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Response of a maize composite to selfed progeny recurrent selection for earliness and yield traits

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Abstract

Population improvement through recurrent selection is a traditional breeding method that has been used in maize for over 60 years. Objectives of the research were to: a) evaluate effect of selfed progeny recurrent selection on earliness and yield traits, b) compare responses of cycle-1 (S1-line) and cycle-2 (S2-line) populations, and c) determine better strategy for improvement of maize source population «PSEV3». The experiments were carried out in partially balanced lattice square design with two replications. In cycle-1 and cycle-2 populations, the differences were highly significant for all studied traits. Selfing in both cycles of selection, resulted increase in days to tasseling while reduction in population means for yield traits. In selected progenies, an increase was seen in mean values of yield traits; however, not in days to tasseling and grain moisture in both cycles of selection. Moderate to high heritability values were observed for almost all the traits in both cycles. Selection differential values were positive and high for grain yield, ear height, prolificacy, ear length, and 100-grain weight in cycle-1 and cycle-2. However, negative values of selection differential were seen for days to tasseling and grain moisture in cycle-1 and 2 populations. The expected responses for days to tasseling and grain moisture were negative in first and second selection cycles. Comparatively, larger and positive responses were noted in cycle-2 than cycle-1 for grain yield and its components. Selfed progeny recurrent selection method was found more effective in improving the maize source population «PSEV3" for earliness and yield traits.

Keywords: recurrent-selection, S1 and S2 lines, heritability, selection differential, *Zea mays* L

Introduction

Maize (*Zea mays* L) is an important cereal crop of the world grown in irrigated and rainfed areas, and ranks third after wheat and rice. Being the highest yielding cereal crop, maize attained significant importance for countries like Pakistan, where rapidly increasing population has already out stripped the available food supplies (Ihsan et al, 2005). Maize is an annual short day plant, which utilizes solar radiations more efficiently than other cereals. Maize is grown at sea level to 3,300 meters and from 500N to 400S latitude in temperate, sub-tropical and tropical regions of the world. Medium textured soil (pH 6.5 to 7.5) is most suitable for maize production, however, it can be cultivated on soils ranging from sandy loam to clay loam. Currently in Pakistan, maize is grown on an area of 1,130 thousand hectares and total production was 6,695 thousand tones with average seed yield of 4155 kg ha^{-1} (PBS, 2014-15).

Recurrent selection is a cyclical breeding technique which has been widely used for maize improvement (Dudley and Lambert, 2004). Recurrent selection increases the frequency of favourable genes by repeated cycles of selection while maintaining genetic variation in the breeding populations (Ajala et al, 2009). A cycle of recurrent selection involves three stages: a) development of progenies, b) progeny evaluation and c) recombination of selected families. Recurrent selection methods have been effectively used to improve the performance of maize populations for quantitatively inherited traits (Pixley et al, 2006).

The S1-recurrent selection provides a good option for achieving improvement within the maize populations (Hallauer and Carena, 2012). The S2-recurrent selection is equally effective to improve the performance of maize populations, therefore, progeny recurrent selection using either S1 or S2 lines is considered superior to other methods of recurrent selection for improvement of maize population (Wardyn et al, 2009). Thus, selfed progeny recurrent selection is effective to improve maize for grain yield and other agronomic traits. Therefore, present research was planned with aim to effectively utilize the S1 and S2 line recurrent selection to achieve the objectives, a) to evaluate the effect of selfed progeny selection

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on maize performance, b) to compare the predicted responses of cycle-1 (S1-line) and cycle-2 (S2-line), and c) to determine better strategy for improvement of PSEV3 maize base population for earliness and yield traits.

Materials and Methods

Maize source population

The base population «PSEV3» has derived from the cross between Azam (a white improved white flint composite variety of medium maturity) and CHSW (a single cross hybrid of white dent kernel with late maturity from CIMMYT, Mexico). The population was subjected to two cycles of selfed progeny recurrent selection, and the first and second cycles were based on S1 and S2 lines, respectively.

Development of maize breeding material

To develop S1 lines, the source population PSEV3 was sown in spring 2004 (February-June) with rows and plants spacing of 75 and 25 cm, respectively at Cereal Crops Research Institute (CCRI), Nowshera, Pakistan. Two to three maize seeds were planted in each hill, and were later thinned to one plant per hill at two-leaf stage. Standard cultural practices were applied to produce healthy and vigorous plants for selfing. More than 500 plants were manually self-pollinated and at physiological maturity, the selfed ears were separately harvested, shelled and labeled.

