Full Length Article

Assessment of Maize S_1 and S_2 Lines for Earliness and Yield Traits Developed from Base Population - PSEV3-S_0 Using Recurrent Selection

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Abstract

The recurrent selection system was introduced to enhance the occurrence of promising genes for quantitatively inherited traits and to genetically improve the germplasm for breeding purposes. Maize base population 'PSEV3-S_0' was used to develop the S_1 and S_2 lines through selfed progeny recurrent selection in five consecutive spring and summer crop seasons during 2014 to 2016. During summer 2017, the present research was carried out with objective to assess the performance S_1 and S_2 selfed and selected populations in comparison to base population (PSEV3-S_0) for earliness and yield traits. A partial balanced lattice square design with two replications was used to layout the experiments. The S_1 and S_2 populations revealed significant ($P \leq$ 0.01) differences for all the traits in cycle-1 and cycle-2, respectively. In S_1 and S_2 selected families, a significant increase was observed for plant height, ears per m², ears per plant, kernel rows per ear, and grain yield; however, the days to silking were reduced in both cycles of selection. Heritability (broad sense) values were moderate to high for all the traits in both cycles of selection. In S_1 and S_2 selected populations, the values for selection differential and expected responses were negative for days to silking in cycle-1 and cycle-2. However, for plant height and yield attributes, the selection differential and expected responses estimates were positive and significantly higher in S_1 and S_2 selected families as compared to selfed and base populations. On average, the S_2 selected lines performed better than S_1 for earliness and yield traits. In crux, selfed progeny recurrent selection method was found more efficient in improving the maize original population. © 2020 Friends Science Publishers

Introduction

Maize (*Zea mays* L.) being the highest yielding cereal crop in the world, attained significant importance for countries like Pakistan (Ali *et al*. 2019, 2020). Maize accomplished a greater role in rewarding the demand of generously increasing population which has already exceeded food supplies (Sajjad *et al*. 2016, 2020a, b). Maize has a wide range of uses and its grain contains starch (72%), vitamins A and B (3 to 5%), proteins (10%), oil (4.8%), fiber (5.8%), sugar (3.0%) and ash (1.7%) (Chaudhary 1983). 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 (Kumar *et al*. 2013). Ethanol obtained from maize can be used as a biomass fuel. Stigmas from female corn flowers, known as corn silk, can be used as herbal supplements. Maize is largely used as the main source of calories in animal feeding and feed formulation. Maize gives the highest conversion of a dry substance to meat, milk and eggs compared to other cereal grains.

Recurrent selection is a cyclical method of germplasm advancement which does not lead directly to the release of cultivars in maize and other crops. In recurrent selection, three basic steps are involved *i.e*., inter-mating, assessment, and selection (Darrah *et al*. 2019; Sheikh *et al*. 2019). Recurrent selection is used for traits that are polygenically inherited. Polygenic inheritance occurs when many genes, each with a small effect, control the expression of a trait. Recurrent selection is designed to

improve the frequency of favorable alleles in a population for quantitative traits in maize (Andorf *et al.* 2019) and further breeding efforts are required to release a cultivar from an improved maize population (Hallauer and Carena 2012; Kolawole *et al.* 2017).

The recurrent selection includes many types *i.e.*, S_0, S_1, S_2, full-sib, half-sib, ear-to-row, reciprocal recurrent, and reciprocal full-sib in maize (Sohail *et al.* 2018; Khamkoh *et al.* 2019). These procedures vary in the progeny which are evaluated through field testing and are recombined to shape the next cycle. In the methods involving selfing, selfed progenies are also evaluated. With S_0 plant selection (*vs.* progeny for S_1 and S_2), selection must be made before flowering and selected plants are recombined, allowing one cycle of selection to be completed per season. The S_0 plant selection is considerably effective for simply inherited traits of maize (Noor *et al.* 2013).

The S_1 and S_2 progeny recurrent selections are admirable choices for acquiring improvement within maize populations, particularly improving grain yield (Badu-Apraku *et al.* 2013). Selection in cycle-2 produced maximum grain yield with significant hereditary gain and concluded that S_1 recurrent selection was found more effective for innate improvement in maize for yield traits (Khan *et al.* 2018; Chen *et al.* 2019). A significant decrease was recorded for morphological traits while an increase in yield traits with S_1 recurrent selection in maize (Horne *et al.* 2016). Maize populations in selection cycle-2 produced maximum grain yield with significant genetic gain and concluded that S_1 recurrent selection has been found effective for genetic improvement in maize (Sajjad *et al.* 2016).

