



Full Length Article

Maize Cyclical Populations (PSEV3-C₀, C₁ and C₂) Response over Diverse Environments

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Abstract

Recurrent selection is an efficient breeding method used to improve the maize and other cross-pollinated species. Present study was aimed to assess the performance of maize cyclical populations *i.e.*, PSEV3(S₁)-C₁ and PSEV3(S₂)-C₂ in comparison to base population PSEV3-C₀ over environments. Maize base population (PSEV3-C₀) was developed through selfed progeny recurrent selection in five consecutive crop seasons for three years (spring and summer-2014 and 2015, and spring-2016). During summer-2016 and 2017, the improved maize populations C₁, C₂ and base population C₀ were grown in a randomized complete block design with four replications over four environments *i.e.*, two each years (2016 and 2017), and locations. Significant ($P \leq 0.01$) differences were observed among cyclical populations (C) for days to silking, plant height and grain yield. The interactions due to population by year and population by location also revealed significant ($P \leq 0.01$) variation for the majority of the traits. The highest grain yield was produced by C₂ population during 2017 at CCRI, followed by C₁ grown during 2016 at UAP. Base population C₀ revealed late flowering with minimum grain yield over environments. In improved populations C₁ and C₂, the observed responses were greater than expected in selection cycle-1 and cycle-2. The cycle-wise and average genetic gain values were greater in C₂ populations than C₁ families for all the traits. The selfed progeny recurrent selection was found more effective in improving maize populations for earliness and yield traits. Similarity, improvement made due to said breeding method suggests further screening of maize populations through advanced cycles. © 2020 Friends Science Publishers

Keywords: Recurrent selection; Improved populations C₁ and C₂; Observed and expected responses; Genetic gain; *Zea mays*

Introduction

Maize (*Zea mays* L.) is one of the most resourceful and multipurpose crops, having widest adaptability in distinct ecologies (Khan *et al.* 2018; Ali *et al.* 2020). Universally, it is also known as queen of cereals due to its highest genetic potential and provides food, feed, fodder for human and animal consumption (Kumar *et al.* 2013). Maize provides raw material to the industry for the preparation of corn oil and starch, corn syrup and flakes, dextrose, cosmetics, wax, alcohol and tanning material for leather industry (Arain 2013). During 2018-2019, the maize was grown on an area of 1.374 million hectares which produced 6.826 million tons of grains with average grain yield of 4968 kg ha⁻¹ in Pakistan (Anonymous 2018–2019). Though maize exceeds other cereals in productivity, however, in Pakistan the

farming community is still getting low yield as compared to other growing countries (Sajjad *et al.* 2016). Maize low yield is attributable to many factors including, genotypes low potential, soil variation, fertility gradient, water shortage and temperature fluctuations (Sajjad 2018; Hussain *et al.* 2019; Minhas *et al.* 2020).

Development of high yielding and well-adapted genotypes with desirable traits usually remains the main objective of plant breeding (Ali 2015; Ali *et al.* 2017). Large number of breeding methods has been developed to enhance the economic yield of the various crops (Ali *et al.* 2018, 2019). However, recurrent selection is a commendable breeding method used to improve the populations particularly those of cross-pollinated species. Being an important breeding strategy, restoration of genetic variability and subsequent improvement within the

population can be made through recurrent selection (Sampoux *et al.* 2020). Recurrent selection can accrue desirable genes and create new gene complexes for genetic variation and improvement within population.

Recurrent selection is a reselection made generation after generation, with reunion of selected plants to produce a population for the next cycle of the selection (Darrah *et al.* 2019; Sheikh *et al.* 2019). Germplasm subjected to recurrent selection with the idea to ensure isolation of superior inbreds from the original population. However, isolation of an outstanding inbred line depends on two factors, a) the ratio of promising genotypes found in the original population, and b) the efficiency of selection during the inbreeding of desirable genes (Pixley *et al.* 2006; Ahmad *et al.* 2010). Based on visual observations for yield related traits in improved populations C_1 and C_2 , the simple recurrent selection was found more suitable for improvement in waxy corn (Khamkoh *et al.* 2019).

Selfed progeny recurrent selection is considered more efficient than full-sib and half-sib family's selection in maize (Hallauer and Carena 2012; Sheikh *et al.* 2019). The S_1 selfed progeny recurrent selection was found is an excellent option for attaining improvement within maize populations and enhancement of grain yield in maize (Chen *et al.* 2019). The S_1 selection was conducted for grain yield under different environments and concluded that S_1 family selection has been found efficient for improving grain yield in maize (Badu-Apraku *et al.* 2013). Selfed progeny recurrent selection using either S_1 or S_2 lines is considered more useful for population improvement compared to other methods of recurrent selection (Hallauer *et al.* 2010).