Evaluation of maize S1 lines

Half of the seed of 255 selected S1 progenies and control (S0) were evaluated in a 16 x 16 partially balanced square lattice design with two replications during summer season 2004 at CCRI, Nowshera, Pakistan. The remnant seed was kept for later use in recombining the selected S1 lines to constitute a source population for further field evaluation (Hallauer and Carena, 2012). A plot size of two rows, 5 meter long and 0.75 m apart was maintained. All the recommended inputs and cultural practices were equally applied during the crop season. Data were recorded on ten competitive plants in each sub-plot for traits i.e. days to tasseling, ear height (cm), prolificacy (%), ear length (cm), 100-grain weight (g), grain moisture at harvest (%) and grain yield (kg ha^{-1}). To determine grain yield, grain weight per plot was obtained and converted to kg ha^{-1} at 15% moisture content using following relationship (Carangal et al, 1971).

$$\text{Grain yield (kg ha}^{-1}\text{)} = \frac{(100 - \text{MC}) \times \text{FEW} \times \text{Shelling coefficient} \times 10{,}000}{(100 - 15) \times \text{Plot area}}$$

where MC = Moisture content (%) in grains at harvest; FEW = Fresh ear weight (kg) at harvest; Shelling coefficient = 0.80.

Recombination of maize selected S1 progenies

Twenty-five best S1 lines were selected on basis of high grain yield and early maturity. Half seed of the selected lines was sown (1:2 rows as male and female, respectively) for recombination during spring season 2005. Seed in equal quantity from all selected lines was bulked and grown as male. The female rows were detasseled before anthesis to eliminate self-pollination and to facilitate cross-pollination. Ears from female rows were harvested, dried, shelled and preserved as C1 population for cycle comparison.

Development of maize S2 lines

During the same spring crop season 2005, remnant seed from the selected S1 lines was sown in two rows having 3 m length with rows and plants spacings of 75 and 25 cm, respectively. Four hundred plants were selfed in the same way as discussed earlier. All the recommended inputs and cultural practices were equally applied during the crop season.

Evaluation of maize S2 progeny

One hundred and sixty nine S2 lines were evaluated in 13 x 13 partially balanced square lattice design with two replications during summer 2005 at CCRI, Nowshera. Same procedure was followed for evaluation of S2 progenies as mentioned earlier for S1 progenies. All the recommended inputs and standard cultural practices were equally applied.

Recombination of maize S2 progenies

Seventeen selected S2 progenies were grown in isolation during spring season 2006 at CCRI, Nowshera, Pakistan. Seeds from the recombined S2 lines constituted the C2 population.

Statistical analysis

Data were recorded in S1 and S2 progeny testing trials, were subjected to analysis of variance appropriate for lattice square design using ANOVALAT procedure of MStat C program.

The complete statistical model used was:

$$Y_{il(j)} = \mu + t_i + r_j + (b/r)_{l(j)} + e_{il(j)}$$

where $Y_{il(j)}$ is the observation of the genotype i (i = 1,…, v = k2), in the block l (l = 1,…, k) of the replication j (j = 1,..., m); μ is a constant common to all observations; t_i is the effect of the treatment I; r_j is the effect of the replication j; $(b/r)_{l(j)}$ is the effect of the block l of the replication j; $e_{il(j)}$ is the error associated to the observation $Y_{il(j)}$.

Expected mean squares were calculated through lattice square (partially balanced) design for both cycles of selection.

Heritability estimation

Heritability (broad sense) was estimated according to Allard (1960) as under:

$\sigma^2e = M1$; $\sigma^2g = (M2-M1)/r$; $h^2_{(bs)} = \sigma^2g / (\sigma^2e + \sigma^2g)$

where σ^2e : environmental variance; σ^2g : genetic variance; $h^2_{(bs)}$: heritability (broad sense).

Selection differential

Selection differential (S) was computed as: $S = \mu_s - \mu$, where μ: selfed populations (S1, S2) of the first and second selection cycles before selection; μ_s: means for selected S1 and S2 lines in cycles-1 and 2, respectively.

Estimation of expected response

Expected response to selection (R_e) was estimat-

Table 1 - Mean squares of maize PSEV3 – S1 lines evaluated for earliness, morphological and yield traits.