Maize breeders are mostly interested in generating heritable variations in the base population for further selection (Ali *et al.* 2017; Sampoux *et al.* 2020). However, the observed variations in the population might be due to genotypic and environmental factors and genotype by environment interactions. Genotypic variance is heritable and durable while environmental variance is non-assignable to the next generation and oscillates with the environment in maize populations (Ali 2015; Annor *et al.* 2019; Cobb *et al.* 2019). Heritability has a key role in the inheritance of the traits and also to partition the total variance into genetic and environmental components in maize germplasm (Ullah *et al.* 2013; Rahman *et al.* 2015). Estimates of genetic variability and heritability are of greater importance for the maize breeders and used as an indication of selection pressure in the segregating populations, and to gauge that the phenotypic change is heritable or not to the next generation (Ali *et al.* 2011a, b). High heritability showed that the trait of interest was least affected by the environment and will contribute to the overall improvement of the original population in maize (Noor *et al.* 2013; Ishaq *et al.* 2014).

Previous findings revealed that S_1 progeny recurrent selection was the most effective method to simultaneously improve earliness, morphological and yield traits in maize (Sajjad *et al.* 2016; Sajjad 2018). Therefore, the current study was designed with the objectives to; a) assess the performance of maize population under selfed progeny selection, b) evaluate the responses of S_1 and S_2 lines in cycle-1 cycle-2, respectively and c) determine a better approach for improvement of maize base population 'PSEV3' for earliness and grain yield traits.

Materials and Methods

Maize source population

Maize 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). Maize base population 'PSEV3 - S_0' was used to develop the S_1 and S_2 selfed and selected lines through selfed progeny recurrent selection for three years in five consecutive crop seasons (during spring and summer - 2014 and 2015 and spring - 2016) at Cereal Crops Research Institute (CCRI), - Nowshera, Pakistan (Table 1). The improved populations (S_1 and S_2 lines) in comparison with the original population (PSEV3-S_0) and selfed populations were evaluated during the summer season 2017 at the CCRI, Nowshera, Pakistan.

Development of maize breeding material

To develop S_1 lines, the source population PSEV3 was sown in spring season 2014 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 the 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, dried, shelled, and labelled.

Evaluation of maize S_1 lines

Half of the seed of 255 selected S_1 progenies and control/base population (S_0) was evaluated in a 16×16 partially balanced square lattice design with two replications during summer season 2014 at CCRI, Nowshera, Pakistan. The remnant seed was kept for later use in recombining the selected S_1 lines to constitute a source population for further field evaluation (Hallauer and Carena 2012). A plot size of two rows, 5 meters long, and 0.75 m apart was maintained. All the recommended inputs and cultural practices were equally applied during the crop season.

Recombination of maize selected S_1 progenies

Twenty-five best S_1 lines were selected based on grain yield and early maturity. The half seed of the selected lines was

sown (1:2 rows as male and female, respectively) for recombination during spring season 2015. 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 C_1 population for cycle comparison.

Development of maize S_2 lines

During the same spring season 2015, remnant seed from the selected S_1 lines was sown in two rows having 3 m length with row and plant spacing of 75 and 25 cm, respectively. Four hundred plants were selfed in the same way as mentioned above. All the recommended inputs and cultural practices were equally applied during the crop season.

Evaluation of maize S_2 progeny

One hundred and sixty-nine S_2 lines were evaluated in 13×13 partially balanced square lattice design with two replications during summer 2015 at CCRI, Nowshera. The same procedure was followed for evaluation of S_2 progenies as mentioned earlier for S_1 progenies. All the recommended inputs and standard cultural practices were equally applied.

Recombination of maize S_2 progenies

Seventeen selected S_2 progenies were grown in isolation during spring season 2016 at CCRI, Nowshera, Pakistan. Seeds from the recombined S_2 lines constituted the C_2 population.

Evaluation of S_1 and S_2 lines

The improved populations (S_1 and S_2 lines) in comparison with the original population (PSEV3-S_0) and selfed populations were evaluated during the summer season 2017 at the CCRI, Nowshera, Pakistan.