In selfed progeny recurrent selection, the desirable alleles are fixed rapidly and deleterious alleles are exposed and eliminated early in selection (Abdulmalik *et al.* 2017; Guimaraes *et al.* 2018). However, several studies suggested that genetic diversity in the populations reduced after the initial cycles, limiting opportunities for selection (Noor *et al.* 2013; Udo *et al.* 2017). Significant decrease was recorded for morphological traits while increase in yield traits was achieved with S_1 recurrent selection (Horne *et al.* 2016; Kolawole *et al.* 2017, 2019). Selection in cycle-2 produced maximum grain yield with significant genetic gain and hence, S_1 recurrent selection was recommended for significant improvement in maize (Bedada and Jifar 2010).

Genotype performance depends on population, environment and genotype by environment interaction (GEI) (Gomez and Gomez 1984). Genotype is an individual's genetic make-up and its phenotypic expression depends on the environments surrounding it (Andorf *et al.* 2019). Genotypes may perform well in one environment but not so well in other. Genotypes exhibits different behaviour in different environments (years and locations) due to their varied genetic makeup (Annor *et al.* 2019). Genotypes, environments, and genotype by environment interaction determine the individual's phenotype and that is why GEI is an important aspect of plant breeding.

Similarly, selection differential and genetic gain are also very important breeding tools which guides the breeder about the genetic potential of selected populations in maize (Ullah *et al.* 2013; Cobb *et al.* 2019). Likewise, expected and observed responses, and genetic gain substantiate that how much improvement is expected and realized during selection in maize (Sajjad *et al.* 2016; Udo *et al.* 2017). Maize S_1 and S_2 selfed families revealed significant enhancement in grain yield with desirable genetic gain (Ali *et al.* 2012; Chen *et al.* 2019). Past studies revealed that S_1 and S_2 based selections were found effective in improving maize populations for earliness and yield related traits (Bedada and Jifar 2010; Ayiga-Aluba *et al.* 2015).

Therefore, after development of maize improved cyclical populations (PSEV3- C_1 and PSEV3- C_2) from base population (PSEV3- C_0) through recurrent selection, the present study was designed with the objectives a) to assess the performance of C_1 and C_2 populations in comparison to original population C_0 in different environments for earliness and yield traits, b) to ascertain the expected and observed responses in selection cycle-1 and cycle-2, and c) to quantify the cycle-wise and average genetic gain in the maize improved populations.

Materials and Methods

Development of breeding material, sites and procedure

Maize original population PSEV3- C_0 was derived from a cross between maize cultivar Azam and hybrid CHSW (Single cross hybrid, white kernels with late maturity from CIMMYT). For improving maize base population 'PSEV3- C_0 ' for earliness and yield traits through selfed progeny recurrent selection, the breeding material was developed in five consecutive crop seasons for three years (during spring and summer - 2014 and 2015, and spring - 2016) at Cereal Crops Research Institute (CCRI), Pirsabak - Nowshera, Pakistan (Table 1).

The first selection cycle (C_1) was based on S_1 -lines while 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) were 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 S₂ plants. During Summer 2015, the seeds from 169 selected S₂ families along with base population were tested in partially balanced lattice design (13 × 13), replicated twice. Same plot size was maintained as described earlier for S₁. At maturity, seventeen best S₂ families were selected and stored to study in the next season. During spring - 2016, the selected S₂ families were recombined and their seeds were bulked to develop PSEV3 (S₂)-C₂ population (C₂).

Cyclical populations PSEV3(S₁)-C₁, PSEV3(S₂)-C₂ and base population PSEV3-C₀ were evaluated during summer season over four environments *i.e.*, two consecutive years (2016 and 2017) and two locations *i.e.*, a) Cereal Crops Research Institute (CCRI), Pirsabak - Nowshera, Pakistan, (situated between 32° N latitude and 72°E longitude with an altitude of 288 m), and b) the University of Agriculture (UAP), Peshawar, Pakistan (situated between 34° N latitude and 71° E longitude with an altitude of 350 m). At CCRI, the soil was sandy loam and moderately calcareous having pH (7.7), organic matter (0.34%), nitrogen (0.034%), P₂O₅ (0.0029%), K₂O (0.051%). At UAP, the soil was silt clay loam with alkaline nature having pH (7.8), organic matter (0.81%), nitrogen (0.063%), P₂O₅ (7.18 mg kg⁻¹) and K₂O (112 ppm). At each location, the experiment was carried out in a randomized complete block design (RCBD) with four replications. Four-row sub-plots were maintained, 10 m long with 0.25 m and 0.75 m distance between plants and rows, respectively.