Source of variation	d.f.	Days to Tasseling	Ear height	Prolificacy	Ear length	100-grain weight	Grain moisture	Grain yield
Replication	1	0.705	1521.69	658.051	1.38	0.76	0.29	142174.45
S1 lines								
Unadjusted	255	4.66**	203.08**	338.62**	1.86**	2.12**	1.22**	2599062.37**
Adjusted	255	4.40**	193.35**	339.04**	-	2.12**	-	-
Blocks	30	2.288	74..13	189.13	0.17	0.27	0.19	214556.64
Error								
Effective	225	0.65	33.88	177.62	-	0.26	-	-
RCBD 255	0.80	36.73	177.72	0.27	0.26	0.216	218485.73	
Intra-block	225	0.60	31.74	176.20	0.28	0.26	0.220	219009.61
CV (%)		1.49	8.23	14.33	3.66	1.69	2.15	11.40

ed as follows: $R_e = S \times h^2$, where S: selection differential; h^2 : heritability.

Results

According to analysis of variance, highly significant ($P \leq 0.01$) differences were observed among maize populations of both cycles of selection for all the studies traits (Tables 1 and 2).

Days to tasseling

By comparing the performance of S1 and S2 selfed lines, days to tasseling reduced from 54.21 to 53.51 days with selection cycles (Table 3). In cycle-1, the fewest days to tasseling were observed for base population S0 (52.30 days), followed by S1 selected families (53.16 days) and S1 selfed population (54.21 days). Similarly, in cycle-2, the least days to tasseling were noticed for source population S0 (51.00 days), followed by S2 selected lines (51.79 days) and S2 selfed population (53.51 days). Comparing the performance of selected families in both selection cycles, days to tasseling have been reduced to 51.79 days (S2 selected) from 53.16 (S1 selected) which showing early maturity in the developed population.

High broad sense heritabilities (0.83 and 0.84) were recorded for days to tasseling in cycle-1 and cycle-2 populations, respectively (Table 4). Negative values of selection differential were observed for both selection cycles which showing earliness in flowering initiation in the selected progenies (S1 and S2 selected) over selfed populations (S1 and S2 selfed) which were desirable. Negative selection differential (-1.05 and -1.72 days) with corresponding negative expected responses (-0.87 and -1.45 days) showed reduction in days to tasseling in the succeeding selection cycle (Table 5).

Ear height

Ear height was reduced from 70.71 cm (S1 selfed) to 58.66 cm (S2 selfed) with both selection cycles (Table 3). In cycle-1, maximum ear height was recorded for S1 selected families (77.11 cm) which was followed by base population S0 (73.28 cm) and selfed S1 population (70.71 cm). Similarly, in cycle-2 the maximum ear height was recorded for source population S0 (72.40 cm) followed by S2 selected families (67.37 cm) and S2 selfed population (58.66 cm). On average, the ear height was decreased in S2 selected families (67.37 cm) in cycle-2 than S1 selected families (77.11 cm) in cycle-1.

Heritability (b_s) estimates were high for ear height in both selection cycles (Table 4). Maximum values of heritability were seen in cycle-2 (0.87) followed by cycle-1 (0.82). Selection differential also indicated an increasing trend in ear height with selection cycles i.e. 6.40 to 8.71 cm in cycle-1 and cycle-2, respectively. Similarly, comparatively larger predicted gains for said trait was observed in cycle-2 (7.59 cm) than cycle-1 (5.24 cm) (Table 5).

Prolificacy %

Prolificacy was increased from 93.01% (S1 selfed) to 94.66% (S2 selfed) with both selection cycles (Table 3). Highest prolificacy was observed for base population S0 (97.00%) followed by S1 selected population (96.00%) and S1 selfed population (93.01%) in cycle-1. However, in cycle-2 the highest prolificacy was seen for S2 selected lines (100.00%) followed by original population S0 (97.96%) and S2 selfed population (94.66%). Overall, prolificacy was higher for the S2 selected families (100.00%) than S1 selected

Table 2 - Mean squares of maize PSEV3 - S2 lines evaluated for earliness, morphological and yield traits.

Source of variation	d.f.	Days to Tasseling	Ear height	Prolificacy	Ear length	100-grain weight	Grain moisture	Grain yield
Replication	1	37.11	2.37	32.25	0.57	4.65	0.13	2844533.09
S2 lines								
Unadjusted	168	8.82**	235.58**	331.21**	4.14**	7.35**	4.10**	4216193.00**
Adjusted	168	8.05**	214.98**	322.73**	-	7.48**	-	4121578.52**
Blocks	24	4.52	59.67	227.13	0.83	2.41	0.35	1351808.98
Error								
Effective	144	0.99	27.36	184.46	-	1.36	-	641809.54
RCBD 168	1.41	30.22	185.91	0.84	1.44	0.53	702460.28	
Intra-block	144	0.89	25.28	179.04	0.84	1.28	0.56	594235.50
CV (%)		1.86	8.92	14.35	6.98	4.11	3.39	22.62

Table 3 - Mean performance of selfed (S1, S2), selected (S1s, S2s) and original (PSEV3-S0) populations for earliness, morphological and yield traits during two cycles of selfed-progeny recurrent selection.

