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MAIZE IMPROVEMENT THROUGH SELFED PROGENY RECURRENT SELECTION ACROSS DIFFERENT ENVIRONMENTS

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Abstract

Recurrent selection is a cyclical breeding procedure which has been mostly used for the improvement of maize populations. This study was aimed at comparing the responses of maize S_1 and S_2-lines through selfed progeny recurrent selection under genotype by environment interactions. During spring-2014, for developing S_1 (selfed) lines in cycle-1, 500 plants were selfed. Two-cycle populations [PSEV3 (S_1)-C_1 and PSEV3 (S_2)-C_2] and base population (PSEV3-C_0) were studied during summer season across four environments i.e., two each years (2016 and 2017) and locations. Cyclical populations revealed significant ($p \leq 0.01$) differences for all the traits. The cycle × year interactions were significant for ear length, 100-grain weight, and grain yield. The cycle × year × location interactions were significant for kernel rows per ear and 100-grain weight. In C_2 population, the improvement in earliness and yield traits was recorded followed by C_1 population. Performance of C_2 was overwhelming at CCRI during 2017 while base population (PSEV3-C_0) exhibited poor performance across years and locations. The responses to selection were encouraging for days to tasseling, cobs per m^2, cob length, kernel rows per cob, 100-kernel weight and grain yield. Overall and average genetic gains per cycle were persuading for days to tasseling, cobs per m^2, cob length, kernel rows per cob, 100-kernel weight and grain yield. The recurrent selection was found more effective in improving maize base population (PSEV3-C_0) for maturity and yield related traits. Simultaneous improvement owing to selfed-progeny recurrent selection suggests further testing of advance cycles in the maize population.

Key words: Cyclical populations, S_1 and S_2 improved lines, Genetic gain, Earliness and yield traits, *Zea mays* L.

Abbreviations used: Base population PSEV3: Cross between maize cultivar Azam and hybrid CHSW), S_1-line: Selfed lines in cycle-1, S_2-line: Selfed lines in cycle-2, C_0: Mean of the base population, C_1: Mean of cycle one, C_2: Mean of cycle two, MC: Grain moisture content at harvest, FEW: Fresh ear weight at harvest.

Introduction

Maize (*Zea mays* L.) is one of the most important cereal grains grown worldwide in a wider range of environments because of its greater adaptability. It ranks third in world production after wheat and rice and also an imperative food and feed crop of Pakistan (Khan *et al*., 2018; Ali *et al*., 2019). It is cultivated almost in all climatic regions of the world (Da-Cunha *et al*., 2012), with 3300 meters altitude and 50°N to 40°S latitude. Maize has attained significant importance for developing countries, like Pakistan for their increasing food requirements (Shahwar *et al*., 2008; Ali, 2015). In the hilly areas i.e., northern areas of Pakistan and Azad Jammu and Kashmir, maize is an important cereal due to the short growing season and chilling conditions (Rahman *et al*., 2015).

In plant breeding, the combined with thoughtful management of elite genetic variation and a clear separation between the parental selection process, product development and advancement processes are needed to be designed to support selection decisions and novel approaches to accelerate breeding cycles to be routinely evaluated and deployed (Cobb *et al*., 2019). Selfed progeny selection has been found useful for yield enhancement in various maize populations (Sajjad *et al*., 2016). Recurrent selection is a cyclical breeding method which is effective to improve maize populations for quantitative traits through the increased gathering of favorable alleles (Ajala *et al*., 2009). Recurrent selection procedures were framed to ensure systematic and incremental genetic improvement (e.g., increase the frequency of desirable alleles) for quantitative traits, that are controlled by a large number of genes, each having a small effect that varies with environments (Hallauer & Carena, 2012). Different recurrent selection procedures have been successfully used for improving the maize populations for important agronomic characters (Pixley *et al*., 2006; Noor *et al*., 2013; Ali *et al*., 2018).

Preliminary data and interpretation of recurrent selection programs showed that additive genetic effects, varying partial to complete dominance, were more important to influence the response to selection for grain yield (Hallauer *et al*., 2010). Selfed-progeny recurrent selection is considered more effective as compared to other breeding methods used for selection and improvement in maize (Wardyn *et al*., 2009). Studies during the 1920s to 1930s revealed that grain yield was a complex character whose expression was influenced by several plant and cob traits associated with yield; and grain yield was also affected by environmental effects experienced across locations and time; therefore, grain yields of inbred lines was not a good indicator of their hybrid yields (Ali *et al*., 2017; Khan *et al*., 2018). Suitable breeding and selection methods are needed for the improvement of quantitatively inherited traits, like grain yield. Therefore, recurrent selection methods looked appropriate for the systematic genetic improvement of germplasm resources to significantly sustain the yield improvements.

Recurrent selection methods vary in their efficiency for improvement; however, the selfed progeny recurrent selection is anticipated to be more efficient than other methods (Hallauer *et al*., 2010). A significant increase in grain yield and yield attributes have been achieved with S_1 recurrent selection in maize (Deletic *et al*., 2005; Bedada & Jifar, 2010; Ayiga-Aluba *et al*., 2015). The S_2 based recurrent selection is also effective to improve the performance of lines and hybrids evolved from base populations. Seven methods of recurrent selection were used for improving maize population for yield and other relevant characters, and the S_2 progeny recurrent selection method was found most effective (Hallauer & Carena, 2012). Previous studies revealed that increase in grain yield of maize in various experiments was based on the evaluation of either S_1 or S_2 selfed families (Wardyn *et al*., 2009; Chen *et al*., 2019).

Therefore, the present study was designed to pursue the objectives a) to assess the impact of selection on earliness and yield traits with S_1 and S_2selfed progeny recurrent selection, b) to evaluate the responses of cycle-1 (S_1-based) with cycle-2 (S_2-based), and c) to ascertain the most efficient selection approach for improvement of yield traits in PSEV3 maize base population.