Crop husbandry

Maize is a shallow-rooted crop, and it requires fine good tilth and well-prepared soil for successful germination and growth of the 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), full 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 one month after germination. Weeds were controlled with Primextra Gold at 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 controlled by using Confidor (WP-60) at the rate of 50 g per 10 kg of maize seed through seed treatment before planting. After one month of germination, Furadon (3%) granules at 20 kg ha^{-1} were applied in the whirls. The crop was irrigated at the proper interval when required, until one week before harvesting. All the entries were equally treated in the field during the cropping season.

Data recorded

Data were recorded on ten competitive plants in each sub-plot for the traits *i.e.*, days to silking, plant height (cm), ears per m^2, ears per plant, kernel rows per ear and grain yield (kg ha). To determine grain yield, grain weight per plot was obtained and converted to kg per ha at 15% moisture content using the following relationship (Carangal *et al.* 1971).

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

Where MC: Moisture content (%) in grains at harvest, FEW: Fresh ear weight (kg) at harvest, Shelling coefficient: 0.80.

Statistical analysis

All the recorded data on S_1 and S_2 progeny testing trials were subjected to analysis of variance appropriate for lattice square design using ANOVALAT procedure of MstatC program.
The complete statistical model used was:

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

Where,
$Y_{il(j)}$: the observation of the genotype i (i = 1,…, v = k^2), in the block l (l = 1,…, k) of the replication j (j = 1,..., m)
μ: the constant common to all the observations
t_i: the effect of the treatment I
r_ji: the effect of the replication j
$(b/r)_{l(j)}$: the effect of the block l of the replication j
$e_{il(j)}$: the error associated to the observation Yil(j).
        where eil(j)~N(0,s), independent.
        Expected mean squares were calculated through a lattice square (partially balanced) design for both cycles of selection.

Heritability (broad sense) estimation

Broad sense heritability (h^2_{bs}) was estimated according to Allard (1960) as under:

$$\sigma^2 e: M_1$$

$$\sigma^2 g: (M_2 - M_1)/r$$

$$h^2_{(bs)}: \sigma^2 g / (\sigma^2 e + \sigma^2 g)$$

Where $\sigma^2 e$: environmental variance, $\sigma^2 g$: genetic variance, $h^2_{(bs)}$: heritability (broad sense).

Selection differential

Selection differential (S) was computed as:

$$S: \mu_s - \mu$$

Where μ_s: means for selected S_1 and S_2 lines in cycles-1 and cycle-2, respectively, μ: selfed populations (S_1 and S_2) of the first and second selection cycles before selection

Estimation of expected response

Expected response to selection (R_e) was estimated as follows:

$$R_e: S \times h^2 (bs)$$

Where S: selection differential, h^2 (bs): heritability (broad sense).

Results

According to the analysis of variance, the S_1-unadjusted and adjusted lines showed significant ($P \leq 0.01$) differences for all the studied traits in cycle-1 (Table 2). Similarly, the S_2-unadjusted and adjusted populations also revealed significant ($P \leq 0.01$) variations for all the variables in cycle-2 (Table 3). The base population (S_0), S_1 and S_2 selfed populations, and S_1 and S_2 selected families revealed greater genetic variability under the existing environment. Such type of genetic variability is direly needed by breeders which can be used for further improvement in maize through intensive selection. However, some of the traits were recorded with low values of coefficient of variation (CV%) (Table 2 and 3). By using Latin Square and Factorial Designs in the field experiments, there is an advantage that the experimental error is reduced because it removes row and column variations from the error which eventually reduced the coefficient of variation (CV%) (Taye *et al.* 2002; Kozak *et al.* 2013).

Heritability (broad sense) and selection differential were determined for all the traits in both selection cycles to formulate the magnitude of genetic variability among S_1 and S_2 populations. For heritability (bs) and selection differential, different trends were observed among the S_1 and S_2 populations for various traits in selection cycle-1 and cycle-2. The trait-wise results are discussed herein.

