002). It has great nutritional value as it contains approximately 66.7% starch, 10% protein, 4.8% oil, 8.5% fiber, 3% sugar, and 7% ash (Chaudhry, 1983).

Maize breeders have used several methods of maize improvement, particularly mass selection, modified ear-to-row selection, S_1 line, reciprocal, and full- and half-sib (HS) recurrent selection (RS) methods to develop high-yielding maize varieties with improved yield per unit area. In any RS program, progress from selection is directly related to the expected change in allelic frequency and the magnitude of genetic variance in the breeding population (Helms et al., 1989). Therefore, population improvement through recurrent methodology focuses on two main objectives: first, improvement of the mean performance of a population through an increase in the frequency of favorable alleles, and second, maintaining adequate genetic variability in the improved population for continued selection and genetic improvement in subsequent generations. Evaluation of RS programs can lead to increased knowledge of methods, population, and traits and provide support for better management of breeding programs (Guimaraes, 2001). Realized progress with any breeding scheme, however, depends largely upon the ability of the breeder to identify superior genotypes and the accuracy with which the experiments are conducted (Alam, 1999). The S_1 progeny selection and HS family selection are of particular interest in this regard (Tanner and Smith, 1987; Beavis et al., 1994).

"HS" is defined as the progeny from a cross that has one parent in common. In maize population improvement, grain yield has historically been the most important trait and hence the most frequently selected. Previous estimates for grain yield improvement indicated that one may expect to observe a 2-4% increase per cycle in grain yield for different methods of selection in different populations, the same methods in different populations, or different methods in the same population, depending on the type of method used for selection (CIMMYT, 1981). Eyherabide and Hallauer (1991) reported a 6.5% per cycle increase in grain yield for a population cross in a reciprocal full-sib selection program between BS10 (formerly Iowa two-ear synthetic) and BS11 (formerly Pioneer two-ear composite). Keertinijakal and Lamkey (1993) also reported a 7.0% per cycle increase in yield in the population cross between Iowa Stiff Stalk Synthetic (BSSS) and

Iowa Corn Borer Synthetic No. 1 (BSCB1). Lamkey (1992) reported that 7 cycles of HS family selection in BSSS increased grain yield by 3.9% per cycle, whereas 6 cycles of S_2 progeny selection following 7 cycles of HS selection produced no increase.

Identification of superior genotypes in a mixed or base population is one of the major aims of plant breeders (Khan, 2004). The objectives of this study were to evaluate HS families derived from the maize variety Pahari and to identify superior HS families for yield and yield-related traits that can be used in future maize breeding programs.

MATERIAL AND METHODS

The procedure, material, and methods used in the present study are as follows.

Breeding material

The breeding materials used in this experiment comprised 144 and 121 HS lines developed from the maize variety Pahari in 2009 and 2010, respectively. Pahari is a composite of Shaheen x PS-7930. It is a white, semi-dent variety of medium-tall stature, and semi-dense tassel with profuse branching. The base population was used as a control.

Procedure and field experiment

During the spring crop seasons (March-June) of 2009-2010, 144 and 121 HS lines derived from the maize variety Pahari were developed by growing the selected HS lines with composite males of selected HS lines in isolation at the Cereal Crops Research Institute, Pirsabak, Nowshera. Regular visits to the farm were made to detassel female lines that displayed tassels. The detasseled HS lines were allowed to be pollinated naturally by the bulk male lines. Plants were hand-harvested at physiological maturity (black layer formation at hilum of maize kernel). HS lines with maximum grain filling, ear length, and good-looking cobs were selected, while the rest were discarded. During the summer of 2009 and 2010, HS lines, along with one check, were evaluated in a replicate trial using a partially balanced lattice square design with 2 replications at the Agricultural University Peshawar research farm. Row length was kept at 5 m, with 0.25-m plant-to-plant spacing and 0.75-m row-to-row spacing. At the 4 to 6 leaf stage, the number of plants was reduced to one plant per hill through thinning to maintain a population size of 53,300 plants per hectare. Standard cultural practices were carried out in both seasons. Fertilizer was applied in the form of diammonium phosphate and urea at the rate of 125 and 250 kg/ha, respectively. All of the diammonium phosphate was applied at the time of sowing, while half the urea was applied before sowing, with the rest being applied when plants were at knee height. The crop was irrigated weekly. Data were recorded for the following parameters as and when appropriate: days to mid-silking, mid-anthesis, anthesis-silking interval (ASI), 100-grain weight (g), and grain yield (kg/ha).