Crop husbandry

Maize is a shallow-rooted crop, and it requires fine good tilth and well-prepared soil for successful germination and growth of crop. To get this, the field was ploughed with deep plough then harrowed with planking each time to make the soil loose, fine, levelled and pulverized. The stubbles of the previous crop left in the field were also removed. A recommended fertilizer dose at the rate of 200:90:90 NPK kg ha⁻¹ was applied. Half dose of nitrogen (N), whole doses of phosphorus (P₂O₅) and Potash (K₂SO₄) 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. The leftover weeds were manually controlled carrying out weeding and earthing-up operations. Maize borer was eradicated with Confidor-WP60 @ 50 g per 10 kg of maize seed through seed treatment before sowing. After one month, Furadon-3% granules @ 20 kg ha⁻¹ were applied in the whirls. The crop was irrigated at the proper interval as and when required, until one week before harvesting. All the entries were equally treated during the cropping seasons. Maximum and minimum temperatures data for maize spring and summer crop seasons during 2014 to 2017 at CCRI and UAP is provided in Fig. 1.

Data recorded

Data were recorded on days to silking (days counted from planting to silk emergence in 50% plants of each plot), plant height (plant height was measured as an average distance from soil surface to the node of flag leaf on 10 competitive plants in each plot and then averaged), ear height (ear height was recorded as an average distance from soil surface to the node bearing the primary ear shoot on 10 competitive plants per plot and then averaged), ears per plant (ears per plant were estimated as ratio of total number of ears to number of plants). Prolificacy (%), and grain yield (kg ha⁻¹) (Carangal *et al.* 1971) were estimated with the help of the following relationships.

$$\text{Prolificacy (\%)} = \frac{\text{Cobs plot}^{-1}}{\text{Plants plot}^{-1}} \times 100$$

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

Where,

MC = Moisture content (%) in grains at harvest

FEW = Fresh ear weight (kg) at harvest

Shelling coefficient = 0.80

Statistical analyses

Analysis of variance: The recorded data for each trait was subjected to analysis of variance techniques using Statistix 8.1 software (Statistix, Analytical Software, Tallahassee, FL, USA, 1985–2003) appropriate for genotype by environment interaction (Gomez and Gomez 1984). After getting the significant mean squares, the means were further compared and separated by using LSD_{0.05} test.

Response to selection

Response to selection and genetic gain are tools for measuring the 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,

C₀: Mean of the parent population

C₁: Mean of cycle one

C₂: Mean of cycle two

Genetic gain

Genetic gain (%) was estimated using the relationship as 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

Three maize cyclical populations (PSEV3- C_0 , PSEV3- C_1 and PSEV3- C_2) were evaluated under four different environments *i.e.*, two each years (2016 and 2017) and locations (CCRI and UAP). Combined analysis of variance revealed that years were significant for ear per plant ($P \leq 0.05$) and grain yield ($P \leq 0.01$) (Table 2). Locations revealed significant ($P \leq 0.01$) mean differences for the majority of the traits while merely significant ($P \leq 0.05$) for ears per plant and prolificacy. In year by location ($Y \times L$), the mean squares were significant ($P \leq 0.01$) for almost all traits. Significant ($P \leq 0.01$) differences were recorded among cyclical populations (C) for days to silking, plant height and grain yield. However, in interactions, varied trends were observed for different traits. The cyclical population by year ($C \times Y$) interactions were highly significant for all the traits except prolificacy and ears per plant. Similarly, population by location ($C \times L$) interactions were significant ($P \leq 0.01$) for days to silking and plant height. Likewise, for population-year-location ($C \times Y \times L$) interactions, significant ($P \leq 0.01$) variations were recorded for plant height, and non-significant for all other traits. The trait-wise results are discussed herein.