Days to silking

Days to silking reduced from 57.01 (base population - S_0) to 52.85 days (S_2 selected populations) and showed a 7.30% reduction with succeeding selection cycles (Table 4). On average, in cycle-1 the minimum days to silking were observed for S_1 selected populations (54.00 days), followed by S_1 selfed families (55.43 days), while the maximum days were utilized by base population - S_0 (57.01 days). Similarly, in cycle-2 the least days to silking were recorded in S_2 selected families (52.85 days), followed by S_2 selfed

populations (53.85 days), whereas the highest number of days was recorded in base population S_0 (55.74 days). Overall, the S_2 selected families took lesser days to silking (52.85 days) as compared to S_1 selected lines (54.00 days) which is very encouraging and needs further exploitation. The highest and same values of broad-sense heritability (0.83) were observed in both cycles of selection (Table 5). The highest negative value of selection differential was recorded in cycle-2 (-1.89 days) as compared to cycle-1 (-1.43 days), with corresponding negative expected responses (-0.83 and -1.19 days) in cycle-2 and cycle-1, respectively and showed a reduction in days to silking in the succeeding selection cycle (Table 6).

Plant height

Plant height reduced from 157 (S_0) to 149 cm (S_2 selected populations) and showed a reduction of 5.10% with succeeding selection cycle (Table 4). In cycle-1, the maximum plant height was observed in S_1 selected families (160 cm), followed by base population S_0 (157 cm) and S_1 selfed population (149 cm). In cycle-2, the utmost plant height was recorded in S_2 selected families (149 cm), followed by base population S_0 (146 cm) and S_2 selfed population (126 cm). By comparing the performance of the S_1 and S_2 selected families, the minimum plant height was observed in S_2 selected (149 cm) as compared to S_1 selected populations (160 cm) with succeeding generation. However, in selfed populations of both cycles the reduction in plant stature ranged from 149 (S_1 selfed) to 126 cm (S_2 selfed). High magnitudes of heritability (broad sense) were observed for plant height in both selection cycles (Table 5). Heritability (bs) was the highest in cycle-2 (0.86), followed by cycle-1 (0.83). Likewise, the selection differential also showed an increasing trend in plant height with a succeeding selection cycle (ranging from 11.00 to 23.00 cm) in cycle-1 and cycle-2, respectively (Table 6). Similarly, comparatively larger predicted gains were observed in cycle-2 (19.78 cm) as compared to cycle-1 (9.13 cm) for the said trait.

Ears per square meter

Ears per square meter were increased by 8.25% from 4.85 (base population) to 5.25 (S_2 selected population) while reduced by 3.75% with selfing from 4.53 to 4.36, respectively in cycle-1 and cycle-2 populations (Table 4). Ears per square meter varied with selection cycles; however, in cycle-1 the maximum ears per square meter were recorded for S_1 selected families (4.96), followed by base population S_0 (4.85) and S_1 selfed population (4.53). A similar trend was also observed in cycle-2, and the highest number of ears per square meter was recorded in S_2 selected families (5.25), followed by base population S_0 (4.80) and S_2 selfed population (4.36). On average, maximum ears per square meter were noted in S_2 selected lines (5.25) in cycle-2 as compared to S_1 selected families (4.96) in cycle-1.

Table 1: Genotypes with various characteristics used in the study

Populations	Source	Type	Kernel shape / Colour	Plant height	Maturity	Pedigree
PSEV3C$_0$	CCRI	OPP	Flint white	Medium	Medium	Cross between Azam and CHSW (Single cross hybrid, white kernels with late maturity from CIMMYT)
S$_1$ lines	CCRI	SP	Flint white	Short	Medium	Derived from selfing PSEV3-C$_0$
S$_2$ lines	CCRI	SP	Flint white	Short	Medium	Derived from selfing S$_1$ lines

CCRI: Cereal Crops Research Institute (CCRI), Nowshera, Pakistan, OPP: Open pollinated population, SP: Selfed population, PSEV3-C$_0$: Base population (C$_0$)

Table 2: Mean squares for earliness and yield traits in maize PSEV3 - S$_1$ lines