ASI

The ASI was calculated with the following formula on a per-plot basis:
ASI = days to 50% silking - days to 50% pollen shedding

Grain yield (kg/ha)

Grain yield was calculated from the data of fresh ear weight per plot with the following formula (Carangal et al., 1971):

$$\text{Grain yield (kg/ha) (15\% GM)} = \frac{\text{Fresh ear weight (kg/plot)} \times (100 - MC) \times 0.8 \times 10,000}{(100 - 15) \times \text{Area harvested (plot size)}}$$

where *GM* is the grain moisture; *MC* is the moisture content (%) in grains at harvest; 0.8 is the shelling coefficient; area per plot is 3.75 m^2; 1 hectare is 10,000 m^2; 15% is the moisture content required in grain at storage.

Statistical analysis

Analysis of variance (ANOVA) based on a randomized complete block design was computed according to format (Table 1) for the data of each year and trait (Milles et al., 1980) to derive mean squares for HS families using the MSTATC computer package (Director Crop and Siol Science Department, Machigan State University, Version 2.00).

Table 1. ANOVA format for single cycle.

SOV	d.f.	MS	Expected MS
Replication (r)	r - 1		
Block (k)	r (k - 1)		
Treatments	(k^2 - 1)	M2	$\sigma^2_E + r\sigma^2_G$
Error	(k - 1) (rk - k - 1)	M1	σ^2_E

SOV = source of variation; d.f. = degrees of freedom; MS = mean square.

Estimates of genotypic and phenotypic components were calculated from ANOVA and used to calculate heritability on an entry-mean basis (Penny and Elbert, 1971; Carson et al., 2004) as follows:

$\delta^2 e = M1$ (error mean squares)
$\delta^2 e + r\, \delta^2 G = M2$ (genotypic/families mean squares)
$\delta^2 G = M2 - M1$ [genotypic variance ($\delta^2 G$)]
$\delta^2 G + \delta^2_{E/r} = $ phenotypic variance ($\delta^2 P$)
$h^2_{BS} = $ broad-sense heritability
$h^2_{BS} = \delta^2 g / \delta^2 g + \delta^2 e$ (Fehr, 1987)
The selection differential was calculated as:

$$S = \mu_{HS} - \mu,$$

where *S* is the selection differential; μ_{HS} is the mean of selected HS families; μ is the population mean.
The expected response (Re) was calculated as:

$$Re = S \times h^2$$

The observed response (Ro) was calculated by subtracting the population mean from the mean of the progenies of the selected S$_1$ lines (μ_P) (Lush, 1940):

$$Ro = R_o = \mu_P - \mu$$

The percent gain per selection was estimated as follows (Keeling, 1982):

$$\% \text{ gain per cycle (C)} = \frac{C_1 - C_0}{C_0} \times 100$$

RESULTS

Flowering traits

Highly significant differences ($P \leq 0.01$) were observed in both C_0 and C_1 among the HS families for days to mid-silking, anthesis, and ASI (Table 2). High and moderate heritability estimates were observed for all flowering traits in both C_0 and C_1 (Table 2). The mean values for days to mid-silking, anthesis, and ASI in C_0 were 48.39, 47.59, and 0.79, respectively. Similarly in C_1, the mean values for flowering were 49.88, 49.42, and 0.45, respectively (Table 3). The selection differential for days to mid-silking, anthesis, and ASI in C_0 was 0.61, 0.61, and 0.01, respectively. Similarly in C_1, the selection differential values for days to mid-silking, anthesis, and ASI were -0.57, -0.38, and -0.16, respectively (Table 2). The Re in C_0 for days to mid-silking, anthesis, and ASI were 0.54, 0.45, and 0.00, respectively (Table 2). Similarly in C_1, the expected responses for flowering traits were -0.33, -0.18, and -0.07, respectively (Table 2). The Ro for days to mid-silking, anthesis, and ASI in C_0 was 0.61, 0.61, and 0.21, respectively (Table 3). The gain per cycle for days to mid-silking, anthesis, and ASI was 3.08, 3.85, and -43.04%, respectively (Table 3). Days to mid-silking was positively correlated with days to mid-anthesis, ASI, and grain yield, while it was negatively and highly significantly correlated with 100-grain weight in C_0. Similarly, days to mid-silking in C_1 was positively and significantly correlated with days to mid-anthesis and ASI. Days to mid-anthesis was positively and highly significantly correlated with ASI and grain yield in C_0, while it negatively correlated with 100-grain weight. Likewise, days to mid-anthesis in C_1 was positively and significantly correlated with ASI (Table 4).