Days to silking

Overall, the maize populations grown during 2017 showed less days to silking than 2016 (Table 3). In locations, populations grown at CCRI revealed fewer days to silking than UAP. For year's \times location means, minimum and at par days to silking were recorded for all the populations grown at CCRI during 2016 and 2017. Minimum days to silking at CCRI confirmed that almost all the populations comparatively matured earlier due to high temperature (Fig. 1). However, maximum days to silking were observed in populations grown during 2016 at UAP. Population (C) means over environments revealed that on average, minimum days to silking were observed in population C_2 (50.31 days), followed by C_1 (52.25 days) and C_0 (54.88 days). On average, days to silking were decreased from 54.88 (base population - C_0) to 52.25 and 50.31 days in improved populations C_1 and C_2 , respectively. In interactions of population by year by location ($C \times Y \times L$) means, minimum and same days to silking were recorded in improved population C_2 grown during 2016 and 2017 at CCRI and UAP, respectively. However, base population C_0 grown at UAP revealed maximum days to silking during both years. For days to silking, the values of expected responses were lesser than observed in cycle-1 and cycle-2 populations (Table 5). In cycle-1 and cycle-2, the genetic gain values were -2.63 and -1.94 days, respectively with an

average reduction of -2.29 days (-4.16%) (Table 6). Days to silking were reduced from 54.88 (C_0) to 50.31 days (C_2) with overall genetic gain of -4.57 days (-8.33%).

Plant height

For years, the least plant height was observed in maize populations grown during 2017 compared to 2016 (Table 3). On average the populations showed minimum plant height at UAP than CCRI. In year \times location interaction, the populations grown during 2017 at UAP revealed minimum plant height compared to CCRI. Maximum and same plant height was recorded in populations grown during 2016 and 2017 at CCRI (175.92 cm). Cyclical population means over environments revealed that minimum and alike plant height was observed in C_0 (164.81 cm) and C_1 (168.00 cm), while C_2 showed maximum plant height (175.69 cm). The cyclical population-year-location interactions revealed that minimum and similar plant height was obtained in original population- C_0 grown during 2017 and improved population- C_1 grown during 2016 at UAP. Maximum and same plant height was obtained in improved populations C_2 and C_1 grown during 2016 and 2017 at CCRI. The improved populations C_1 and C_2 showed significant increase in plant height compared to original population. In cyclical populations for plant height, the observed responses were larger than the corresponding expected responses in cycle-1 and cycle-2 (Table 5). Plant height increased with succeeding cycles with overall genetic gain of 10.88 cm (6.60%) (Table 6). Cycle wise gains were 3.19 and 7.69 cm in cycle-1 and cycle-2, respectively while average genetic gain was 5.44 cm (3.30%) for plant height.

Ear height

For years, the minimum ear height was recorded for populations grown during 2017, followed by 2016 (Table 3). In locations, the populations grown at UAP revealed minimum ear height while maximum at CCRI. Cyclical population means over environments ranged from 75.38 (C_0) to 79.13 cm (C_2). Similarly, interaction means for population \times year \times location ranged from 67.75 to 89.25 cm. However, minimum ear height was observed in base population- C_0 grown during 2017 at UAP, followed by improved populations C_2 and C_1 during 2016 and 2017, respectively at UAP. The increased ear height was observed in population C_2 and C_1 grown during 2017 and 2016, respectively at CCRI. Ear height was significantly increased in improved populations C_1 and C_2 compared to base population. Among populations for ear height, the observed responses were greater than expected responses (Table 5). Ear height was increased with succeeding selection cycles with overall genetic gain of 3.75 cm (4.97%) (Table 6). Cycle-wise gain values were 3.12 and 0.63 cm in cycle-1 and cycle-2, respectively, with average genetic gain of 1.88 cm (2.49%) for ear height.

Table 1: Maize base and improved populations with various characteristics used in the study

Genotypes	Source	Type	Kernel shape/color	Plant height	Maturity	Pedigree
Base population PSEV3-C ₀	CCRI	OPP	Flint white	Medium	Medium	Cross between maize cultivar Azam and CHSW (Single cross hybrid, white kernels with late maturity from CIMMYT)
PSEV3 (S ₁)-C ₁	CCRI	OPP	Flint white	Medium	Medium	Derived from recombination of S ₁ selected maize families
PSEV3 (S ₁)-C ₂	CCRI	OPP	Flint white	Medium	Medium	Derived from recombination of S ₂ selected maize families

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

Table 2: Mean squares of maize cyclical populations (PSEV3-C₀, C₁, C₂) for varioustraitsevaluatedduring2016and 2017 at CCRI and UAP

Source of variation	df	Days to silking	Plant height	Ear height	Ears plant ⁻¹	Prolificacy	Grain yield
Years (Y)	1	3.52	36.75	0.08	0.005*	55.32	6411366.89**
Locations (L)	1	54.19**	3201.33**	1200.00**	0.031*	299.75*	14920507.57**
Y × L	1	13.02**	330.75**	0.75	0.030*	291.026*	38889863.71**
R (LY)	12	1.60	62.10	33.26	0.005	47.44	989818.87*
Cycles (C)	2	83.90**	500.06**	64.58	0.001	13.04	10638602.17**
C × Y	2	0.52	286.19**	236.33*	0.001	8.24	2244654.65*
C × L	2	19.56**	282.02**	7.75	0.001	7.97	25336.99
C × Y × L	2	0.77	244.31**	25.00	0.001	11.97	39442.18
Error	24	1.27	38.37	46.22	0.006	59.67	438449.48
CV (%)	-	2.15	3.65	8.75	8.26	8.28	10.22