	Cycle-1			Cycle-2		
Traits	Original population (S0)	Selfed population (S1)	Selected families (S1s)	Original population (S0)	Selfed population (S2)	Selected families (S2s)
Days to tasseling (days)	52.30	54.21	53.16	51.00	53.51	51.79
Ear height (cm)	73.28	70.71	77.11	72.40	58.66	67.37
Prolificacy (%)	97.00	93.01	96.00	97.96	94.66	100.00
Ear length (cm)	15.00	14.07	16.02	14.30	13.08	16.40
100-grain weigh (g)	30.00	30.11	31.01	27.00	28.41	31.41
Grain moisture (%)	22.00	21.64	21.39	21.46	21.53	19.99
Grain yield (kg ha^{-1})	5638.02	4101.87	6175.28	5525.45	3541.94	6216.56

(96.00%) which indicating improvement from selection in the next generation.

Moderate heritabilities were seen for prolificacy during both selection cycles (Table 4). Comparatively, the heritability was high during cycle-1 (0.48) followed by cycle-2 (0.42). The selection differential values were also medium (2.99%, 5.34%), resulting into moderate gains (1.44%, 2.25%), respectively in two selection cycles (Table 5).

Ear length

With selfing, the ear length in cycle-1 was decreased in succeeding selection cycles from 14.07 (S1 selfed) to 13.08 (S2 selfed) (Table 3). However, maximum ear length was recorded for S1 selected families (16.02 cm) followed by source population S0 (15.00 cm) and S1 selfed (14.07 cm). Likewise, in cycle-2 maximum ear length was also seen for S2 selected lines (16.40 cm) followed by original population S0 (14.30 cm) and S2 selfed population (13.08 cm). By comparing the performance of selected families in both selection cycles, ear length was increased in S2 selected (16.40 cm) than S1 selected families (16.02 cm) which was also encouraging for yield enhancement.

Declining trend in heritability (bs) was also observed for ear length with succeeding selection cycles (Table 4). Maximum value of heritability (0.85) was observed in cycle-1 followed by cycle-2 (0.58). Significant increase was observed for selection differential with succeeding cycles i.e. 1.95 (cycle-1) to 3.32 cm (cycle-2), while expected responses were 1.67% and 1.93%, respectively (Table 5).

100-grain weight

With selfing in base population, the hundred grains weight was reduced from 30.11 g to 28.41 g in S1 and S2, respectively (Table 3). However, in cycle-1 maximum 100-grain weight was recorded in S1 selected lines (31.01 g) followed by S1 selfed population (30.11 g) and base population S0 (30.00 g). For 100-grain weight, improvement was seen in S2 selected families (31.41 g) followed by S2 selfed population (28.41 g) and original population S0 (27.00 g) in cycle-2. By comparing the performance, the S2 selected families showed maximum 100-grain weight (31.41 g) than S1 selected families (31.01 g).

In broad sense heritability, high estimates were observed for 100-grain weight during both selection cycles (Table 4). For both cycles, the heritability values were 0.80 to 0.88 in cycles-2 and cycle-1, respectively. For selection differential, significant increase was observed with succeeding cycles i.e. 0.90 g (cycle-1) and 3.0 g (cycle-2). The expected responses of two selection cycles were 0.97 and 2.41 g, respectively (Table 5).

Grain moisture at harvest

With selfing, the grain moisture at harvest slightly varied in both selection cycles (Table 3). However, least moisture content was recorded for S1 selected families (21.39%) and S1 selfed population (21.64%) while highest for original population S0 (22.00%) in cycle-1. Similarly, in cycle-2 minimum grain moisture at harvest was obtained from S2 selected lines (19.99%) while maximum in original population S0 (21.46%) and S2 selfed population (21.53%). Grain moisture at harvest reduced in S2 selected families (19.99%) than S1 selected (21.39%), and said trend was desirable for ensuring early maturity in the improved cyclical population.

High heritability (b_s) estimates were recorded for grain moisture at harvest in both selection cycles (Table 4). Broad sense heritability values were 0.82

Table 4 - Genetic components of variance of S1 and S2 selfed families for earliness, morphological and yield traits during two cycles of selfed-progeny recurrent selection.