Materials and Methods

Development of breeding material, sites and procedure: Maize base population PSEV3 was derived from cross between maize cultivar Azam and hybrid CHSW (Single cross hybrid, white kernels with late maturity from CIMMYT). With the objective to improve maize base population (PSEV3) for earliness and grain yield traits, the breeding material was further developed using selfed progeny recurrent selection and evaluated through two selfed progeny recurrent selection cycles during 2014 to 2017 utilizing both spring and summer crop seasons at the two locations i.e., a) Cereal Crops Research Institute (CCRI), Pirsabak - Nowshera, and b) University of Agriculture, Peshawar (UAP), Pakistan (Table 1, Fig. 1).

The first selection cycle (C_1) was based on S_1-lines while the second cycle (C_2) was on S_2-lines. During Spring-2014, for developing S_1 (selfed) lines in cycle-1, 500 plants were selfed. At harvest time, 255 selfed ears were selected and stored for evaluation in the next summer season. In the second stage during Summer-2014, a part of seed from 255 selected selfed progenies along with base population (PSEV3-C_0) was sown in ear-to-row method and evaluated in a 16 × 16 partially balanced lattice design with two replications. While the remnant seed of S_1-selected progenies was saved for use in the recombination of selected families in the next spring season. A plot size of four rows, 10 meters long with 0.25 m and 0.75 m distance between plants and rows, respectively was maintained. In the third stage during Spring-2015, 25 selected S_1 families were recombined and their seeds were bulked to form PSEV3 (S_1)-C_1 population (C_1). During the same growing season (Spring 2015), a part of seed from the selected S_1 families was grown and selfed to produce S_2 plants. During Summer-2015, the seeds from 169 selected S_2 families along with the base population were tested in partially balanced lattice design (13 × 13), twice replicated. Same plot size was maintained as described earlier for S_1. At maturity, seventeen best S_2 families were selected and stored to study in the next season. During spring 2016, the selected S_2 families were recombined and their seeds were bulked to develop PSEV3 (S_2)-C_2 population (C_2).

Cyclical populations (PSEV3(S_1)-C_1, PSEV3(S_2)-C_2) and base population (PSEV3) were evaluated during summer season across four environments i.e., two consecutive years (2016-2017) and two locations (CCRI and UAP). At each location, the experiment was carried out in a randomized complete block design (RCBD) with four replications. Four-row plots were maintained, 10 m long with 0.25 m and 0.75 m distance between plants and rows, respectively.

Crop husbandry: A recommended fertilizer dose @ 200:90:90 NPK kg ha^{-1} was applied. Half dose of nitrogen (N), whole doses of phosphorus (P_2O_5) and Potash (K_2SO_4) were applied during land preparation and just before planting in the form of Urea, Single Super Phosphate (SSP) and Sulphate of Potash (SOP), respectively. The remaining half N was applied in the form of Urea as side dressing about 4-5 weeks after germination. Weeds were controlled with Primextra Gold @ 1.5 L ha^{-1} as a pre-emergence application. Maize borer was eradicated with Confidor (WP-60) @ 50 g per 10 kg of maize seed through seed treatment before sowing. After one month, Furadon (3%) granules @ 20 kg ha^{-1} was applied in the whirls. Weeds were manually controlled carrying out weeding and earthing-up operations. The crop was irrigated at the proper interval when required, until one week before harvesting. All entries were equally treated during the cropping seasons. Maximum and minimum temperatures data for maize spring and summer crop seasons during 2015 to 2017 at CCRI and UAP is provided in Fig. 1.

Table 1. Maize populations with various characteristics used in the study.

Genotypes	Source	Type	Kernel shape / color	Stature	Maturity	Pedigree
Base population PSEV3-C_0	CCRI	OPP	Flint white	Medium stature	Medium	Cross between maize cultivar Azam and CHSW (Single cross hybrid, white kernels with late maturity from CIMMYT)
PSEV3(S1)-C_1	CCRI	OPP	Flint white	Medium stature	Medium	Derived from recombination of S_1 selected maize families
PSEV3(S1)-C_2	CCRI	OPP	Flint white	Medium stature	Medium	Derived from recombination of S_2 selected maize families

CCRI — Cereal Crops Research Institute, Pirsabak - Nowshera, Khyber Pakhtunkhwa, Pakistan; OPP — Open pollinated population

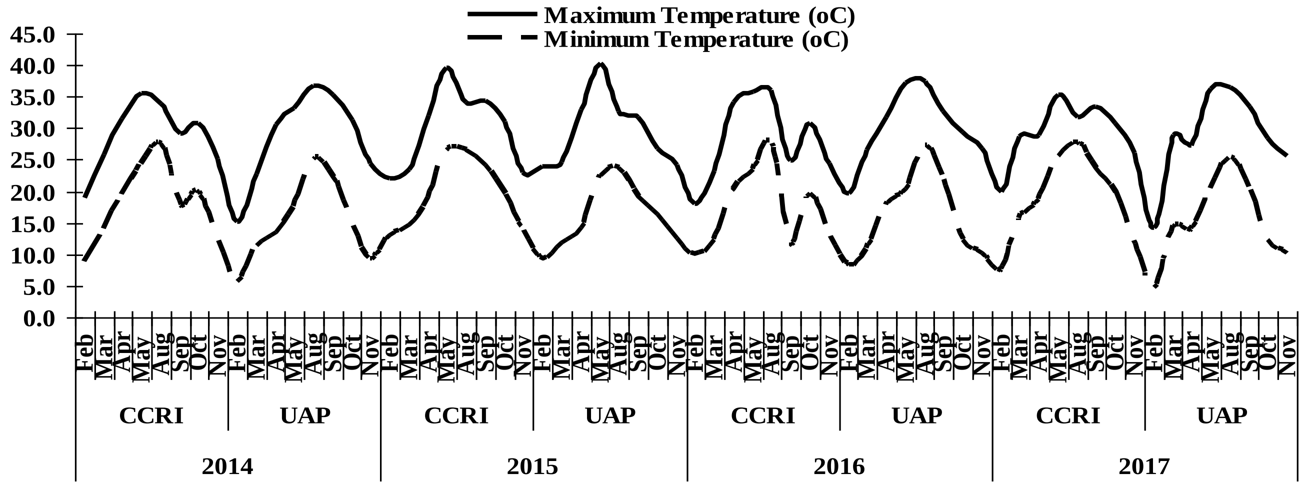

Fig. 1. Maximum and minimum temperatures for spring and summer maize crop seasons during 2014 to 2017 at CCRI and UAP.