Table 2. Mean square values, heritability (h^2_{BS}), selection differential (S), and expected response (Re) for various parameters observed during C_0 and C_1 in maize population Pahari.

Parameter	Mean squares		h^2_{BS}		S		Re	
	C_0	C_1	C_0	C_1	C_0	C_1	C_0	C_1
Days to silking	9.94**	6.01**	0.88	0.57	0.61	-0.57	0.54	-0.33
Days to anthesis	5.34**	2.48**	0.74	0.48	0.61	-0.38	0.45	-0.18
Anthesis silking interval	2.37**	2.39**	0.48	0.45	0.01	-0.16	0.00	-0.07
100-grain weight (g)	12.11**	16.75*	0.59	0.42	0.67	0.98	0.39	0.41
Grain yield (kg/ha)	1274827.78**	676804.11**	0.74	0.64	927.22	639.84	681.76	410.20**

**Highly significant; *significant.

Table 3. Means of population (μ), selected half-sib families (μHS), progeny (μP), observed response (Ro), and gain/cycle for different parameters observed during C_0 and C_1 in maize population Pahari.

Parameter	μ		μHS		μP	Ro	Gain (%)
	C_0	C_1	C_0	C_1	C_1	C_0	
Days to silking	48.39	49.88	49.00	49.31	49.00	0.61	3.08
Days to anthesis	47.59	49.42	48.20	49.04	48.20	0.61	3.85
Anthesis silking interval	0.79	0.45	0.80	0.29	1.00	0.21	-43.04
100-grain weight (g)	25.26	27.33	25.93	28.31	25.93	0.67	8.19
Grain yield (kg/ha)	3150.61	3309.26	4077.83	3949.10	3966.00	815.74	5.05

Table 4. Phenotypic correlation among flowering and grain yield-related traits in cycle 0 (above diagonal) and cycle 1 (below diagonal).

	DS	DA	ASI	GWT	YLD
DS	-	0.86**	0.67**	-0.23**	0.13*
DA	0.76**	-	0.19**	-0.16**	0.17**
ASI	0.75**	0.14*	-	-0.21**	0.002[NS]
GWT	-0.05[NS]	-0.05[NS]	-0.03[NS]	-	0.24**
YLD	-0.09[NS]	-0.09[NS]	-0.04[NS]	0.20**	-

DS = days to mid-silking; DA = days to mid-anthesis; ASI = anthesis-silking interval; GWT = 100-grain weight; YLD = grain yield. **Highly significant; *significant; NS = non-significant.

Hundred-grain weight (g)

The data presented in Table 2 indicate highly significant ($P \leq 0.01$) differences for 100-grain weight in C_0, while significant differences ($P \leq 0.05$) were observed in C_1. Moderate heritability was observed for grain weight in both cycles (Table 2). The population mean of 25.26 g and mean of selected HS lines of 25.93 g were observed in C_0. Similarly, the population mean of 27.33 g and mean of selected HS lines of 28.31 g were observed in C_1 (Table 3). The selection differential and Re observed in C_0 were 0.67 and 0.39 g, and 0.98 and 0.41 g in C_1, respectively (Table 2). An Ro of 0.67 g was observed for 100-grain weight (Table 3). The gain per cycle for grain weight was 8.19% (Table 3). The 100-grain weight in both cycles was positively and highly significantly correlated with grain yield (Table 4).