	Cycle-1 (S1 lines)				Cycle-2 (S2 lines)			
Traits	σ^2g	σ^2e	σ^2p	h^2	σ^2g	σ^2e	σ^2p	h^2
Days to tasseling	1.93	0.80	2.33	0.83	3.71	1.41	4.41	0.84
Ear height	83.18	36.73	101.54	0.82	102.68	30.22	117.79	0.87
Prolificacy	80.45	177.72	169.31	0.48	67.53	185.91	160.49	0.42
Ear length	0.80	0.27	0.93	0.85	0.59	0.84	1.01	0.58
100-grain weight	0.93	0.26	1.06	0.88	2.97	1.44	3.69	0.80
Grain moisture	0.50	0.22	0.61	0.82	1.78	0.53	2.05	0.87
Grain yield	1190288.32	218485.73	1299531.19	0.92	1756279.72	702460.28	2107509.86	0.83

σ^2g: genotypic variance; σ^2e: environmental variance; σ^2p: phenotypic variance; h^2 = heritability

Table 5 - Selection differential and expected responses of maize PSEV3 population during two cycles of selfed progeny recurrent selection for maturity, morphological and grain yield traits.

	Selection cycle-1		Selection cycle-2	
Traits	Selection differential (S)	Expected response (Re)	Selection differential (S)	Expected response (Re)
Days to tasseling (days)	-1.05	-0.87	-1.72	-1.45
Ear height (cm)	6.40	5.24	8.71	7.59
Prolificacy (%)	2.99	1.44	5.34	2.25
Ear length (cm)	1.95	1.67	3.32	1.93
100-grain weigh (g)	0.90	0.79	3.00	2.41
Grain moisture (%)	-0.25	-0.21	-1.54	-1.34
Grain yield (kg ha^{-1})	2073.41	1899.11	2674.62	2228.88

to 0.87 in selection cycle-1 and cycle-2, respectively and showed promise increase with succeeding generations. Desirable negative and declining trend in selection differential was observed for grain moisture content with succeeding selection cycles i.e. -0.25% (cycle-1) and -1.54% (cycle-2). Similarly, negative genetic gains were noted in both selection cycles i.e. -0.21 and -1.34%, respectively (Table 5).

Grain yield

With selfing, the grain yield was reduced from 4101.87 (S1 selfed) to 3541.94 kg ha^{-1} (S2 selfed) and showed 13.65% reduction with succeeding selection cycles (Table 3). In cycle-1, highest grain yield was produced by S1 selected lines (6175.28 kg ha^{-1}) followed by base population S0 (5638.02 kg ha^{-1} and S1 selfed population (4101.87 kg ha^{-1}). Similarly, in cycle-2 the highest grain yield was obtained from S2 selected lines (6216.56 kg ha^{-1}) followed by original population S0 (5525.45 kg ha^{-1}) and S2 selfed population (3541.94 kg ha^{-1}). The S2 selected families revealed higher grain yield (6216.56 kg ha^{-1}) than S1 selected families (6175.28 kg ha^{-1}) which showed progress from selection through succeeding generations and need to work on the mentioned population in the future generation.

Large broad sense heritability estimates were observed for grain yield in both cycles of selection (Table 4). However, comparatively high heritability was seen in cycle-1 (0.92), followed by cycle-2 (0.83). Likewise, large values of selection differential were observed in both cycles of selection ranging from 2073.41 to 2674.62 kg ha^{-1} resulting in large gains i.e. 1899.11 and 2228.88 kg ha^{-1} in cycle-1 and cycle-2, respectively (Table 5).

Discussion

Present study revealed that both S1 and S2 selfed progeny recurrent selection were effective to improve maturity, morphological and yield traits in PSEV3 maize base population. Numerous past studies also showed that selfed progeny recurrent selection was the most effective breeding procedure for improving maize populations for yield and other agronomic traits as compared to other methods (Weyhrich et al, 1998; Ali et al, 2012).

Highly significant differences among genotypes of both selection cycles indicated that wide genetic variability existed within the S1 and S2 selfed populations and potential of recurrent selection to improve maize population for yield related traits. Past studies revealed that highly significant differences were observed among S1 lines for ear length, kernel rows per ear, 1,000-kernel weight and grain yield of maize (Shahwar et al, 2008; Wardyn et al, 2009). Ruiz-de-Galarreta and Alvarez (2007) recorded significant improvement in morphological and yield traits with six cycles of S1 recurrent selection in maize.