Data recorded: Data were recorded on days to tasseling (days counted from planting when 50% of the plants were tasseled in the plot), cobs per m^2 (total cobs were counted at harvest in each plot and then cobs per m^2 were calculated on simple calibration), cob length (average length in centimeters of 10 selected ears in each plot, measured with the help of a ruler), kernel rows per cob (average number of kernel rows per cob of ten selected cobs in each plot) and 100-kernel weight (a hundred kernels were taken randomly from the grain lot of each entry and weighed with the help of an electric balance). Grain yield (kg ha^{-1}) was calculated by using the following formula (Carangal *et al.*, 1971).

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

where;

MC = Moisture content (%) in grains at harvest

FEW = Fresh ear weight (kg) at harvest

Shelling coefficient = 0.80

Statistical analyses

Analysis of variance: All the recorded data were individually subjected to analysis of variance techniques using Statistix 8.1 software (Statistix, Analytical Software, Tallahassee, FL, USA 1985-2003) appropriate for genotype by environment interactions (Gomez & Gomez, 1984). After getting the significant F-values, the means were further compared and separated by using $LSD_{0.05}$.

Response to selection: Response to selection and genetic gains are tools for measuring improvement in a parental population with the selection.

Response to selection was formulated as suggested by Lush (1940):

$$R_1 = C_1 - C_0$$
$$R_2 = C_2 - C_1$$

where:

C_0: Mean of the parent population

C_1: Mean of cycle one

C_2: Mean of cycle two

Genetic gain

Genetic gain (%) was estimated using relationship suggested by Keeling (1982):

$$\text{Genetic gain(\%)} = [(C_n - C_{n-1}) / C_n] \times 100$$

where:

C_n : advanced cycle population after selection

C_{n-1}: cycle population before selection

Results and Discussion

The present study revealed that different recurrent selection methods could be effectively used for improving the maize populations, and the same were authenticated by earlier findings (Hallauer & Carena, 2012; Sajjad *et al.*, 2016). In the current method of recurrent selection, the two objectives were always remained common: (i) to improve the overall performance of the population, and (ii) to maintain the population with greater genetic variability for ensuring long-term selection. Improvement in maize populations is indispensable to achieve higher grain yield. Present results revealed that both selfed progeny recurrent selection methods were found effective in improving PSEV3 base population over two cycles of selection in the form of earliness and yield traits. Recurrent selection is an efficient method of maize improvement because it increases the number of favorable genes through frequent selection cycles and maintain the genetic variation in the breeding population as well (Ajala *et al.*, 2009).

Combined analysis of variance for years indicated significant differences for days to tasseling, ears per square meter, ear length, 100-grain weight and grain yield (Table 2). For location, all traits showed highly significant mean differences. Mean squares for environments (year × location) were significantly different in the majority of the traits except for kernel rows per cob. Significant mean differences were recorded in the cycle populations (C) for all the measured traits. Among S_1-lines, highly significant differences were reported for yield and yield attributes while evaluating the efficiency of recurrent selection in two maize populations (Shah *et al*., 2007; Shahwar *et al*., 2008; Ayiga-Aluba *et al*., 2015). In cycle-1 and cycle-2 maize populations, the differences were highly significant for all studied traits (Sajjad *et al*., 2016). Highly significant variations were noted among different maize populations using recurrent selection to improve earliness, grain yield, and resistance to maydis leaf blight (Khalil *et al*., 2010). Ishaq *et al*., (2014). Sohail *et al*., (2018), and Sheikh *et al*., (2019) reported that maize half-sib families were significantly ($p \le 0.01$) different for various earliness and grain yield characters.

However, in interaction mean squares, varied patterns were noticed for various traits. The cycle × year (C × Y) interactions were significant for cob length, 100-kernel weight and grain yield which indicated that improved and base populations could not sustain same phenotypic behavior under different environments. The cycle × location interactions were nonsignificant for the majority of the traits except days to tasseling. Mean squares due to genotype × year × location (G × Y × L) were significant for kernel rows per cob and 100-kernel weight whereas, nonsignificant for other traits. Significant genotype × environment interactions were observed for earliness, ears per square meter and grain yield through recurrent selection in maize (Tardin *et al*., 2007; Da-Cunha *et al*., 2012). Earlier studies indicated that G × E interaction effects were significant ($p \le 0.01$) for earliness, cob length, 1000-kernel weight and grain yield in different maize composites (Rahman *et al*., 2009).

Days to 50% tasseling: On average, least days to 50% tasseling were recorded for all the populations grown during 2017 (49.58 days), followed by 2016 (50.58 days) (Table 3). The values of location means revealed that days to tasseling were less at CCRI (48.88 days) compared with UAP (51.29 days). Year × location means for days to tasseling were comparatively fewer during 2016 and 2017 (48.83 days and 48.92 days, respectively) at CCRI which might be due to warmer climate at this location (Fig. 1). However, average maximum days to tasseling were noticed in all populations grown during 2016 at UAP (52.33 days). Population means across years and locations ranged from 48.19 (PSEV3(S_2)-C_2) to 52.06 days (PSEV3-C_0). Reduction in days to tasseling in the base population C_0 (52.06) occurred with progressive selection cycles C_1 (50.00 days) and C_2 (48.19 days). The cyclical population by year by location (C × Y × L) interaction means were non-significant however, numerically fewer days to tasseling were recorded in population C2 during 2017 at UAP (47.50 days) and CCRI (47.75 days). However, relatively maximum days to tasseling were recorded for base population C_0 (55.25 days) grown during 2016 at UAP. The overall reduction in days to tasseling ranged from 52.06 (C_0) to 48.19 days (C_2) (Table 5). Maximum response to selection in reduction of days to tasseling was observed in population C_1 (-2.06 days) followed by C_2 (-1.81 days), while overall and average responses were -3.87 and -1.94 days, respectively. Similarly, the higher genetic gain was seen in population C_1 (-3.96%) followed by C_2 (-3.62%). However, overall and average gains in C_1 and C_2 populations were -7.43% and -3.72%, respectively (Table 5). In the phenotypic recurrent selection of 71 genotypes of maize, the losses in genetic gain were -0.10 and -2.50 days in days to 50% tasseling and silking, respectively (Okporie *et al*., 2013).