Source of variation	d.f.	Days to Silking	Plant height	Ears m^{-2}	Ears plant^{-1}	Kernel rows ear^{-1}	Grain yield
Replications	1	3.78	1591.54	7.75	0.109	0.03	142174.45
S$_1$ lines-unadjusted	255	7.98**	418.38**	1.15**	0.036**	1.26**	2599062.37**
S$_1$ lines-adjusted	255	7.62**	410.59**	1.15**	0.036**	-	-
Blocks	30	3.51	88.41	0.47	0.016	0.11	214556.64
Error effective	225	1.19	70.02	0.34	0.015	-	-
RCBD 255	255	1.39	70.56	0.35	0.015	0.16	218485.73
Intra - blocks	225	1.10	68.18	0.33	0.014	0.16	219009.61
CV (%)		1.91¥	5.63	12.93	12.986	3.02	11.40

¥ - In Latin Square design, the experimental error is reduced because it removes row and column variations from the error which eventually reduced the coefficient of variation (CV%) (Taye *et al.* 2002; Kozak *et al.* 2013)

Table 3: Mean squares for earliness and yield traits in maize PSEV3 - S$_2$ lines

Source of variation	d.f.	Days to Silking	Plant height	Ears m^{-2}	Ears plant^{-1}	Kernel rows ear^{-1}	Grain yield
Replications	1	25.59	1.48	1.19	0.004	2.79	2844533.09
S$_2$ lines-unadjusted	168	10.18**	756.61**	1.23**	0.033**	3.87**	4216193.00**
S$_2$ lines-adjusted	168	9.93**	655.84**	1.22**	0.032**	-	4121578.52**
Blocks	24	2.07	286.01	0.54	0.023	0.47	1351808.98
Error effective	144	1.75	90.47	0.49	0.018	-	641809.54
RCBD 168	168	1.76	111.24	0.49	0.019	0.53	702460.28
Intra - blocks	144	1.71	82.11	0.48	0.018	0.54	594235.50
CV (%)		2.38¥	7.57	16.01	14.357	5.98	22.62

¥ - In Latin Square design, the experimental error is reduced because it removes row and column variations from the error which eventually reduced the coefficient of variation (CV%) (Taye *et al.* 2002; Kozak *et al.* 2013)

Table 4: Mean performance of maize base (PSEV3-S$_0$ - as check), selfed (S$_1$, S$_2$), and selected (S$_1$s, S$_2$s) populations for various traits

Traits	Cycle-1			Cycle-2		
	Base population (S$_0$)	Selfed population (S$_1$)	Selected families (S$_1$s)	Base population (S$_0$)	Selfed population (S$_2$)	Selected families (S$_2$s)
Days to silking (days)	57.01	55.43	54.00	55.74	53.85	52.85
Plant height (cm)	157	149	160	146	126	149
Ears per m^2 (#)	4.85	4.53	4.96	4.80	4.36	5.25
Ears per plant (#)	0.97	0.93	0.96	0.98	0.95	1.00
Kernel rows ear^{-1} (#)	14.00	13.19	15.03	13.00	12.15	15.50
Grain yield (kg ha^{-1})	5638	4102	6175	5525	3542	6217

Table 5: Genetic components of variance in maize PSEV3 - selfed and selected populations for various traits

Traits	Cycle-1 (S$_1$ lines)				Cycle-2 (S$_2$ lines)			
	σ^2g	Σ^2e	Σ^2p	h^2 (bs)	σ^2g	σ^2e	σ^2p	h^2 (bs)
Days to silking	3.30	1.39	3.99	0.83	4.22	1.76	5.10	0.83
Plant height	173.91	70.56	209.19	0.83	329.75	111.24	385.37	0.86
Ears per m^2	0.40	0.35	0.58	0.70	0.37	0.49	0.62	0.60
Ears per plant	0.01	0.02	0.02	0.58	0.01	0.019	0.02	0.56
Kernel rows ear^{-1}	0.55	0.16	0.63	0.87	0.70	0.53	0.96	0.72
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 (bs): broad sense heritability

High broad-sense heritability values were recorded for ears per square meter in both cycles (Table 5). However, comparatively the highest heritability was recorded in cycle-1 (0.70) as compared to cycle-2 (0.60). The selection differential was also increased in the S$_2$ population (0.89) as compared to S$_1$ families (0.43) in both cycles (Table 6). The moderate and positive genetic gains (0.53 and 0.31) were also observed for the said trait in cycle-2 and cycle-1, respectively.