Flowering initiation symbolizes maturity and transition from vegetative to reproductive phase. Early flowering is desirable in the existing intensive cropping pattern which also helps to escape the insect pests and diseases. Tasseling and silking durations were shorter for the selected families than selfed ones in both cycles of selection which is desirable. Fewest days to tasseling and silking were recorded for selected S1 families compared to selfed populations during two cycles of S1 recurrent selection in maize (Khalil et al, 2010). However, some past findings were in contradiction with present results by showing more days to tasseling and silking for the selected lines than base and selfed populations in maize (Ali et al, 2011), however, equal number of days to tasseling and pollen shedding were noted in selected and original population in maize (Rahman et al, 2005). Fewest days to tasseling and silking were reported in two maize populations with selfed progeny recurrent selection (Shah et al, 2007). Contradictory findings might be due to varied genetic make-up of the breeding material and the environmental conditions where the material was studied.

For plant architectural traits (plant and ear heights), medium stature plants are preferred over tall ones for controlling lodging and ultimately getting higher yield (Noor et al, 2010). Anyhow, a little increase in ear and plant height is manageable. In present studies, the selected populations showed comparatively more ear height than selfed and base populations in the two selection cycles. However, by comparing the selected families of cycle-1 with the selected families of cycle-2, the latter were less tall than the former ones which is desirable and showing improvement within the population. Maize response to selection was evaluated under maydis leaf blight stress environment and reported reduction in ear height in the selected lines than selfed populations during two cycles of S1 recurrent selection (Khalil et al, 2010). Increased ear height was exhibited by selected lines than parent populations while estimating genetic analysis of maturity and morphological traits under maydis leaf blight epiphytotics in maize (Ali et al, 2011). For grain moisture, least moisture content was observed for S1 and S2-selected families compared to the base population and selfed lines in each cycle. Lowest grain moisture content at harvest is desirable for attaining early maturity in maize. Some past studies revealed that selection for yield alone had caused undesirable responses in other agronomic traits such as lodging and grain moisture at harvest in various maize populations (Shah et al, 2007; Tardin et al, 2007).

Grain yield is the cumulative effect of various yield attributes, i.e. plants m^{-2}, ears per m^{-2}, prolificacy, ear length, kernel rows per ear, and 100-grain weight. Different trends in the means of the three types of genotypes (base population, selfed population, and selected families) were observed in both cycles of selection: i) reduction in means of the selfed population with selfing, ii) increase in means of the selected families due to accumulation of favourable genes, and iii) larger means for S2-selected families, compared to S1 selected lines in the subsequent cycle.

Present results revealed greater genetic variations within and between populations and genetic progress was made through two cycles of selection resulting significant improvement in yield contributing traits. This achievement could be due to accumulation of favorable alleles in the selected versions of the maize population. Significant increase in yield traits for the selected populations might be contributing to improvement in agronomic and yield related traits of maize (Rahman et al, 2007). Several past studies revealed highly significant differences for grain yield and other agronomic traits. Significant increase was noted in grain yield and its components using S1 recurrent selection in maize synthetic populations (Vales et al, 2001). Highly significant differences were reported among maize S1 lines for ear length, kernel rows, 1,000-kernel weight and grain yield in maize (Wardyn et al, 2009).

Achieving improvement in any crop depends on genetic variability, heritability and genetic gain from selection in maize (Khan et al, 2006). Heritability has key role in the inheritance of traits and to partition the total phenotypic variance into genetic and environmental components (Falconer and Mackay, 1996). Therefore, knowledge of heritability helps breeder in choosing suitable selection procedure for improving particular plant characters and to predict gain from selection (Haq et al, 2008; Kashiani et al, 2010). Plant traits having reasonable variability, high heritability and genetic advance (predicted gain) would be an effective tool for crop improvement (Noor et al, 2010; Hussain et al, 2011). Therefore, developing high yielding varieties of maize necessitates critical evaluation of existing genetic variability, heritability and genetic advance (Mahmood et al, 2004).

In the present study, genetic variance and heritability were high for majority of the traits in both selection cycles. This indicates sufficient genetic variability and strong potential of improvement in the breeding material with selection. Several past studies also revealed great genetic variability and high heritability for maturity, morphological and yield traits in maize with selfed progeny recurrent selection in maize (Najeeb et al, 2009; Asghar and Mehdi, 2010; Khalil et al, 2010; Da-Cunha et al, 2012; Ullah et al, 2013). These results elucidates that genetic variance over dominates environmental variances for improving S1 and S2 progenies in both cycles of selection. Some past studies showed low heritability for maturity (Kashiani et al, 2014) and yield traits (Badu-Apraku et al, 2013) with S1 recurrent selection in maize.