Several other researchers have been reported the effectiveness of recurrent selection based on selfed families. Two maize populations were studied for improving earliness, grain yield and resistance to maydis leaf blight through S_1 recurrent selection (Shah *et al*., 2007; Ayiga-Aluba *et al*., 2015).The response to S_1 recurrent selection in maize was investigated and observed the greater response in earliness and increased grain yield (Bedada & Jifar, 2010). Two maize populations were subjected to S_1 selection and observed increased grain yield with earliness and reduced lodging (Ruiz-de-Galarreta & Alvarez, 2007). Selfed-progeny recurrent selection (based on S_1 or S_2-lines) is considered more efficient than other breeding methods of recurrent selection used for the improvement of maize populations (Wardyn *et al*., 2009; Hallauer & Carena, 2012; Chen *et al*., 2019). Earliness in maturity through selfed progeny recurrent selection was confirmed by the negative selection differential values for days to tasseling and grain moisture in cycle-1 and cycle-2 maize populations through S_1 and S_2 recurrent selection (Sajjad *et al*., 2016).

Table 2. Mean squares for various traits in three maize cycle populations (PSEV3-C_0, C_1, C_2) evaluated during 2016 and 2017 at CCRI and UAP.

Source of variation	d.f.	Days to tasseling	Ears m^{-2}	Ear length	Kernel rows ear^{-1}	100-grain weight	Grain yield
Year (Y)	1	12.00**	0.563*	4.26**	0.021	80.08**	6411366.89**
Location (L)	1	70.08**	5.880**	5.67**	1.02**	14.08**	14920507.57**
YL	1	14.08**	5.880**	8.76**	0.52	12.00**	38889863.71**
R (LY)	12	1.57	0.265	0.23	0.15	3.32	989818.87*
Cycle (C)	2	60.15**	2.576**	5.47**	49.13**	68.31**	10638602.17**
C × Y	2	1.31	0.021	1.82**	0.15	7.52**	2244654.65*
C × L	2	22.65**	0.008	0.42	0.02	0.19	25336.99
C × Y × L	2	1.90	0.008	0.47	0.77**	3.06*	39442.18
Error	24	1.19	0.143	0.33	0.15	0.72	438449.48
CV (%)		2.18	8.22	3.43	2.59	3.83	10.22

*, ** Significant at $p \le 0.05$ and $p \le 0.01$, respectively

Table 3. Mean performance of three maize cyclical populations (PSEV3-C_0, C_1, C_2) for days to tasseling, ears m^2 and ear length evaluated during 2016 and 2017 at CCRI and UAP.

Genotypes with cycles	2016		2017		Means
	CCRI	UAP	CCRI	UAP	
Days to tasseling (days)					
PSEV3C0	49.25	55.25	50.00	53.75	52.06
PSEV3(S_1) C1	48.75	52.75	49.00	49.50	50.00
PSEV3(S_2) C2	48.50	49.00	47.75	47.50	48.19
Means (days)	48.83	52.33	48.92	50.25	
Location means (CCRI: 48.88, UAP: 51.29), Year means (2016: 50.58, 2017: 49.58)					
$LSD_{0.05}$ Cycles: 0.82, Y × L: 0.92, C × Y × L: NS					
Ears m^{-2} (#)					
PSEV3C0	4.78	3.46	4.28	4.28	4.20
PSEV3(S_1) C1	5.20	3.70	4.75	4.75`	4.60
PSEV3(S_2) C2	5.60	4.22	5.10	5.10	5.00
Means (number)	5.19	3.79	4.71	4.71	
Location means (CCRI: 4.95, UAP: 4.25), Year means (2016: 4.49, 2017: 4.71)					
$LSD_{0.05}$ Cycles: 0.28, Y × L: 0.32, C × Y × L: NS					
Ear length (cm)					
PSEV3C0	16.62	15.52	15.92	16.32	16.10
PSEV3(S_1) C1	16.89	15.32	17.67	17.24	16.78
PSEV3(S_2) C2	18.04	16.09	17.19	17.72	17.26
Means (cm)	17.18	15.64	16.93	17.09	
Location means (CCRI: 17.05, UAP: 16.37), Year means (2016: 16.41, 2017: 17.01)					
$LSD_{0.05}$ Cycles: 0.42, Y × L: 0.48, C × Y × L: NS					

Cobs per square meter: On average in populations, the ears per square meter were significantly ($p \leq 0.05$) high during 2017 (4.71) compared to that in 2016 (4.49) (Table 3). Similarly, across locations, the cycle populations yielded maximum cobs per square meter at CCRI (4.95) followed by UAP (4.25). Ears per square meter ranged from 3.79 (during 2016 at UAP) to 5.19 (during 2016 at CCRI) in individual environments. Cycle means were significantly highest for population C_2 (5.0) followed by C_1 (4.60) while lowest for base population C_0 (4.20). Means due to genotype by environment (C × Y × L) interaction ranged from 3.46 (C_0 population grown at UAP in 2016) to 5.60 (C_2 population grown at CCRI in 2016). Ears per square meter significantly increased with response to selection of 0.40 in each cycle while overall and average responses were 0.80 and 0.40, respectively (Table 5). Correspondingly, cycle-wise genetic gains for populations C_1 and C_2 were 9.52% and 8.70%, respectively. However, overall and average gains in C_1 and C_2 populations were 19.05% and 9.52%, respectively (Table 5). The 42 families of maize were evaluated and reported significant improvement through recurrent selection for yield traits i.e., ears per square meter (1.79), 100-kernel weight (0.58 g), cob weight per plot (308.21 g), and grain yield (261.83 kg ha^{-1}) (Da-Cunha *et al*., 2012). Previous research work revealed that improved population showed best performance than original population, and bears maximum ears per square meter, ear length, fresh ear weight and grain yield in maize (Rahman *et al*., 2009, 2015).