*, ** = Significant at P≤0.05 and P≤0.01, respectively

Table 3: Performance of maize cyclical populations (PSEV3-C₀, C₁, C₂) over environments for various traits

Cyclical populations	2016		2017		Means
	CCRI	UAP	CCRI	UAP	
Days to silking (days)					
PSEV3-C ₀	52.50	58.00	52.75	56.25	54.88
PSEV3 (S ₁)-C ₁	51.00	54.25	51.75	52.00	52.25
PSEV3 (S ₂)-C ₂	50.00	50.75	50.50	50.00	50.31
Means	51.17	54.33	51.67	52.75	-
Means (years)	52.75	-	52.21	-	-
Means (locations)	51.42	-	-	53.54	-
LSD _{0.05} Cycles: 0.80, Locations: 0.69, Years: NS, Y × L: 0.95, C × Y × L: NS					
Plant height (cm)					
PSEV3-C ₀	169.25	171.75	170.00	148.25	164.81
PSEV3 (S ₁)-C ₁	180.25	151.25	181.50	159.00	168.00
PSEV3 (S ₂)-C ₂	178.25	171.50	186.75	166.25	175.69
Means (cm)	175.92	164.83	179.42	157.83	-
Means (years)	170.38	-	168.63	-	-
Means (locations)	177.67	-	-	161.33	-
LSD _{0.05} Cycles: 4.52, Locations: 3.69, Years: NS, Y × L: 5.22, C × Y × L: 9.04					
Ear height (cm)					
PSEV3-C ₀	82.75	73.25	77.75	67.75	75.38
PSEV3 (S ₁)-C ₁	87.25	73.50	81.25	72.00	78.50
PSEV3 (S ₂)-C ₂	77.75	71.75	89.25	77.75	79.13
Means (cm)	82.58	72.83	82.75	72.50	-
Means (years)	77.71	-	77.63	-	-
Means (locations)	82.67	-	-	72.67	-
LSD _{0.05} Cycles: NS, Locations: 4.10, Years: NS, Y × L: NS, C × Y × L: NS					

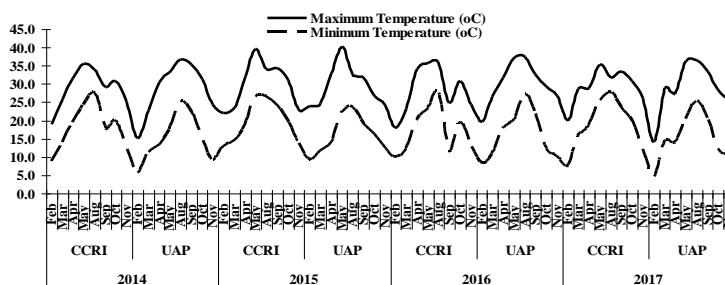


Fig. 1: Maximum and minimum temperatures for spring and summer maize crop seasons during 2014 to 2017 at CCRI and UAP
Source: Pakistan Forest Institute (PFI), Peshawar, Pakistan; Cereal Crops Research Institute (CCRI), Pirsabak - Nowshera, Pakistan

Table 4: Performance of maize cyclical populations (PSEV3-C₀, C₁, C₂) over environments for yield related traits

