

FULL-SIB VERSUS S_1 FAMILY SELECTION METHOD IN IMPROVEMENT OF A TROPICAL QUALITY PROTEIN MAIZE (QPM) POPULATION

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Abstract

Different selection procedures differ in effectiveness when applied for improvement of the same population. A study was conducted at Ilora and Ikenne out-stations of the Institute of Agricultural Research and Training, (IAR&T), Moor plantation, to assess the effectiveness of full-sib (FS) and S_1 family in improving a quality protein maize population (QPM), ART/98/SW6-OB. One hundred S_1 and 96 FS were generated from the maize population and evaluated in 2015 and 2016. The experimental design was alpha lattice design in three replications. Data were collected on agronomic and yield traits. Genetic variance and heritability were estimated from combined analysis of variance. Genetic gains were determined and correlation analysis was also carried out. Means were significantly higher in FS for plant height and grain yield with wide ranges. Significant mean square of entry was recorded in both family types for most of the traits studied. Correlation among traits followed similar trend in both families. Heritability and genetic gains were higher in FS for number of ears per plant and grain yield, while higher increase would be recorded with selection for plant height and days to anthesis in S_1 . Full-sib family would be better in improving ART/98/SW6-OB for yield and related traits.

Keywords: Full-sib family, Quality protein maize, Genetic gains, Recurrent selection, S_1 family

Running title: Full-sib versus S_1 selection in QPM population.

Introduction

Recurrent selection has been widely used for maize inter and intra-population improvement. The most common recurrent selection methods for maize intra-population improvement are classified as mass (phenotypic) selection and family selection. Family selection methods are Half-sib family selection (HS), Full-sib family selection (FS), Selfed or inbred progeny selection (S_1 or S_2) and Combined selection (Hallauer *et al.*, 2010). Reports from earlier workers (Burton *et al.*, 1971; Genter, 1973) indicated that methods which are effective in improving one population may not be effective for another. Also, different selection procedures differ in effectiveness when applied for the improvement of the same population (Adeyemo, 1986). Therefore, information on the magnitude of various components of genetic variation for different family selection procedures (Obilana and Hallauer, 1974; Subandi and Compton, 1974), effectiveness and ease of generating the family, the cost and time in terms of number of generations per cycle (Ajala *et al.*, 2009), would help in identifying the best selection method for improving a specific maize population under given circumstances.

Dhillon and Khehra (1989) and Ajala *et al.* (2007) proposed modifications to the S_1 and full-sib recurrent selection procedures respectively which allow a cycle

to be completed in two seasons instead of three. Tanner and Smith (1987) reported that selection based on S_1 was expected to utilize additive genetic variance. However, heritability estimates differed according to population (genetic variance) traits, selection methods and environmental conditions. The reports of Walters *et al.* (1991), Mahmoud *et al.* (1999), El-Morshidy *et al.* (2002), Shah *et al.* (2007), and Saini and Malhi (2001) indicated that S_1 family selection was more effective than full-sib and half-sib selection in improving populations. Ajala *et al.* (2009) concluded that the best selection method for yield improvement that would increase plant height the least would be FS family selection. El-Seidy *et al.* (2013) however reported that genetic gains were conflicting among different studied traits for HS and S_1 selection methods. Peng *et al.* (2007) studied three recurrent selection methods: modified S_1 family selection, modified S_1 -HS and Modified Half-sib reciprocal recurrent selection (MHRRS). They demonstrated that the three recurrent methods were effective for increasing grain yield in test crosses and improvement of general combining ability in maize populations.

Maize variety, ART/98/SW6-OB, is a Quality Protein Maize (QPM) population developed by the Institute of Agricultural Research and Training. It is an intermediate maturing, white-grained maize now being

promoted among farmers in southern part of Nigeria. QPM varieties are alternative maize varieties to alleviate problem of malnutrition especially in infants, due to the presence of two essential amino acids- lysine and tryptophan, which are deficient in the normal maize. This study was conducted to determine the amount of genetic variation present in the maize population, ART/98/SW6-OB, for grain yield by using FS and S_1 families, and to use this information in determining the best selection method to improve the maize population.