Cob length: Cob length varied with cropping years however, maximum cob length was produced by three maize populations in 2017 (17.01 cm) proceeded by 2016 (16.41 cm) (Table 3). Similarly, cob length differed with the location, and the populations showed maximum cob length at CCRI (17.06 cm) followed by UAP (16.37 cm). Cob length at different environments (year-location) ranged from 15.64 (2016-UAP) to 17.18 cm (2016-CCRI). Cycle means significantly differed with maximum cob length in population C_2 (17.26 cm), followed by C_1 (16.78 cm) whereas minimum in C_0 (16.10 cm). The cycle × year × location interaction means showed nonsignificant differences among the populations grown across different environments. However, cob length ranged from 15.32 cm (C_1 population grown during 2016 at UAP) to 18.04 cm (C_2 population grown during 2016 at CCRI). Ear length significantly increased and maximum response to selection was achieved in population C_1 (0.68 cm) followed by C_2 (0.48 cm) (Table 5). However, overall and average responses were 1.16 and 0.58 cm, respectively. The similarly larger genetic gain was recorded in population C_1 (4.22%) followed by C_2 (2.86%), whereas overall and average genetic gains were 7.20% and 3.60%, respectively (Table 5). The S_1-line recurrent selection brings improvement in the maize populations for cob length, grain rows per cob, 1000-grain weight and grain yield (Shahwar *et al*., 2008; Ayiga-Aluba *et al*., 2015). Likewise, another study indicated a significant improvement in various yield traits including cob length and grain yield through S1-line recurrent selection in various maize populations (Shah *et al*., 2007).

Table 4. Mean performance of three maize cyclical populations (PSEV3-C_0, C_1, C_2) for kernel rows per ear, 100-grain weight and grain yield evaluated during 2016 and 2017 at CCRI and UAP.

Genotypes with cycles	2016		2017		Means
	CCRI	UAP	CCRI	UAP	
Kernel rows per ear (#)					
PSEV3C0	12.87	12.37	12.87	12.87	12.75
PSEV3(S_1) C1	16.06	15.06	15.31	15.56	15.50
PSEV3(S_2) C2	16.00	16.00	16.25	15.75	16.00
Means (#)	14.98	14.48	14.81	14.73	
Location means (CCRI: 14.89, UAP: 14.60), Year means (2016: 14.73, 2017: 14.77)					
LSD$_{0.05}$ Cycles: 0.28, Y × L: NS, C × Y × L: 0.58					
100-grain weight (g)					
PSEV3C0	32.56	29.81	31.31	31.56	31.31
PSEV3(S_1) C1	29.69	32.19	35.94	32.94	32.69
PSEV3(S_2) C2	33.38	33.38	39.13	35.63	35.38
Means (g)	31.88	31.80	35.46	33.38	
Location means (CCRI: 33.67, UAP: 32.59), Year means (2016: 31.84, 2017: 34.42)					
LSD$_{0.05}$ Cycles: 0.93, Y × L: 1.07, C × Y × L: 1.85					
Grain yield (kg ha^{-1})					
PSEV3C0	4080.77	6921.11	5963.87	5256.42	5555.54
PSEV3(S_1) C1	4956.33	8073.28	7387.38	6684.25	6775.31
PSEV3(S_2) C2	4927.30	7715.88	8206.67	7561.76	7102.90
Means (kg ha^{-1})	4654.80	7570.09	7185.97	6500.81	
Location means (CCRI: 5920.38, UAP: 7035.45), Year means (2016: 6112.45, 2017:6843.39)					
LSD$_{0.05}$ Cycles: 483.20, Y × L: 557.90, C × Y × L: NS					

Table 5. Responses to selection and genetic gains (cycle-wise, overall and average) in three maize cyclical populations (PSEV3-C_0, C_1, C_2) for various traits evaluated during 2016 and 2017 at CCRI and UAP.

Traits	Cycle populations			Response to selection (unit)				Genetic gain (%)			
	C_0	C_1	C_2	R_1	R_2	R (Overall)	R (Average)	GG_1	GG_2	GG (Overall)	GG (Average)
Days to tasseling (#)	52.06	50.00	48.19	-2.06	-1.81	-3.87	-1.94	-3.96**	-3.62**	-7.43**	-3.72**
Ears per m^2 (#)	4.20	4.60	5.00	0.40	0.40	0.80	0.40	9.52**	8.70**	19.05**	9.52**
Ear length (cm)	16.10	16.78	17.26	0.68	0.48	1.16	0.58	4.22**	2.86**	7.20**	3.60**
Kernel rows ear^{-1} (#)	12.75	15.50	16.00	2.75	0.50	3.25	1.63	21.57**	3.23**	25.49**	12.75**
100-Grain weight (g)	31.31	32.69	35.38	1.38	2.69	4.07	2.04	4.41**	8.23**	13.00**	6.50**
Grain yield (kg ha^{-1})	5555.54	6775.31	7102.90	1219.77	327.59	1547.36	773.68	21.96**	4.84**	27.85**	13.93**

**Genetic gain significant at $p<0.01$, R_1: Response to cycle-1, R_2: Response to cycle-2, GG_1: Genetic gain in cycle-1, GG_2: Genetic gain in cycle-2, R (overall): Overall response, R (average): Average response, GG (overall): Overall genetic gain, GG (average): Average genetic gain