Cyclical populations	2016		2017		Means
	CCRI	UAP	CCRI	UAP	
	Ears per plant (#)				
PSEV3-C ₀	0.98	0.89	0.95	0.93	0.93
PSEV3 (S ₁)-C ₁	0.96	0.86	0.93	0.96	0.92
PSEV3 (S ₂)-C ₂	0.99	0.88	0.95	0.95	0.94
Means (#)	0.97	0.87	0.94	0.94	-
Means (years)	0.92	-	0.94	-	-
Means (locations)	0.96	-	-	0.91	-
	LSD _{0.05} Cycles: 0.06, Locations 0.05, Years: 0.05, Y × L: 0.07, C × Y × L: NS				
	Prolificacy (%)				
PSEV3-C ₀	97.33	88.57	95.14	92.42	93.36
PSEV3 (S ₁)-C ₁	95.40	85.67	92.72	95.71	92.38
PSEV3 (S ₂)-C ₂	98.85	87.58	95.39	94.90	94.18
Means (%)	97.19	87.27	94.42	94.34	-
Means (years)	92.23	-	94.38	-	-
Means (locations)	95.81	-	-	90.81	-
	LSD _{0.05} Cycles: NS, Locations: 4.60, Years: NS, Y × L: 6.51, C × Y × L: NS				
	Grain yield (kg ha ⁻¹)				
PSEV3-C ₀	4081	6921	5964	5256	5556
PSEV3 (S ₁)-C ₁	4956	8073	7387	6684	6775
PSEV3 (S ₂)-C ₂	4927	7716	8207	7562	7103
Means (kg ha ⁻¹)	4655	7570	7186	6501	6478
Means (years)	6113	-	6844	-	-
Means (locations)	5921	-	-	7036	-
	LSD _{0.05} Cycles: 483.20, Locations: 394.50, Years: 394.50, Y × L: 557.90, C × Y × L: NS				

Table 5: Expected and observed responses in maize cyclical populations over two cycles of selection for various traits

Traits	Selection cycle-1		Selection cycle-2	
	Expected response (R _e)	Observed response (R _o)	Expected response (R _e)	Observed response (R _o)
Days to silking (days)	-1.30	-4.76	-1.56	-5.43
Plant height (cm)	8.95	19.27	20.14	50.05
Ear height (cm)	5.24	7.79	7.59	20.47
Ears per plant (#)	0.02	-0.01	0.03	-0.01
Prolificacy (%)	1.44	-0.63	2.25	-0.48
Grain yield (kg ha ⁻¹)	1899.11	2673.44	2228.88	3560.96

R_e = Expected response (h²*S); R_o = Observed response (μ_p - μ)

Table 6: Genetic gains (cycle-wise, overall and average) in maize cyclical populations over two cycles of selection for various traits

Traits	Cyclical populations			Cycle-wise gain				Overall gain		Average gain	
	C ₀	C ₁	C ₂	Cycle-1		Cycle-2		(unit)	(%)	(unit)	(%)
				(unit)	(%)	(unit)	(%)				
Days to silking (days)	54.88	52.25	50.31	-2.63	-4.79**	-1.94	-3.71**	-4.57	-8.33**	-2.29	-4.16**
Plant height (cm)	164.81	168.00	175.69	3.19	1.94**	7.69	4.58*	10.88	6.60**	5.44	3.30*
Ear height (cm)	75.38	78.50	79.13	3.12	4.14 ^{NS}	0.63	0.80 ^{NS}	3.75	4.97 ^{NS}	1.88	2.49 ^{NS}
Ears per plant (#)	0.934	0.924	0.942	-0.010	-1.071 ^{NS}	0.018	1.948 ^{NS}	0.008	0.857 ^{NS}	0.004	0.428 ^{NS}
Prolificacy (%)	93.36	92.38	94.18	-0.98	-1.05 ^{NS}	1.80	1.95 ^{NS}	0.82	0.88 ^{NS}	0.41	0.44 ^{NS}
Grain yield (kg ha ⁻¹)	5555.54	6775.31	7102.90	1219.77	21.96**	327.59	4.84 ^{NS}	1547.36	27.85**	773.68	13.93**

*, ** = Significant at P ≤ 0.05 and P ≤ 0.01, respectively; NS = Non-significant

Ears per plant

For years, the ears per plant produced by the maize populations during 2016 and 2017 were comparable with least differences (Table 4). For locations, the highest number of ears per plant was produced by populations at CCRI, followed by UAP. In year × location means, the populations revealed maximum ears during 2016 at CCRI, followed by the populations grown during 2017 at CCRI and UAP. The cyclical population means enunciated non-significant variations over years and locations *i.e.*, 0.93 (C₀),

0.92 (C₁) and 0.94 (C₂). Interaction means of cyclical population × year × location ranged from 0.86 to 0.99. The interaction means were also nonsignificant for the said trait; however, comparatively larger value was recorded in C₂ (0.99) grown during 2016 at CCRI while smaller value stood for C₁ (0.86) grown during 2016 at UAP. Among cyclical populations for ears per plant, the expected responses were higher than observed responses in both selection cycles (Table 5). The ears per plant were non-significantly enhanced and hence, the genetic gain was not formulated for the said trait.