Ears per plant

For ears per plant, the S$_2$ selfed families (0.95) as compared to S$_1$ selfed populations (0.93) increased by 2.15%,

Table 6: Selection differential and expected response in maize S$_1$ and S$_2$ families for various traits

Traits	Selection cycle-1		Selection cycle-2	
	Selection differential (S)	Expected response (Re)	Selection differential (S)	Expected response (Re)
Days to silking (days)	-1.43	-1.19	-1.89	-0.83
Plant height (cm)	11.00	9.13	23.00	19.78
Ears per m^2 (#)	0.43	0.31	0.89	0.53
Ears per plant (#)	0.03	0.02	0.05	0.03
Kernel rows ear^{-1} (#)	1.84	1.60	3.35	2.41
Grain yield (kg ha^{-1})	2073.00	1907.16	2675.00	2220.25

S: Selection differential, R$_e$: Expected response (h^2*S)

while S$_2$ selected population (1.00) as compared to base populations (0.97) increased by 3.09% in both selection cycles (Table 4). In cycle-1, the values for ears per plant were comparable in S$_0$, S$_1$ selfed and S$_1$ selected populations, however, numerically the highest number of ears per plant were recorded in the base population (0.97), followed by S$_1$ selected families (0.96) and S$_1$ selfed population (0.93). In cycle-2, the maximum ears per plant were recorded in S$_2$ selected families (1.00), followed by base population (0.98) and S$_2$ selfed population (0.95). By comparing the performance of selected families in both cycles, the highest number of ears per plant was recorded in S$_2$ selected (1.00) as compared to the S$_1$ selected populations (0.96). Moderate estimates of heritability (bs) were recorded for ears per plant during both cycles of selection (Table 5). Comparatively the heritability (broad sense) was highest during cycle-1 (0.58) as compared to cycle-2 (0.56). For ears per plant, the selection differential value was the highest in cycle-2 (0.05) as compared to cycle-1 (0.03), while the expected response was also more in cycle-2 (0.03) than cycle-1 (0.02), respectively (Table 6).

Kernel rows per ear

Kernel rows per ear were reduced by 7.88% with selfing from 13.19 (S$_1$ selfed) to 12.15 (S$_2$ selfed) in cycle-1 and cycle-2, respectively (Table 4). The S$_2$ selected populations (15.50) compared to the base population - S$_0$ (14.00) showed an increase of 10.71%. However, in cycle-1 the maximum kernel rows per ear were recorded for S$_1$ selected families (15.03), followed by base population S$_0$ (14.00) and S$_1$ selfed population (13.19). Similarly, in cycle-2 the highest kernel rows per ear were also noted for S$_2$ selected lines (15.50), followed by the base population S$_0$ (13.00) while minimum in S$_2$ selfed population (12.15). In S$_2$ selected families (15.50), the kernel rows per ear were increased as compared to S$_1$ selected families (15.03). High heritability (bs) values were recorded for kernel rows per ear in both cycles of selection (Table 5). However, in cycle-1 the heritability (0.87) was higher as compared to cycle-2 (0.72). By comparing the selection differential in both cycles, the selection differential was significantly increased in cycle-2 (3.35) as compared to cycle-1 (1.84) for kernel rows per ear (Table 6). Similarly, positive and enhanced expected genetic gain values (2.41 and 1.60) were noted in cycle-2 and cycle-1, respectively for the said trait.

Grain yield

Grain yield reduced by 13.63% with selfing from 4102 (S$_1$ selfed) to 3542 kg ha^{-1} (S$_2$ selfed), while S$_2$ selected populations (6217 kg ha^{-1}) compared to S$_0$ (5638 kg ha^{-1}) showed an increase of 10.27% in the succeeding selection cycles (Table 4). In cycle-1, the highest grain yield was produced by S$_1$ selected lines (6175 kg ha^{-1}), followed by base population S$_0$ (5638 kg ha^{-1}) and S$_1$ selfed population (4102 kg ha^{-1}). Similarly, in cycle-2 the highest grain yield was obtained in S$_2$ selected populations (6217 kg ha^{-1}), followed by base population S$_0$ (5525 kg ha^{-1}) and S$_2$ selfed families (3542 kg ha^{-1}). On average, the S$_2$ selected families (6217 kg ha^{-1}) revealed higher grain yield than S$_1$ selected families (6175 kg ha^{-1}) which showed improvement through selection in succeeding generations. A higher magnitude of broad sense heritabilities was observed for grain yield in both cycles of selection (Table 5). However, comparatively, the maximum heritability was observed in cycle-1 (0.92) as compared to cycle-2 (0.83). Likewise, the highest values of selection differential and expected genetic gains were observed in both cycles of selection, ranging from 2073.00 to 2675.00 kg ha^{-1} and 1907.16 to 2220.25 kg ha^{-1} in cycle-1 and cycle-2, respectively (Table 6).