Kernel rows per cob: Effect of cropping year was nonsignificant for kernel rows per cob; however, it ranged from 14.73 (2016) to 14.77 (2017) (Table 4). Similarly, kernel rows per ear in different populations were varied with location and ranging from 14.60 (UAP) to 14.89 (CCRI). Environment effect on three populations for said trait was nonsignificant; however, ranging from 14.48 (UAP) to 14.98 (CCRI) grown during 2016. The cycle population × year × location interaction effects on the said trait were significant and ranging from 12.37 (C_0 population grown in 2016 at UAP) to 16.25 (C_2 population grown in 2017 at CCRI). Kernel rows per ear over four environments significantly changed with selection cycles. Maximum kernel rows per ear were observed in the second selection cycle (16.00) followed by the first cycle (15.50) while minimum in the original population (12.75). Response to selection was higher in the first selection cycle (2.75) as compared to second cycle (0.50) while overall and average responses were 3.25 and 1.63 per cycle, respectively (Table 5). Similarly, the larger genetic gain was observed in population C_1 (21.57%) followed by C_2 (3.23%), whereas overall and average genetic gains were 25.49% and 12.75% per cycle, respectively (Table 5). In S_1 recurrent selection, significant genetic gain was reported for grain yield and yield attributing traits in different maize populations (Okporie *et al.*, 2013; Ayiga-Aluba *et al.*, 2015). In selected progenies, an enhancement was reported for mean values of yield traits including grain rows per ear; however, no increase was observed for days to tasseling and grain moisture in cycle-1 and cycle-2 populations of maize (Sajjad *et al.*, 2016). Beside genetic variation in maize breeding populations, the recurrent selection was found very effective in improvement of yield components including kernel rows and kernels per row which eventually increased the grain yield through repeated cycles of selection (Ajala *et al*., 2009).

100-kernel weight: On average, all the populations produced maximum 100-kernel weight during the crop year 2017 (34.42 g) proceeded by 2016 (31.84 g) (Table 4). The 100-grain weight also varied at two locations and ranging from 32.59 g (UAP) to 33.67 g (CCRI). Effect of four environments was significant on 100-grain weight, and on average, minimum 100-grain weight was produced by three cycle populations grown during 2016 at UAP (31.80 g) while maximum during 2017 at CCRI (35.46 g). Cycle population's means were significantly different for 100-grain weight. The highest 100-kernel weight was recorded in population C_2 (35.38 g) and was followed by C_1 (32.69 g) whereas the lowest value was observed in base population C_0 (31.31 g). The cycle population × year × location interaction effects were significant, and ranging from 29.69 g (population C_1 grown during 2016 at CCRI) to 39.13 g (population C_2 grown during 2017 at CCRI). The 100-grain weight was significantly improved with selection cycles. Higher response to selection was recorded in population C_2 (2.69 g) compared to C_1 (1.38 g) (Table 5). However, overall and average responses were 4.07 g and 2.04 g, respectively. Correspondingly, the maximum genetic gain was achieved in population C_2 (8.23%) followed by C_1 (4.41%), whereas overall and average genetic gains per cycle were 13.00% and 6.50%, respectively (Table 5). Significant improvement in positive selection response was reported in 100-kernel weight, cob length and grain yield in two maize cycle populations (Sajjad *et al*., 2016). Highest expected response (based on broad sense heritability and selection differential) was observed for 1000-kernel weight, grain yield, plant height, and ear height in maize population improved through recurrent selection (Ishaq *et al*., 2014).

Grain yield: The growing conditions for maize populations i.e., PSEV3-C0, PSEV3(S1)-C1 and PSEV3(S_2)-C_2 were optimum during 2016 and 2017 at CCRI and UAP; however, comparatively high temperature resulted in higher grain yield during 2017 (6843.39 kg ha^{-1}) than 2016 (6112.45 kg ha^{-1}) (Table 4, Fig. 1). For location means, the higher grain yield was produced by the populations at UAP (7035.45 kg ha^{-1}) than CCRI (5920.38 kg ha^{-1}) (Table 4). The location means over populations varied from 4654.80 kg ha^{-1} (CCRI) to 7570.09 kg ha^{-1} (UAP) grown during 2016. Cycle means were significantly different with maximum grain yield in population C_2 (7102.90 kg ha^{-1}) followed by C_1 (6775.31 kg ha^{-1}) while minimum in parent base population C_0 (5555.54 kg ha^{-1}). The cycle population × year × location interaction effect was nonsignificant; however, it varied from 4080.77 kg ha^{-1} (C_0 population grown in 2016 at CCRI) to 8073.28 kg ha^{-1} (C_1 population grown in 2016 at UAP). Grain yield increased significantly with selection cycles (Table 5). The larger response was seen in population C_1 (1219.77 kg ha^{-1}) than C_2 (327.59 kg ha^{-1}). However, overall and average responses were in C_1 and C_2 populations were 1547.36 and 773.68 kg ha^{-1}, respectively. Likewise, the larger genetic gain was achieved in population C_1 (21.96%) while comparatively lower gain was observed in population C_2 (4.84%). Overall and average genetic gains per cycle were 27.85% and 13.93%, respectively. In past studies, 19% increase per cycle was reported in maize grain yield (Shah *et al*., 2007). However, Ayiga-Aluba *et al*., (2015) and Sajjad *et al*., (2016) reported significant genetic gain per cycle for grain yield using S_1 and S_2 maize populations through recurrent selection. By comparing the selected lines in cycle-0 and cycle-3 maize populations, a significant direct gain was reported for Fusarium ear rot, however, no improvement seen for yield and lodging (Horne *et al*., 2016).