Grain yield (kg/ha)

The grain yield ANOVA revealed highly significant variations ($P \leq 0.01$) among HS lines in C_0 and C_1 (Table 2). Heritability of 0.74 and 0.64 was revealed for grain yield in C_0 and C_1, respectively (Table 2). The population mean and mean of selected HS lines for grain yield were 3150.61 and 4077.83 kg/ha in C_0, respectively; likewise in C_1, the population mean of 3309.26 kg/ha and mean of selected HS lines of 3949.10 kg/ha were observed. The selection differential and Re for grain yield in C_0 were 927.22 and 681.76 kg/ha, respectively. Similarly in C_1, the selection differential was 639.84 kg/ha and the expected response was 410.20 kg/ha (Table 2). A greater Ro of 815.74 kg/ha compared to the expected 681.76 kg/ha was observed for grain yield. The gain per cycle observed for grain yield was 5.05% (Table 3). The coefficients of variation 18.36 and 14.49% were observed in both C_0 and C_1, respectively (Table 4).

DISCUSSION

Flowering traits

Maize is a monoecious plant where male and female flowers are present on the same plant at different positions, with male flower (tassel) at the top and the female flower (ear) centrally located. Flowering traits measured included days to mid-tasseling, mid-silking, and mid-anthesis. To measure the synchronization of male and female flowers, the ASI was ascertained by subtracting days to mid-anthesis from days to mid-silking. Maturity is an important

character in plants; along with days to mid-anthesis and to silking, the days to tasseling determine the duration of maturity of plants. The results revealed highly significant variation among HS families for days to mid-silking, anthesis, and ASI in both cycles. These results are in agreement with those of Hidayat et al. (2006), who observed highly significant differences for mid-anthesis and silking while evaluating the performance of local and exotic inbred lines of maize under agro-ecological conditions in Peshawar. Carlone Jr. and Russell (1989) observed similar results in testcross evaluation of maize synthetic BSSS lines. Akbar et al. (2008) also reported significant differences for days to mid-silking while evaluating 3-way crosses of maize through genetic variability, broad-sense heritability, character association, and path analysis. Similarly, other authors estimated significant differences for flowering traits among their experimental material (Rahman et al., 2005).

A short ASI is desirable because it has been reported that a short ASI increases maize tolerance to stress during flowering and ensures good grain filling (Edmeades et al., 1993; Bolaños and Edmeades, 1996). A negative ASI indicates protandry, i.e., silks emerge after pollen shed, whereas a positive ASI indicates protogyny, i.e., silks emerge before pollen shed. In both cases, as the value for ASI diverges from zero, there would be disparity between the time for silking and pollen shed, which is undesirable. A low coefficient of variation was observed for days to mid-tasseling, mid-silking, and mid-anthesis in both C_0 and C_1, which demonstrated the reliability of the data. Our findings were in agreement with that of Ajala et al. (2009) and Akbar et al. (2008). They also reported a low coefficient of variation for days to mid-silking. After 2 cycles of HS RS, the gain per cycle observed for days to mid-tasseling, silking, and anthesis was 2.99, 3.08, and 3.85%, respectively. High and moderate heritability was observed for maturity traits, indicating low environmental variance and more genetic variance. Our findings for days to mid-silking were in agreement with those of Ajala et al. (2009) when comparing predicted responses to 3 types of RS procedures for the improvement of a maize population. Akbar et al. (2008), Bekavac et al. (2006), Wolf et al. (2000), and Keeratinijakal and Lamkey (1993) also reported similar results. In contrast, Salami et al. (2007) observed low heritability for days to mid-silking and anthesis. The low selection differential demonstrated that progress was made for maturity traits. A possible reason for the low selection differential is that the selection was specifically practiced for yield and maturity traits. A positive and highly significant correlation was found among the flowering traits in both cycles. In C_0, days to mid-anthesis was positively and highly significantly correlated with grain yield, while a significant positive correlation was observed between days to mid-silking and grain yield. Galarreta and Álvarez (2007) observed a highly significant (0.92) positive correlation between days to mid-silking and grain yield. Flowering traits were negatively correlated with grain yield in C_1. Our results are in accordance with those of Bekavac et al. (2008), who also reported a negative correlation between ASI and grain yield.