Materials and Methods

Generation of Families

The maize population was planted and about 200 individual plants were self-pollinated to produce S_1 family. Out of these, 100 S_1 individuals were selected for evaluation for the S_1 family. Full-sib family was developed using NCI mating scheme of Comstock and Robinson, (1952). One hundred and twenty-five S_0 individuals were selected from the population. Twenty-five S_0 individuals were designated as males and the remaining were females. Each male was mated to four females each to generate a total of 100 full-sib individuals. A group was lost due to poor flower synchrony, thus leaving a total of 96 FS families for evaluation.

Evaluation of Families

A total of 100 S_1 families and 96 FS families were evaluated. The evaluation was conducted at Ilora, in derived savanna, and at Ikenne, in humid rain forest, in southwestern Nigeria in 2015 and 2016 cropping seasons. The experiment was laid out in a 10 x 10 (for S_1) and 12 x 8 (for FS) alpha lattice design in three replications. A plot was a two-row plot of 2m long. Plant spacing was 0.75 m space between rows and 0.25 m apart within rows. Thinning was done three weeks after planting to one plant per hill to have a plant population of 53,333 plants/ha. N.P.K fertilizer was applied at 2 weeks, while urea was applied at 6 weeks after planting at rate of 90kgN/ha. Fields were kept weed-free throughout the trials.

Data Collection

Days to 50% anthesis and silking were recorded in each of the plot as the number of days from sowing to when half of the plants in a plot shed pollen and emerge silks, respectively. Anthesis-silking interval (ASI) computed as the interval in number of days between silking and anthesis. Plant and ear height were measured in centimeters as the distance from the base of the plant to the base of the tassel, and node bearing the first ear respectively. Root lodging was taken at maturity as number of plants that made angle 90° to the ground level or laid flat on the ground expressed as percentage of number of plant stands per plot. The number of ears per plant (EPP) was estimated as proportion of total number of ears divided by the number of harvested plants. Few ears were shelled from each plot to determine Percentage moisture. Grain yield adjusted to 14% moisture was estimated from field weight at 80% shelling percentage.

Statistical Analyses

Mean, CV and ranges were estimated. Combined analyses of variance (ANOVA) was performed separately for S_1 and FS family using a random model in SAS version 9.2 ([SAS Institute, 2009](#)). From ANOVA, genetic variances and broad-sense heritability were estimated as described by Hallauer and Miranda (1988). The expected response from selection (Gs) was also computed according to Hallauer and Miranda (1988) as:

$$Gs = k \sigma^2_g / \sigma_p$$

Where σ_p is the square root of phenotypic variance, and k is selection intensity (10% selection intensity was used). Gains were expressed as percentage of means as gains per cycle. Pearson's correlation analysis was done to determine the relationship among measured traits.

Results

Mean Performance of S_1 And Fs Families for the Traits Measured

Mean performance of the two family types is as shown in Table 1. Mean days to 50% pollen shed and silking, and ASI were higher in S_1 than in FS. Plant and ear height were however higher

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Table 1. Mean ± SE, range and coefficient of variation of the traits measured in S_i and FS family of ART/98/SW6-OB at Ilora and Ikenne in 2015 and 2016.

Traits	Family	Mean±SE	Range	CV (%)
Days to 50% pollen shed	S _i	58.82±0.11	49 -75	2.37
	FS	57.32±0.09	50- 69	5.69
Days to 50% silking	S _i	61.19±0.12	50 - 79	6.17
	FS	59.79±0.11	51 -72	3.12
ASI	S _i	2.81±0.05	-1 – 7	265.52
	FS	2.30±0.05	-4 - 7	51.51
Plant height (cm)	S _i	125.30±0.82	33 -216.3	10.16
	FS	147.12±0.70	80 - 280	13.15
Ear height (cm)	S _i	51.99±0.49	10 - 115.5	16.06
	FS	64.90 ±0.42	22 - 115	20.64
Root lodging (%)	S _i	21.54±0.90	0 - 100	91.56
	FS	18.57±0.79	0 - 100	106.88
Ears per plant	S _i	1.15±0.90	0 - 2.0	198.68
	FS	0.91±0.01	0 - 2.5	34.79
Grain yield (tons/ha)	S _i	2.40±0.06	0.2 - 10.6	54.50
	FS	3.05±0.04	0 - 11.16	26.49