Selection differential indicates progress as well as direction of the selection process. Positive selection differential shows an increase in the means of the selected progenies while negative values indicate a decrease in the means of the selected progenies. Some time, positive values of selection differential are desirable and some time negative values, depending on the trait. In the present study, selection differential values were negative for days to tasseling, and grain moisture at harvest during both cycles of selection. In grain moisture, reduction was reported with S1 recurrent selection in various maize populations (Ajala et al, 2009; Weyhrich et al, 1998). For days to tasseling, silking and pollen shedding, negative values of selection differential were reported in maize populations (Ali et al, 2011). Selection differential values were smaller for S2 selected than S1 selected progenies, showing that response of the S2-base selection was stronger than S1-base to bring early maturity and reduction in grain moisture content at harvest of the maize population. On the other hand, selection differential values were positive for prolificacy, ear length, 100-grain weight and grain yield which are desirable. Several past studies revealed positive values of selection differential for yield related traits, and negative for earliness and plant architectural traits in evaluation of selfed progeny recurrent selection for improving maize populations (Shah et al, 2007; Khalil et al, 2010).

Results revealed that responses to selection for days to tasseling and grain moisture content at harvest time were negative, showing a decrease in the estimates of these traits which is desirable. Several previous studies were in support of our findings (Khalil et al, 2010; Da-Cunha et al, 2012). Positive gains in yield traits are the prime target of any breeding programme. Ear height is associated with grain yield, and an increase in grain yield correspondingly causes increase in height. Comparing the responses, S2 recurrent selection seems more effective in improving performance of the original population. For grain yield and yield related traits, highest predicted gain was observed via S1 selection (using S2 seeds of selected lines for recombination) while comparing predicted responses to full-sib, half-sib and S1 recurrent selection in a maize population (Ajala et al, 2009). Weyhrich et al (1998) also reported largest predicted response to S2 recurrent selection for grain yield while evaluating effect of seven methods of recurrent selection in a maize population.

Both S1 and S2 populations showed decline in vigor due to inbreeding which is not uncommon. However, a look at the performance of the selected families during the two selection cycles, showing better responses for yield and earliness traits. Therefore, improvement in PSEV3 base population after recombination of the selected families in the improved cycle populations (PSEV3 C1 and PSEV3 C2) is expected. Expected responses of cycle-2 were better than cycle-1 for yield attributes and earliness traits.

Conclusion

Selfed progeny recurrent selection is effective to improve PSEV3 maize base population. The S2 progeny recurrent selection is more efficient for improving the performance of PSEV3 maize source population. Further evaluation of the improved cycle populations, C1 and C2 across different environments is suggested to investigate their performance and choose better selection strategy.

References

Ajala SO, Ago CE, Olaoye G, 2009. Comparison of predicted responses to three types of recurrent selection procedures for the improvement of a maize (*Z. mays* L.) population. J Plant Breed Crop Sci 1(8): 284-292

Ali F, Muneer M, Xu J, Shahwar D, Rahman H, Lu Y, Hassan W, Ullah H, Noor M, Ullah I, Yan J, 2012. Accumulation of desirable alleles for southern leaf blight (SLB) in maize (*Z. mays* L.) under the epiphytotic of Helminthosporium maydis. Aust J Crop Sci 6(8): 1283-1289

Ali F, Rahman H, Shahwar D, Nawaz I, Munir M, Ullah H, 2011. Genetic analysis of maturity and morphological traits under maydis leaf blight (MLB) epiphytotics in maize (*Z. mays* L.). APRN J Agric Biol Sci 6(8): 13-19

Allard RW, 1960. Principles of Plant Breeding. John Wiley and Sons Inc, New York

Asghar MJ, Mehdi SS, 2010. Selection indices for yield and quality traits in sweet corn. Pakistan J Bot 42(2): 775-789

Badu-Apraku B, Oyekunle M, Fakorede MAB, Aderounmu M, 2013. Effects of three cycles of S1 selection on genetic variances and correlations of an early maize population under drought and well-watered environments. ASA, CSSA, and SSSA Int. Annual Meetings, Nov. 3-6, Tampa, Florida, USA

Carangal VR, Ali SM, Koble AF, Rinke EH, Sentz JC, 1971. Comparison of S1 with testcross evaluation for recurrent selection in maize. Crop Sci 11: 658-661

Da-Cunha KS, Pereira MG, Gonçalves LSA, Berilli APCG, de-Oliveira EC, Ramos HCC, Júnior ATA, 2012. Full-sib reciprocal recurrent selection in the maize populations CIMMYT and Piranão. Genet Mol Res 11(3): 3398-3408

Dudley JW, Lambert RJ, 2004. 100 generations of selection for oil and protein in corn. Plant Breed Rev 24 (part 1): 79-110

Falconer DS, Mackay TFC, 1996. Introduction to quantitative genetics, pp. 245-247. 4th ed. Benjamin Cummings, England