Discussion

Recurrent selection has been contentedly used for evaluating S$_1$ lines through mean performance, heritability, and genetic gain from selection and improvement of maize populations (Ali 2015; Kolawole *et al*. 2017; Sajjad *et al*. 2020a, b). In the present study, maize populations (S$_0$, S$_1$ and S$_2$) derived from the base population - PSEV3, revealed highly significant differences for earliness, morphological, and yield traits in selection cycle-1 and cycle-2. These populations revealed a greater proportion of genetic variation and prospective for recurrent selection to improve their agronomic traits and grain yield. Based on these findings, it can be concluded that one of the main objectives of recurrent selection has been achieved, *i.e.*, the genetic variability within population has been maintained at adequate level, while the variability between populations has enhanced over succeeding cycles of selection which contributing stability in the breeding program. Recurrent selection is enhancing the frequency of favorable genes through regular cycles of selection along with sufficient

genetic variation in maize families for their improvement (Kolawole *et al.* 2017; Sampoux *et al.* 2020). In two cycles of S_1 recurrent selection, the population revealed positive responses for earliness, ear traits, and other yield-related traits in maize (Khalil *et al.* 2010; Khan *et al.* 2018). Past findings revealed that after selection, the genetic variance within and between the maize populations amplified to a significant level in the succeeding cycles of recurrent selection (Berilli *et al.* 2011; Cunha *et al.* 2012). Significant variations were observed among the S_1 lines for flowering, plant and ear height, ear length, kernel rows per ear, 1000-kernel weight, and grain yield in maize (Ahmad *et al.* 2010; Berilli *et al.* 2013; Annor *et al.* 2019). Significant improvement was persuaded in maize populations through six cycles of S_1 recurrent selection with increased grain yield and lodging resistance (Chen *et al.* 2019).

Crop production is influenced by many factors including phenological traits. In maize, the flowering time like tasseling, silking, pollen shedding, and anthesis-silking interval contributes to physiological maturity. In the present study, the S_2 selected families took less days to silking than S_1 and S_2 selfed and base populations, and tending to earliness by showing improvement in early maturity. Past studies revealed that tasseling and silking time had a positive impact on grain yield followed by ear height and flag leaf area in maize (Ahmad *et al.* 2010). Maize populations revealed significant differences for days to tasseling and silking; however, selected S_1 lines showed less days to flowering compared to selfed populations (Khalil *et al.* 2010; Sohail *et al.* 2018; Sheikh *et al.* 2019). With marginal differences and the same number of days to tasseling, silking, and pollen shedding were recorded in selected and base populations in maize (Sajjad *et al.* 2016). However, some studies reported that S_1 selected lines took more days than original population for earliness traits with positive selection differential exercised in improving population mean in maize (Ali *et al.* 2011a, b).

In plant architectural traits (plant and ear height), the least increase is manageable and to protect the crop from lodging. In present studies, within each cycle of selection, the selected populations showed increased plant height compared to selfed and base populations in cycle-1 and cycle-2. On average, with succeeding cycles, the S_2 selected families had the lowest mean values for morphological traits compared to S_1 which are desirable from breeding point of view for population improvement. Significant differences were observed in maize S_1 and S_2 families for plant and ear height; however, on average the selected lines attained least plant and ear height than selfed and original maize populations (Khalil *et al.* 2010). For plant and ear height, the mean values of the S_1 selected populations were higher than the population mean with positive values of selection differential in maize (Ahmad *et al.* 2010). Significant genetic variability was reported among cyclical populations for morphological traits, and maize populations with

moderate plant and ear height were found desirable because of their less exposure to lodging and ultimately contribute to good yield (Noor *et al.* 2013; Ullah *et al.* 2013; Khamkoh *et al.* 2019).