FS: Full-sib; SE: Standard error; CV: Coefficient of variation for FS (147.12 cm, 64.90cm respectively) than S_i (125.3cm, 51.9cm respectively). Root lodging was lower in FS (18.57%) than in S_i (21.54%). FS has lower number of ears per plant but higher grain yield (3.05tons/ha) as against 2.41tons/ha for S_i (Table 1). Range was high for almost all the traits for both family types. Coefficient of variation (CV) was moderate for most traits except for estimated traits such as ASI, root lodging, number of ears per plant and grain yield for both family types.

Mean Squares of the Measured Traits for S_i and FS Family

Result of mean square estimates is presented in Table 2. Mean square of environment was significant for all the traits measured for both family types except ASI in S_i family. Meansquare of entry was significant for most traits except for ASI, root lodging and number of ears per plant for S_i and FS family. Mean squares of environment by entry interaction was not significant for all traits for FS family, but significant for days to 50% pollen shed, ASI, plant and ear height and grain yield for S_i family.

Estimates of Genetic Variance Components and Heritability for S_i and FS Families

Estimates of genetic variances and heritability are presented in Table 3. Estimates of genetic variance were higher for S_i than FS family for all traits except root lodging. Estimates of genetic variance were more than twice their respective standard error except for root lodging, number of ears per plant and grain yield for S_i family showing their level of significance. Environmental variance was relatively large except in few instances where genetic variance was larger. Variance of genetic by environment interaction was negative for all traits for FS except days to 50% pollen shed (Table 3). Except for root lodging and number of ears per plant in S_i, heritability was moderate to high for all traits in both family types. Heritability estimates were higher in FS than S_i family for days to silking, root lodging, number of ears per plant and grain yield. On the other hand, heritability estimates were higher in S_i for days to pollen shed, ASI, plant and ear height. Genetic gains would be positive and higher for most agronomic traits in S_i than FS family. Gains would however be higher for grain yield in FS (9.79%) than in S_i (9.17%) (Table 3).

Table 2. Mean squares from analysis of variance for the traits measured in S₁ and FS family of ART/98/SW6-OB at Ilora and Ikenne in 2015 and 2016.

SOV	df	Days to 50% pollen shed	Days to 50% silking	ASI	Plant height (cm)	Ear height (cm)	Root lodging (%)	Ears per plant	Grain yield (tons/ha)
S									
Env	3	2960.9**	3619.8**	92.94	134615**	34871**	27.61**	14.29*	227.86**
Rep (Env)	8	23.40**	26.21	63.46	8247.7**	4585.1**	1.66**	28.58**	29.43**
Block	108	23.23**	26.26**	56.28	1040.9**	462.54**	0.42**	5.83	6.17**
Entry	99	19.67**	25.25**	74.35	965.52**	362.61**	0.34	5.02	5.33**
Env x Entry	297	6.85**	9.96	24.59**	303.1**	141.88**	0.33	4.82	4.07**
Error	792	1.95	14.27	55.5	162.04	69.68	0.29	5.26	3.2
FS									
Env	3	1348**	2324.3**	248.2**	4248.7**	5639.4**	78287**	0.91**	61.81**
Rep (Env)	8	23.16*	12.45**	4.62**	5156.3**	1948.6**	1627.2**	0.43**	18.24**
Block	108	14.31*	3.98	1.5	325.77	160.08	354.29	0.07	1.84
Entry	95	18.79*	12.06**	1.57	708.73**	268.96**	441.1	0.08	3.07**
Env x Entry	285	11.1	0.25	1.4	279.04	119.65	364.16	0.06	1.77
Error	760	10.64	3.49	1.4	374.12	179.41	393.93	0.1	2.01

FS: full-sib; *, **: significantly different from zero at P= 5% and 1% respectively; Env: environment ; df: degree of freedom

Table 3. Components of genetic variance*, heritability and genetic gains of the traits measured in S₁ and FS family of ART/98/SW6-OB at Ilora and Ikenne in 2015 and 2016.