Hallauer AR, Carena MJ, 2012. Recurrent selection methods to improve germplasm in maize. Maydica 57: 226-283

Haq W, Malik MF, Rashid M, Munir M, Akram Z, 2008. Evaluation of heritability and genetic advancement for yield related attributes in wheat lines. Pakistan J Bot 40: 1699-1702

Hussain N, Khan MY, Baloch MS, 2011. Screening of maize varieties for grain yield at Dera Ismail Khan. J Anim Plant Sci 21(3): 626-628

Ihsan H, Khalil IH, Rahman H, Iqbal M, 2005. Genotypic Variability for orphological traits among exotic maize hybrids. Sarhad J Agric 21(4): 599-602

Kashiani P, Saleh G, Abdulla NAP, Sin MA, 2014. Evaluation of genetic variation and relationships among tropical sweet corn inbred lines using agronomic traits. Maydica 59: 275-282

Kashiani P, Saleh G, Abdullaha NAP, Abdullah SN, 2010. Variation and genetic studies on selected sweet corn inbred lines. Asian J Crop Sci 2(2): 78-84

Khalil IA, Rahman H, Shahwar D, Nawaz I, Ullah H, Ali F, 2010. Response to selection for grain yield under maydis leaf blight stress environment in maize (*Z. mays* L.). Biol Divers Conserv 3(1): 121-127

Khan FA, Ali S, Shakeel A, Saeed A, Abbas G, 2006. Genetic variability and genetic advance analysis for some morphological traits in (*Brassica napus* L.). J Agric Res 44(2): 83-88

Mahmood Z, Malik SR, Akhtar R, Rafique T, 2004. Heritability and genetic advance estimates from maize genotypes in Shishi Lusht a valley of Karakoram. Int J Agric Biol 6: 790-791

Najeeb S, Rather AG, Parray GA, Sheikh FA, Razvi SM, 2009. Studies on genetic variability, genotypic correlation and path coefficient analysis in maize under the high altitude temperate conditions of Kashmir. Maize Genet Coop News letter No. 83: 46

Noor M, Rahman H, Shahwar D, Iqbal M, Shah SMA, Ullah I, 2010. Evaluation of maize half sib families for maturity and grain yield attributes. Sarhad J Agric 26: 545-549

PBS 2014-15. Year Book. Pakistan Bureau of Statistics (PBS). Govt of Pakistan, Islamabad, Pakistan.

Pixley KV, Dhliwayo T, Tongoona P, 2006. Improvement of maize populations by full-sib selection alone versus full-sib selection with selection during inbreeding. Crop Sci 46: 1130-1136

Rahman H, Khalil IH, Islam N, Shahwar D, Rafi A, 2007. Comparison of original and selected maize populations for grain yield traits. Sarhad J Agric 21: 231-235

Rahman H, Raziq F, Ahmad S, 2005. Screening and evaluation of maize genotypes for Southern leaf blight resistance and yield performance. Sarhad J Agric 21(2): 231-235

Ruiz-de-Galaretta JI, Alvarez A, 2007. Six cycles of S1 recurrent selection in two Spanish maize synthetics. Span J Agric Res 5(2): 193-198

Shah SS, Rahman H, Khalil IH, Iqbal M, 2007. Recurrent selection for maydis leaf blight resistance and grain yield improvement in maize. Pakistan J Biol Sci 10(20): 3632-3637

Shahwar D, Rahman H, Shah SMA, Khalil IA, Ali F, 2008. Recurrent selection for yield and yield associated traits under leaf blight (Helminthosporium maydis) stress in maize. Sarhad J Agric 24(4): 599-605

Tardin FD, Pereira MG, Gabriel APC, Júnior ATA, Filho GAS, 2007. Selection index and molecular markers in reciprocal recurrent selection in maize. Crop Breed Appl Biotechnol 7: 225-233

Ullah K, Rahman HU, Noor M, Rehman MU, Iqbal M, Ullah S, 2013. Heritability estimates and yield performance of half sib families derived from maize variety Sarhad White. Sarhad J Agric 29(1):29-32

Vales MI, Valar RA, Revilla P, Ordas A, 2001. Recurrent selection for grain yield in two Spanish maize synthetic populations. Crop Sci 41: 15-19

Wardyn BM, Edwards JW, Lamkey KR, 2009. Inbreeding progeny selection is predicted to be inferior to half-sib selection for three maize populations. Crop Sci 49: 443-450

Weyhrich RA, Lamkey KR, Hallauer AR, 1998. Response to seven methods of recurrent selection in the BS-11 maize population. Crop Sci 38: 308-321