Hundred-grain weight (g)

Grain weight, an important yield component, has a direct effect on the grain yield of maize. The grain weight has a remarkable role in increasing grain yield in relation to other yield-related components (Manivannan, 1998). Highly significant ($P \leq 0.01$) differences were observed for 100-grain weight in C_0, while significant differences ($P \leq 0.05$) were observed in

C_1. Our results were in line with those of Abou-Dief (2007), Mahmood et al. (2004a), Khan et al. (2003), and Alvi et al. (2003), who also reported highly significant differences for grain weight. Moderate heritability estimates were observed for grain weight in both C_0 and C_1. Ojo et al. (2006), Mahmood et al. (2004b), and Alvi et al. (2003) observed high heritability for grain weight. The population mean of 25.26 g and mean of selected HS lines of 25.93 g were observed in C_0. Likewise, the population mean of 27.33 g and mean of selected HS lines of 28.31 g were revealed in C_1. The difference between the means of the selected lines and the population resulted in selection differentials of 0.67 and 0.98 g in C_0 and C_1, respectively. The Re observed in C_0 was 0.39 g. Similarly in C_1, the Re was 0.41 g.

The 100-grain weight in both cycles was positively and highly significantly correlated with grain yield. Mahmood et al. (2004b) reported similar findings in genetic studies for high-yield maize in Chitral Valley. In contrast, Ojo et al. (2006) reported a negative correlation between 100-grain weight and grain yield.

Grain yield (kg/ha)

Increased grain yield is the main objective of every plant breeding program. Grain yield in maize is the most complex character with which a plant breeder works and is controlled by other yield factors such as grain weight, grain rows per ear, ear length, ear diameter, and prolificacy. Therefore, selection for desirable genotypes should be made based on grain yield as well as other yield components that could influence the yield. The grain yield ANOVA revealed highly significant variations ($P \leq 0.01$) among HS lines in both C_0 and C_1. Our results also confirmed the findings of Rahman et al. (2007), who also reported highly significant differences for yield components while comparing original and selected maize populations for grain yield traits. Similarly, Sharifi et al. (2009), Badu-Apraku et al. (2008), Menkir and Kling (2007), and Doerksen et al. (2003) observed highly significant differences for grain yield. The population mean and mean of selected HS families for grain yield in C_0 were 3150.61 and 4077.83 kg/ha, respectively. Similarly in C_1, the population mean of 3309.26 kg/ha and mean of selected HS families of 3949.10 kg/ha were observed for grain yield.

Maximum yield (6932.50 kg/ha) was produced by HS-51 and minimum yield (1259.00 kg/ha) was produced by HS-40 in C_0, similarly in C_1, maximum yield (4419.50 kg/ha) was produced by HS-120 and minimum yield (1564.50 kg/ha) was produced by HS-45. A high heritability of 0.74 and 0.64 for grain yield was revealed in C_0 and C_1, respectively. The heritability estimate decreased because of a decrease in genetic variance, demonstrating stability in the population. Weyhrich et al. (1998) and Betrán and Hallauer (1996) reported moderate heritability for HS and BSSSCO x BSCB1C0, respectively. Similarly, Santos et al. (2005) also observed high heritability (65.63) in C_0 and low heritability (56.61) in C_3. The selection differential for grain yield in C_0 and C_1 was 927.22 and 639.84 kg/ha, respectively. Weyhrich et al. (1998) observed a 0.67 selection differential for grain yield (mg/ha) while comparing responses to 7 RS methods in a BS11 maize population. The Re for grain yield in C_0 was 681.76 and 410.20 kg/ha in C_1. The greater Ro for grain yield compared to the Re demonstrated the usefulness of selection for grain yield. Santos et al. (2005) reported a 6.76% Re for grain yield (g/plant). The gain per cycle observed for grain yield was 5.05%, demonstrating that grain yield was increased by 5.05% after 2 cycles of HS RS.

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