Traits	Family	$\sigma^2_g \pm S.E$	σ^2_{ge}	σ^2_e	σ^2_{ph}	H ² (%) $\pm S.E$	Gs	Gains/cycle (%)
Days to 50% pollen shed	S ₁	1.07± 0.24	1.64	0.16	1.64	65.14±0.03	1.17	1.98
	FS	0.64 ±0.23	0.15	0.88	1.57	40.95±0.03	0.72	1.25
Days to 50% silking	S ₁	1.27± 0.30	-1.44	1.19	2.10	60.55±0.04	1.23	2.01
	FS	0.98± 0.14	-1.08	0.29	1.00	97.91±0.02	1.37	2.30
Anthesis-SilkingInterval	S ₁	4.14± 0.88	-10.30	4.62	6.20	66.92±0.13	2.33	82.91
	FS	0.01± 0.02	-0.001	0.12	0.13	10.76±0.003	0.05	2.18
Plant height (cm)	S ₁	55.20± 11.51	47.02	13.50	80.46	68.60±1.65	8.62	6.88
	FS	35.81± 8.53	-31.69	31.18	59.06	60.62±1.23	6.52	4.43
Ear height (cm)	S ₁	18.39± 4.36	24.06	5.81	30.21	60.87±0.63	4.68	9.01
	FS	12.44± 3.26	-19.92	14.95	22.41	55.51±0.47	3.68	5.67
Root lodging (%)	S ₁	2.30± 6.80	31.01	32.42	42.47	4.86±0.001	0.49	2.29
	FS	6.66± 5.77	-9.93	32.83	37.01	18.00± 0.90	1.53	8.26
Ears per plant	S ₁	0.02± 0.06	-0.15	0.43	0.42	3.90±0.01	0.04	3.08
	FS	0.001± 0.001	-0.01	0.01	0.01	15.61±0.001	0.02	1.93
Grain yield (tons/ha)	S ₁	0.10± 0.06	0.29	0.27	0.44	23.58±0.01	0.22	9.17
	FS	0.11± 0.03	-0.08	0.17	0.26	42.20±0.01	0.30	9.79

* σ^2_g : genetic variance; SE: Standard error; σ^2_{ge} : Variance due to environment by entry interaction; σ^2_e : Variance due to environment; σ^2_{ph} : Phenotypic variance; H²: Broad-sense heritability; Gs: Genetic gains; FS: Full-sib.

Correlation among Traits Studied in S_1 and FS Families

Correlation coefficients were higher in S_1 than FS for most of the traits (Table 4). Correlation followed the same trend in both family types except in few cases. For instance, negative correlation existed between days to silking and ASI, although not significant (-0.01). However, the correlation was positive and significant for FS (0.37**). Also, correlation between root lodging and number of ears per plant was negative for S_1 (-0.06) but positive for FS family (0.04) (Table 4). Days to pollen shed and silking had negative correlation with other traits. Strong and positive correlation existed between days to pollen shed and days to silking, and between plant and ear height in both family types. Correlation between days to silking and grain yield was only significant in S_1 (-0.25**). Grain yield was significantly correlated with number of ears per plant (0.52** for S_1 , 0.50** for FS), plant height (0.21* for S_1 , 0.20* for FS) and ear height (0.22* for S_1 , 0.28** for FS) (Table 4).