Prolificacy

Maize improved and base populations grown during 2017 revealed the highest prolificacy than 2016 (Table 4). However, for locations the higher prolificacy was observed in populations grown at CCRI, followed by UAP. According to year by location interactions, maize populations revealed higher prolificacy at CCRI while least at UAP during 2016. Cyclical populations over years and locations revealed that prolificacy was greater in C₂ (94.18%), followed by C₀ (93.36%) while the least value was recorded in C₁ (92.38%) for the said trait. The cyclical population × year × location interactions enunciated that the highest prolificacy was achieved in improved population-C₂ grown during 2016 at CCRI, followed by base population-C₀ during 2016 at CCRI and C₁ during 2017 at UAP. However, the minimum prolificacy was observed in improved population-C₁ grown during 2016 at UAP. Among cyclical populations, the expected responses were greater than corresponding observed responses for prolificacy in cycle-1 and cycle-2 (Table 5). In selection cycles, the prolificacy was increased in improved population C₂ compared to original population.

Grain yield (kg ha⁻¹)

For maize populations, the highest grain yield was obtained during 2017, followed by 2016 (Table 4). In locations, populations grown at UAP revealed maximum grain yield succeeded by CCRI. Population means for year by location revealed that maximum grain yield was recorded during 2016 at UAP, followed by populations grown during 2017 at CCRI. However, the populations grown during 2016 at CCRI exhibited minimum grain yield. Cyclical population means over years and locations ranged from 5555.54 (C₀) to 7102.90 kg ha⁻¹ (C₂). However, improved populations C₂ (7102.90 kg ha⁻¹) and C₁ (6775.31 kg ha⁻¹) revealed the highest grain yield compared to original population C₀ (5555.54 kg ha⁻¹) over environments. In cyclical population × year × location interactions, the highest grain yield was delivered by improved cyclical populations C₂ grown during 2017 at CCRI, followed by C₁ grown during 2016 at UAP. Minimum grain yield was manifested by base population C₀ grown during 2016 at CCRI. The observed responses were higher in magnitude than expected in both cycles of selection (Table 5). The yield increased with proceeding cycles with overall genetic gain of 1547.36 kg ha⁻¹ (27.85%), with average genetic gain of 773.68 kg ha⁻¹ (13.93%) in both cycles (Table 6). In grain yield, the highest increase in form of genetic gain was recorded in cycle-1, followed by cycle-2.

Discussion

Selection of suitable populations is crucial and very important in maize breeding for getting higher yields and to periodically check the agronomic performance of

recommended populations for specific growing locations (Santos *et al.* 2002). Plant breeding is a vital tool allowing recombination of genes between diversified and superior genotypes, aiming at exploiting the genetic divergence for obtaining genotypes with greater potential and adaptability to different environmental conditions (Allard 1971). Hence, S₁ progeny selection in terms of units of selection and recombination of S₁ progenies is of immense interest for maize breeders (Badu-Apraku *et al.* 2013).

Maize populations and various interactions showed significant differences for majority of the earliness, morphological and yield traits under different environments which authenticated that genotypes have greater genetic variability and scope for further improvement. Significant differences were observed among various maize populations for female and male flowering, plant and ear height, and other yield traits in recurrent selection (Shah *et al.* 2006, 2007; Khalil *et al.* 2010). The S₁ families and genotype × location interactions revealed significant impact on earliness, morphological and yield traits in maize (Ali *et al.* 2011). Environments as well as genotypes were significant for days to flowering, plant and ear height, and 100-grain weight; genotype × environment interactions (GEI) were significant for number of plants and ears, ear weight, and grain weight; while GEI means were nonsignificant for days to flowering, plant height, ear height, and 100-grain weight in maize (Tardin *et al.* 2007). Significant differences revealed by testcrosses of maize S₁ lines and genotype by location interactions for maturity, plant and ear height, yield traits, while nonsignificant for anthesis, silking interval (Rahman *et al.* 2015). Significant effect of genotype by environment interactions was recorded on yield contributing traits while evaluating maize testcrosses for yield and its associated traits (Sajjad *et al.* 2016, 2020b).

Flowering is an important stage of growth in maize because it symbolizes maturity and transition from vegetative phase to reproductive phase (Bolanos and Edmeades 1996). The improved population C₂ took fewer days to silking and attained increased plant and ear height compared to C₁ and C₀ populations. In recurrent selection, the selected maize populations were reported with significant improvement in early flowering (Okporie *et al.* 2013; Reis *et al.* 2013). Based upon negative expected responses, decrease in days to tasseling, silking and pollen shedding was observed in the progenies of selected maize S₁ lines (Khalil *et al.* 2010). Though late flowering genotypes were high yielding due to accumulation of comparatively larger quantity of photosynthate during vegetative growth; however, early flowering is still desirable to protect maize crop from various biotic and abiotic stresses. Present results further revealed that C₂ population was simultaneously improved for flowering traits and showed early maturity. Delay in flowering with increase in plant and ear height were reported in S₁ recurrent selection in two maize populations, however, that

delay was manageable (Ruiz-de-Galarreta and Alvarez 2017; Udo *et al.* 2017).