For yield traits (ears per m^2, ears per plant and kernel rows per ear) and grain yield, the increased mean values were observed with significant improvement in S_1 and S_2 selected families followed by original and S_1 selfed populations in both cycles. However, a significant increase was shown by S_2 selected families than S_1 for yield traits. Present results further revealed greater genetic variation within and between maize populations and the genetic gain made through two cycles of selection resulting in significant improvement in yield traits. This improvement might be due to accumulation of favorable genes in the selected versions of maize populations. Recurrent selection effectively enhanced the accretion of desirable genes for quantitative traits with significant improvement in maize improved populations (Kolawole *et al.* 2017). Selection in cycle-2 provoked maximum grain yield with significant genetic gain and concluded that S_1 recurrent selection has been found efficient for genetic improvement in maize (Ali *et al.* 2018, 2019; Khan *et al.* 2018). Current results also revealed that in improved population C_2 the increased grain yield was associated with early flowering and maturity. Past investigations also reported significant response in maize S_1 populations with a positive association between earliness and yield traits in maize (Khamkoh *et al.* 2019). As compared to selfed and base populations, the maize selected populations showed increased values for yield related traits (Sajjad 2018; Sajjad *et al.* 2020a, b). In breeding programs, the appreciated progress mainly depends upon precise identification of promising populations for the specific environment and the precision with which the studies are conducted.

Genetic variability and heritability among maize populations provides valuable information and assists the breeder to predict the behavior of a trait in succeeding generations (Ali *et al.* 2012a, b; Kashiani *et al.* 2014). Heritability (broad sense) values were moderate to high in S_1 and S_2 selfed families for earliness, morphological and yield traits. Present results highlighted the lower impact of the environment compared to genetic variances in S_1 and S_2 selection cycles, indicating sufficient genetic variability and suggesting further improvement. The highest genetic variability and heritability were observed for earliness traits which assured prospects for future improvement in S_1 populations of maize (Khalil *et al.* 2010; Ishaq *et al.* 2014). High broad-sense heritability was recorded for plant and ear height and yield components in maize selfed progenies (Noor *et al.* 2013; Ullah *et al.* 2013; Annor *et al.* 2019). Past studies on S_1 recurrent selection reported high heritability and selection response for plant and ear height, ear length, kernel rows per ear, and grain yield in maize (Rahman *et al.* 2015; Cobb *et al.* 2019). However, some other studies reported reduced values of genetic variances and heritability

for earliness and yield traits in advanced cycles of selection in maize (Badu-Apraku *et al.* 2013).

Selection differential is the deviation of selected S_1 and S_2 families from their selfed populations, and the change occurred in the population mean is the response to selection. In present studies, the higher negative values of selection differential were reported for days to silking in S_2 selected populations than S_1 lines which help in early maturity of the improved maize populations. Selected S_1 and S_2 lines were observed with smaller mean values than the population mean, resulting in negative values of selection differential for earliness traits in maize (Ali *et al.* 2011a, b; Kolawole *et al.* 2017). For plant height and yield traits, the selection differential values were positive and significantly high with less inbreeding depression which also confirmed improvement in the selected populations through succeeding generations. High heritability and index of variation estimates were exhibited by maize S_1 and S_2 populations for yield traits (Sajjad *et al.* 2016; Sajjad 2018). High heritability and selection response with significant improvement in grain yield suggested that S_1 recurrent selection was found quite effective in improving maize populations (Ahmad *et al.* 2010; Sajjad *et al.* 2020a, b). Therefore, the improvement in present maize selected populations through succeeding generations was dependent both on the genetic variability and heritability in the population which determines the extent of progress through recurrent selection.

Conclusion

The S_1 and S_2 selected population revealed significant decrease for days to silking while increase for yield related traits. Heritability (broad sense) was moderate to high for all the traits in both cycles of selection. The selection differential and expected responses were significantly negative for days to silking while positive for yield related traits in S_2 selected populations as compared to S_1 lines. Overall, the selfed progeny recurrent selection method was found more effective in improving the maize base population 'PSEV3' for earliness and yield traits.

Author Contributions

MS, NUK and SG designed and executed the study; SUK and SA recorded and analyzed the data; SAK and NA made Tables and illustrations; IT and ZB collected the review and drafted the manuscript; IH and SMK 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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