Discussion

Family-based selection has been preferred to mass selection in that it can provide greater accuracy in predicting an individual's breeding value and hence,

give a larger response. The longer days to 50% flowering and ASI in S_1 , but taller plants and higher yield in FS revealed the level of vigour in FS and inbreeding depression in S_1 . Similar result was reported by El-seidy *et al.* (2013). At S_1 , level of inbreeding is 50%, and at this stage, it is expected that plant vigour and yield reduces. Taller plants and high yield in FS is expected because plant height and grain yield have strong correlation in maize. The lower percentage root lodging in FS further revealed high standability and vigour in FS. This is due to the heterozygous nature of FS family. Jalal *et al.* (2006) reported severe inbreeding depression in grain yield using S_1 family.

Significant mean squares for grain yield in this study for S_1 lines was also reported by Taha *et al.* (2016), Environmental variance being larger than genetic variance for most of the traits is not unconnected with the significant mean squares of environment for the traits in both family types. This is an indication that the QPM population performed differently in both environments. The negative variance due to environment by genetic interaction for FS which is equated to zero is associated with the non-significance mean squares of environment by genetic interaction for FS.

Table 4: Pearson correlation coefficients of the traits measured in S_1 and FS family of ART/98/SW6 OB at Ilora and Ikenne in 2015 and 2016.

Traits	Family	Days to 50% pollen shed	Days to 50% silking	Anthesis-Silking interval	Plant height (cm)	Ear height (cm)	Root lodging (%)	Ears per plant	Grain yield (tons/ha)
Days to 50% pollen shed	S_1		0.93**	-0.37**	-0.21*	-0.21*	0.02	-0.18	-0.21*
	FS		0.88**	-0.11	-0.04	-0.04	-0.03	-0.04	-0.03
Days to 50% silking	S_1			-0.01	-0.18	-0.21*	0.05	-0.17	-0.25**
	FS			0.37**	-0.5	-0.04	-0.01	-0.13	-0.17
Anthesis-Silking interval	S_1				0.09	0.04	0.06	0.12	-0.02
	FS				-0.04	-0.01	0.02	-0.19	-0.31*
Plant height (cm)	S_1					0.75**	-0.05	0.07	0.21*
	FS					0.81**	-0.01	0.06	0.20*
Ear height (cm)	S_1						-0.01	0.22*	0.22*
	FS						-0.01	0.04	0.28*
Root lodging (%)	S_1							-0.06	0.04
	FS							0.04	0.14
Ears per plant	S_1								0.52**
	FS								0.50**
Grain yield (tons/ha)	S_1								
	FS								

FS: full-sib; *, **: significantly different from zero at P= 5% and 1% respectively

No genotype x environment interaction observed for all traits evaluated in FS, indicated that a single recurrent selection program can be conducted for both sites. Similar observation was reported by Beriliet *al.*(2013) for FS family. The significant mean squares of entry for most traits in both S_1 and FS and the corresponding moderate to high heritability for these traits suggested appreciable level of variability in both family types for these traits. Mahmood *et al.*(2017) however reported the effectiveness of half-sib family as a potential line in the future maize breeding programs.

Heritability and genetic gains measures level of progress that could be attained in a population improvement program. In the present study, heritability estimate was moderate to high for flowering, plant height and grain yield in both family types indicating wider variability for these traits. Heritability was however higher for days to silking, number of ears per plant and grain yield in FS family than S_1 , while it was higher in S_1 for other traits. This indicated the effectiveness of using FS family selection in improving the maize populations for yield and related traits. Ajala *et al.* (2009) also reported higher heritability for grain yield in FS than S_1 family but higher heritability for days to silking and plant height. The heritability for days to 50% pollen shed and silking for S_1 in the present study is similar to those recorded by Ali *et al.*(2011). El- Seidy *et al.* (2013) however reported higher heritability and gains for grain yield in S_1 .