Present studies revealed that average genetic gains per cycle for days to tasseling, cobs m^{-2}, cob length, kernel rows per cob, 100-kernel weight and grain yield were -3.72%, 9.52%, 3.60%, 12.75%, 6.50% and 13.93%, respectively. Through S_1 recurrent selection, improvement in maize cultivar Azam with genetic gains per cycle were 5%, 2%, 6% and 9% for cob length, kernel rows per cob, 1000-kernel weight and grain yield, respectively (Shahwar *et al*., 2008; Ayiga-Aluba *et al*., 2015). In cycle-1 and cycle-2, the maize grain yield increased by 22% and 27.85%, respectively, while average genetic gain was 24.90% per cycle (Bedada & Jifar, 2010). The 71 genotypes were subjected to a cycle of phenotypic recurrent selection, and the genetic gains of -3.6 cm, 6.7, 0.3, 2.6 cm, 1.10 cm, 9.4 g and 0.1 g cm^3 for plant height, tassel number plant^{-1}, ear number plant^{-1}, cob length, cob circumference, 100 seed weight, and kernel density, respectively (Okporie *et al*., 2013).

These findings further revealed that inbred-progeny selection methods (S_1, S_2) performed well than other selection methods. Negative responses with less days to tasseling, pollen shedding and silking, were reported in selected S_1-lines of cycle-3 and cycle-4 maize populations (Khalil *et al*., 2010). Selection differential values were significantly high and positive for grain yield, cob height, prolificacy, ear length, and 100-grain weight in cycle-1 and cycle-2 maize populations (Sajjad *et al*., 2016).

Grain yield is a complex trait which is affected by various genotypic and environmental factors. Crop improvement based on genotypic variations; however, environments (locations and years) greatly influence the performance of maize genotypes. Genotypes are considered desirable which persistently perform under various environments. Present findings justified that two cycles of selfed progeny recurrent selection (S_1 and S_2-cycles) showed significant genetic improvement in earliness and grain yield in base population PSEV3. Besides other agronomic traits, significant increase per cycle in grain yield (773.68 kg ha^{-1}) has been achieved. Past findings revealed that average yield of maize populations i.e., EZS1 and EZS2 increased by 820 and 930 kg ha^{-1} per cycle after six S1-selection cycles (Ruiz-de-Galarreta and Alvarez, 2007). For grain yield, the positive response was reported in S1 recurrent selection in maize and realized 750 and 1230 kg ha^{-1} increase in grain yield in two cycles (Bedada & Jifar, 2010; Ayiga-Aluba *et al*., 2015). In S_1 recurrent selection, the significant increase was observed in grain yield per cycle in improved maize populations (Ajala *et al*., 2009; Da-Cunha *et al*., 2012).

Present studies confirmed that both methods of selection (S1-progeny, S2-progeny) were found efficient in improving maize population for earliness and yield characters; however, the S_2-progeny selection was more effective. Overall, the performance of C_2 population was best, followed by C_1 over different environments (locations and years). However, C_0-base population demonstrated poor performance in the form of least mean values for yield traits with late maturity under different environments. Relatively, highest positive responses were noted for yield and yield related traits in cycle-2 than cycle-1 corn populations (Sajjad *et al*., 2016). Reciprocal recurrent selection (RRS) increased heterosis in the inter-population hybrid from 12.3% (C_0) to 24.9% (C_3), and the productivity gain [husked ear weight (t ha^{-1})] was 13.5% over the three cycles in maize (Reis *et al*., 2013).

Therefore, the C_2 population can be better used for getting a higher yield with early maturity in maize, which can improve the socio-economic status of farming community. With early maturity, the farmer's can save the labor charges incurred on standing crop, and land will be readily available for following crops.

Conclusion

Present studies revealed that two cycles of selfed progeny recurrent selection enumerated positive response to selection with significant genetic gain for earliness and yield traits under various environments. Environments interaction with cyclical populations revealed that selected maize populations (C_1 and C_2) grown at CCRI owned remarkable performance for maturity and yield traits. The C_2 population showed the best performance than C_1 which confirmed that S_2-progeny recurrent selection was more effective for maize improvement. The C_0 (base population) was not much responsive and showed weaker performance for yield traits with late maturity in various environments, which authenticated that such base population always need cycling to improve it. These evidence indicated that recurrent selection procedures are more capable to improve the performance of different maize base populations. Present findings suggested that further cycling in a wide range of environments will bring more improvement in these improved maize populations.

References

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

Ali, S. 2015. Genetic analysis and genotype by environment studies in maize. Ph.D. Dissertation, Department of Plant Breeding and Genetics, The University of Agriculture, Peshawar, Pakistan.

Ali, S., N.U. Khan, I.H. Khalil, M. Iqbal, S. GuL, S. Ahmed, N. Ali, M. Sajjad, K. Afridi, I. Ali and S.M. Khan. 2017. Environment effects for earliness and grain yield traits in F_1 diallel populations of maize (*Zea mays* L.). *J. Sci. Food Agric*., 97: 4408-4418.

Ali, S., N.U. Khan, R. Gul, I. Naz, R. Goher, N. Ali, S.A. Khan, I. Hussain, M. Saeed and M. Saeed. 2018. Genetic analysis for earliness and yield traits in maize. *Pak. J. Bot*., 50: 1395-1405.

Ali, S., N.U. Khan, S. Gul, R. Goher, I. Naz, S.A. Khan, N. Ali, M. Saeed, I. Hussain, S.M. Khan and I. Ali. 2019. Heterotic effects for yield related attributes in F_1 populations of maize. *Pak. J. Bot*., 51: 1675-1686.

Ayiga-Aluba, J., R. Edema, G. Tusiime, G. Asea and P. Gibson. 2015. Response to two cycles of S_1 recurrent selection for turcicum leave blight in an open pollinated maize variety population (Longe 5). *Adv. Appl. Sci. Res*., 6(12): 4-12.

Bedada, L.T. and H. Jifar. 2010. Maize (*Zea mays* L.) genetic advances through S_1 recurrent selection in Ethiopia. *J. Environ. Issues Agric. Dev. Count*., 2(1): 154-169.

Carangal, V.R., S.M. Ali, A.F. Koble, E.H. Rinke and J.C. Sentz. 1971. Comparison of S_1 with testcross evaluation for recurrent selection in maize. *Crop Sci*., 11: 65S-661.