Moderate plant height and central position of the top ear on the maize plant is favourable due to its least vulnerability to lodging which ultimately contribute to good yield (Noor *et al.* 2013; Rahman *et al.* 2015). Very dwarf cultivars have thick canopy, less air and sun light penetration to the lower parts of the plants, causing substantial reduction in grain yield. On the other hand, taller plants are more vulnerable to lodging, so moderate plant stature is desirable. Under recurrent selection, the sub-tropical maize populations revealed nonsignificant variation for plant and ear height (Sohail *et al.* 2018). Maize breeders therefore, seriously consider these two traits to improve the lodging resistance and to reduce yield losses in maize.

Among genotypes and genotype-year-environment interactions, the improved population C₂ showed best performance with enhanced mean values for yield traits, followed by population C₁. Results further authenticated that C₂ genotypes performed better during 2016 at CCRI, followed by 2017 at UAP. However, base population C₀ demonstrated weaker performance during 2016 and 2017 at both locations. Phenotypic superiority of the selected breeding material over the original population revealed increased ear length, kernel rows per ear, kernel index, and grain yield in maize (Sajjad *et al.* 2016, 2020a). Selection for grain yield provided remarkable genetic gains for ears per plot, ear weight, 100-grain weight and grain yield in full-sib families of maize (Cunha *et al.* 2012). Positive selection differential was observed for ear length, kernel rows per ear, 1000-kernel weight and grain yield (Okporie *et al.* 2013). Past studies authenticated that increase in yield components was based on the evaluation of maize S₁ and S₂ selfed families (Berilli *et al.* 2011, 2013; Chen *et al.* 2019). Selected maize S₁ and S₂ populations effectively enhanced the accretion of desirable genes for quantitative traits with significant enhancement in yield attributing traits (Kolawole *et al.* 2017, 2019). Based on the populations C₁ and C₂ performance, simple recurrent selection was found more effective in improving maize populations for grain yield (Horne *et al.* 2016; Khamkoh *et al.* 2019). Results further revealed greater proportion of genetic variation among selected and original maize populations indicated enhanced genetic disparity and efficiency of recurrent selection for improving grain yield simultaneously.

In present studies, the observed responses were far greater than expected for earliness, morphological and yield traits. For earliness, maximum negative responses were reported to be desirable for flowering which confirmed by improvement in selected populations for earliness traits. The cycle-wise and average genetic gain values were significantly negative for days to silking. In comparison, the C₂ populations were observed with greater negative responses than C₁ families for early flowering. For plant and

ear height and grain yield, the observed responses were positive and greater than expected responses in selected populations of cycle-1 and cycle-2. However, for ears per plant and prolificacy, the values of observed responses were negative and less than expected responses in both cycles. For plant height and yield related traits the values for all the genetic gain were significantly positive. Maize full-sib families with direct selection for earliness and yield attributes revealed negative values of genetic gain for flowering while positive for yield related traits (Cunha *et al.* 2012). Based on selection differential, the highest observed and expected responses were recorded for earliness and yield related traits in improved maize populations, however, the responses were negative for earliness traits in maize (Ishaq *et al.* 2014). Badu-Apraku *et al.* (2013) reported varied and encouraging genetic gain per cycle for yield related traits in maize under recurrent selection. However, Carangal *et al.* (1971) reported close resemblance between observed and expected responses with two cycles of S₁ recurrent selection in maize. Present studies authenticated that two cycles of phenotypic selection helped up to some extent in accumulating favourable alleles in the improved maize populations.

Conclusion

Maize improved population C₂ showed improvement in earliness and grain yield over the environments, followed by C₁ population. Base population C₀ recorded with late flowering and minimum grain yield over environments. Overall, the observed responses were greater than expected for majority of the traits in cycle-1 and cycle-2. Greater values of cycle-wise and average genetic gain were recorded in C₂ populations compared to C₁ families for various traits. The selfed progeny recurrent selection was found more effective in improving maize base population for flowering and yield traits.

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Author Contributions

MS, NUK and SG visualized the idea, designed and executed the study; SUK and IHK recorded and analyzed the data; SAK, SA and NA made Tables and illustrations; IT and ZB collected the review and drafted the manuscript; SMK and IH interpreted the results and reviewed the contents. All authors improved the write-up by reading and approved the final version of the manuscript.

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