Higher genetic gains were observed in S_1 family in the present study for days to flowering and other agronomic traits, indicating that there would be longer days to flowering and taller plants which is not desirable. Flowering and plant height would however increase lesser while grain yield would be higher with selection in FS family indicating the reliability of FS in improving this maize population to make rapid progress. Ajala *et al.* (2009) also reported higher gains/cycle for agronomic traits in S_1 family, but higher gains in FS family for grain yield. Beriliet *al.*(2013) reported wide genotypic variability and heritability estimates ranged from 33 to 73%, and predicted genetic gain of 12.90% for yield in FS family of a maize population indicating prospects of using FS selection. Flachenecker *et al.* (2006) conclude that modified recurrent FS selection is an alternative to other commonly applied intrapopulation recurrent selection schemes, and some of its features may also be useful for increasing the efficiency of interpopulation recurrent selection programs. Tulu and Jifar (2010) however reported short plant height and low ear placement with significant genetic gains using S_1 family. Ayiga *et al.*

(2015) reported that S_1 recurrent selection method was effective in improving a maize population for grain yield and the associated traits. Badu *et al.* (2008), reported S_1 recurrent selection to be effective in improving grain yield and *Striga* resistance in two early maize populations. This further buttress the fact that different family selection method would work for different maize population.

Conclusion

The result of this study revealed that variability is higher in FS family for yield and related traits in this maize population. The selection method that would increase days to flowering and plant height the least, but increase grain yield the most in ART/98/SW6-OB would be FS family selection. Hence, FS selection method would be better in improving this maize population for yield and related traits to make faster progress.

References

- Adeyemo, M.O.(1986). Genetic variability and predicted responses to four types of progeny selection in a Nigerian maize population. Ph.D. Thesis. University of Ife, Ile-Ife, Nigeria p. 123.
- Ajala, S. O., Ago, C. E. and Olaoye, G.(2009). Comparison of predicted responses to three types of recurrent selection procedures for the improvement of a maize (*Zea mays* L.) population. *Journal of Plant Breeding and Crop Science*, 1(8): 284-292.
- Ajala, S.O., Menkir, A., Kamara, A.Y., Alabi, S.O., Abdullai, M.S.(2007). Breeding strategies to improve maize for adaptation to low soil nitrogen in West and Central Africa. *African Crop Science Proceedings*, El-Minia, Egypt pp. 87-94.
- Ali, F., Rahman, H., Durrishahwar, Nawaz, I., Munir, M. and Ullah, H. (2011). Genetic analysis of maturity and morphological traits under Maydis Leaf Blight (MLB) epiphytotics in maize (*Zea mays* L.). *Journal of Agricultural and Biological Science*, 6(8):13-19.
- Ayiga-Aluba, J., Edema, R., Tusiime, G., Asea, G. and Gibson, P. (2015). Response to two cycles of S_1 recurrent selection for turicum leave blight in an open pollinated maize variety population (Longe 5). *Advances in Applied Science Research*, 6(12): 4-12.
- Badu-Apraku, B., Fakorede, M. A. B. and Fontem Lum A. (2008). S_1 family selection in early-maturing maize populations in *Striga*-infested and *Striga*-free environments. *Crop Science*, 8:1984-1994.
- Berilli, A.C.G., Pereira, M.G., Trindade, R.S., da