Chen, Z.H., Y.F. Zhu, A.G. Wang, X.Y. Guo, X. Wu and P.F. Liu. 2019. Effects of reciprocal recurrent selection on grain yield in two tropical-temperate maize synthetic populations tuxpeño-reid and suwan-lancaster. *Am. J. Plant Sci*., 10: 298-308.

Cobb, J.N., R.U. Juma, P.S. Biswas, J.D. Arbelaez, J. Rutkoski, G. Atlin, T. Hagen, M. Quinn and E.H. Ng. 2019. Enhancing the rate of genetic gain in public-sector plant breeding programs: lessons from the breeder's equation. *Theor. Appl. Genet*., 132(3): 627-645.

Da-Cunha, K.S., M.G. Pereira, L.S.A. Gonçalves, A.P.C.G. Berilli, E.C. de-Oliveira, H.C.C. Ramos and A.T.A. Junior. 2012. Full-sib reciprocal recurrent selection in the maize populations CIMMYT and Piranão. *Genet. Mol. Res*., 11(3): 3398-3408.

Deletic, N., S. Stojkovic, V. Duric, S. Gudzic and M. Biberdzic. 2005. The effect of a high selection intensity on the change of maize yield components additive variance. *Genetika*, 37(1): 71-76.

Gomez, K.A. and A.A. Gomez. 1984. Statistical procedures for agricultural research. John Wiley and Sons, New York, USA.

Hallauer, A.R. and M.J. Carena. 2012. Recurrent selection methods to improve germplasm in maize. *Maydica*, 57: 226-283.

Hallauer, A.R., Fo. J.B. Miranda and M.J. Carena. 2010. Quantitative genetics in maize breeding. 3rd, Springer, New York, USA.

Horne, D.W., M.S. Eller and J.B. Holland. 2016. Responses to recurrent index selection for reduced *Fusarium* ear rot and lodging and for increased yield in maize. *Crop Sci*., 56: 85-94.

Ishaq, M., G. Hassan, H. Rahman, M. Iqbal, I.A. Khalil, S.A. Khan, S.A. Khan, Rafiullah and J. Hussain. 2014. Estimates of heritability and expected response for maturity and grain yield related traits in half-sib recurrent families of maize. *Pak. J. Biotechnol*., 11(2): 141-151.

Keeling. B.I. 1982. Effect of soybean mosaic virus on root volume and dry weight of soybean plants. *Crop Sci*., 22(3): 629-639.

Khalil, I.A., H. Rahman, D. Shahwar, I. Nawaz, H. Ullah and F. Ali. 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, K., N.U. Khan, M. Iqbal, H. Sher, S. Gul and N. Ali. 2018. Populations of exotic × locally adapted germplasm - A potential source of inbred lines for superior indigenous maize hybrids. *Tarim Bilim. Derg. - J. Agric. Sci*., 24: 413-421.

Lush, J.L. 1940. Intra-sire correlations or regression of offspring on dam as method of estimating heritability of characteristics. *33rd Ann. Proc. Soc. Anim. Prod*. pp. 293.

Noor, M., D. Shahwar, H. Rahman, H. Ullah, F. Ali, M. Iqbal, I.A. Shah and I. Ullah. 2013. Change in heritability estimates due to half-sib family selection in the maize variety Pahari. *Genet. Mol. Res*., 12(2): 1872-1881.

Okporie E.O., S.C. Chukwu and G.C. Onyishi. 2013. Phenotypic recurrent selection for increase yield and chemical constituents of Maize (*Zea mays* L.). *World Appl. Sci. J.*, 21(7): 994-999.

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

Rahman, H., H. Ullah, L. Shah and A. Ali. 2015. Estimates of heritability and genetic advance for morphological traits improvement in maize (*Z. mays* L.). *Acad. J. Agric. Res.*, 3(1): 9-14.

Rahman, H., I. Nawaz, S.M.A. Shah, D. Shahwar, I.A. Khalil, M. Iqbal, M. Sohail and M.Y. Khan. 2009. Evaluation of testcrosses derived from maize variety Azam for yield and yield associated traits. *Sarhad J. Agric*., 25(2): 197-202.

Reis, M.C.D., F.L. Guedes, G.B. Abreu and J.C. Souza. 2013. Reciprocal recurrent selection in maize enhances heterosis and ears yield. *Euphytica,* 191(2): 217-222.

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

Sajjad, M., N.U. Khan, H. Rahman, K. Khan, G. Hassan, S. Gul, S. Ali, K. Afridi, I. Ali and S.M. Khan. 2016. Response of a maize composite to selfed progeny recurrent selection for earliness and yield traits. *Maydica,* 61(3): 1-8.

Shah, S.S., H. Rahman, I.H. Khalil and M. Iqbal. 2007. Recurrent selection for may dis leaf blight resistance and grain yield improvement in maize. *Pak. J. Biol. Sci*., 10(20): 3632-3637.

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

Sheikh, F., A. Sohail, T. Burni, F. Hadi, M. Asad, A. Aziz, A. Haleem, M. Maryam and Z. Rahman. 2019. Impact of half-sib family recurrent selection on grain yield in maize population ZM-309. *Pure Appl. Biol*., 8(3): 2399-2408.

Sohail, A., Q. Hussain, S. Ali, Manzoor, F. Hadi, S. Uddin, F. Bashir, M. Asad, S. Sami and Z. Yousafzai. 2018. Evidence of improving yield and yield attributes via half-sib family recurrent selection in maize (*Zea mays* L.). *Int. J. Curr. Res. Biosci. Plant Biol.*, 5(12): 45-56.

Tardin, F.D., M.G. Pereira, A.P.C. Gabriel, A.T.A. Júnior and G.A.S. Filho. 2007. Selection index and molecular markers in reciprocal recurrent selection in maize. *Crop Breed. Appl. Biotechnol*., 7: 225-233.

Wardyn, B.M., J.W. Edwards and K.R. Lamkey. 2009. Inbreeding progeny selection is predicted to be inferior to half-sib selection for three maize populations. *Crop Sci*., 49: 443-450.

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