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- Costa, F.R. and da Cunha, K.S. (2013). Response to the selection in the 11th cycle of reciprocal recurrent selection among full-sib families of maize. *Acta Scientiarum. Agronomy*, 35(4): 435-441.
- Burton, J.W., Penny, L.H., Hallauer, A.R. and Eberhart, S.A. (1971). Evaluation of synthetic populations developed from a maize variety (BSK) by two methods of recurrent selection. *Crop Science* 11: 658-661.
- Comstock, R.E. and Robinson, H.F. (1952). Estimation of average dominance of genes. *Heterosis*. J.W. Gowen, Ed. Iowa State University press, Ames, Iowa. 494-516.
- Dhillon, B.S. and Khehra, A.S. (1989). Modified S_1 recurrent selection in maize improvement. *Crop Science*, 29: 226-228.
- El-Morshidy, M.A., Hassaballa, E.A., Abou El-Saad, S.F. and Abd El-Moula, M.A. (2002). Selection for drought tolerance in maize (*Zea mays* L.). The 3rd Sci. Conference. of Agricultural Assiut, Oct. 173-191.
- El-Seidy, E.H., Shehata, A.M. and Alsebaey, R. H. A. (2013). Estimation of some genetical parameters and their implication on yield improvement in maize using two selection methods *Journal of Plant Production, Mansoura Univ.*, 4(8): 1183 - 1196.
- Flachenecker, C., Frisch, M., Falke, K. C. and Melchinger, A. E. (2006). Genetic drift and selection effects of modified recurrent full-sib selection programs in two F_2 populations of European flint maize. *Theoretical and Applied Genetics*, 113:1113–1120.
- Genter, C.F. (1973). Comparison of S_1 and testcross evaluation after two cycles of recurrent selection in maize. *Crop Science*, 13: 524-527.
- Hallauer, A.R., Carena, M.J. and Miranda, J.B. (2010). Quantitative genetics in maize breeding. 3rd ed. Iowa: Iowa State University Press/Springer Science.
- Hallauer, A.R. and Miranda, J.B. Eds. 1988. Heredity variance: Mating designs. *Quantitative genetics in maize breeding*. 2nd edition. USA: Iowa State University Press, Ames. 45-114.
- Jalal, A., Rahman, H., Khan, M.S., Maqbool, K. and Khan, S. (2006). Inbreeding depression for reproductive and yield related traits in S_1 lines of maize (*Zea mays* L.) Songklanakarin. *Journal of Science and Technology*, 28(6): 1169-1173.
- Mahmood, F., Rahman, H., Ahmad, N., Haq, F., Gul, S.I., Hussain, Q., Khalid, A., Iqbal, T. and Rozi, S. (2017). Yield performance with heritability measurements of half sib families obtained from maize variety. *Journal of Experimental Sciences*, 8: 33-36.
- Mahmoud, A.A., Soliman, F.H.S. and Shehata, A.M. (1999). Evaluation of S_1 progenies of maize composite Giza-2 (Ev-8). *Egyptian Journal of Plant Breeding*, 3:115-125.
- Obilana, A.T. and Hallauer, A.R. (1974). Estimation of variability of quantitative traits in BSSS by using unselected maize inbred lines. *Crop Science* 14:99-103.
- Peng-Ze Bin, Li, M., XinZhi, L.U. and Jun-Qiang, L.I. (2007). Comparisons of three recurrent selection methods in the improvement of maize populations. *Crop Science*, Chinese Academy of Agricultural Science 12: 155-162.
- Saini, G.S. and Malhi, N.S. (2001). Direct and correlated response to selection through three methods of population improvement in maize. *Crop Improvement*, 28(1): 62-68.
- SAS Institute (2009). *SAS System for Windows v. 9.3*. Cary, NC: SAS Inst. Inc.
- Shah, S.S., Rahman, H., Khalil, I.H. and Iqbal, M. (2007). Recurrent selection for maydis leaf blight resistance and grain yield improvement in maize. *Pakistan Journal of Biological Science*, 10(20): 3632-3637.
- Subandi and Compton WA (1974). Genetic studies in an exotic population of corn (*Zea mays* L) grown under two plant densities. 1. Estimates of genetic parameters. *Theoretical and Applied Genetics*, 44: 153-159.
- Taha, E.M., Mokadem, S.A., El-Morshidy, M.A. and Abdel-Mageed, M.M. (2016). Effectiveness of S_1 family selection for improving grain yield in two maize populations. *Minia Journal of Agricultural Research and Development*, 36(1):1-13.
- Tanner, A. H. and Smith, O.S. (1987). Comparison of half-sib and S_1 recurrent selection in the Krug Yellow Dent Maize Population. *Crop Science*, 27:509-513.
- Tulu, L. and Jifar, H. (2010). Advances in improving Ukiriguru Composite B maize (*Zea mays* L.) variety through S_1 recurrent selection. *East African Journal of Sciences*, 4(2): 78-85.
- Walters, S. P., Russell, W.A. and Lamkey, K.R. (1991). Performance and genetic variance among S_1 lines and test crosses of Iowa stiff stalk synthetic maize. *Crop Science*, 31: 76-80.