Variability in a Silage Maize "*Zea mays*, L." Base Population *via* Two Types of Families

3. Forage botanical composition and dry matter partitioning

M.Abd El-Sattar Ahmed[1*], M. H. El-Sheikh[1], Kadria M.El-Sayed[1] and Doaa KH. Abd El-Mohsen[2]

1 Crop Science Dept., Fac. Agric. (El-Shatby), Alexandria Univ., Egypt.

2 Postgraduate student, Crop Science Dept., Fac. Agric. (El-Shatby), Alexandria Univ., Egypt.

* Corresponding anther (Mohamed.A@alexu.edu.eg)

ABSTRACT

The base population for the recent study which is a yellow seed synthetic variety of maize was provided by Dr. M. Abd El-Sattar Ahmed, professor of crop science, Crop Science Department, faculty of Agriculture, Egypt. Two types of families had formulated, as a step before selection for high yielding ability. Those were half-sib (H.S) families and the first generation of self-pollination (S_1) families. Variability in the base population gene pool had estimated depending on variance components of the families. Reduction in mean values associated with S_1 families relative to half-sib families reached 0.182, 1.18, 0.98, 3.88, 2.75 and 5.72% for leaves percentage, stem percentage, ear percentage, grain percentage, cob percentage and husk percentage, respectively. Genotypic variances among S_1 families was larger in magnitude than the respective value for half-sib families in each measured botanical composition and dry matter partitioning characters. Meanwhile, within family's variance, (σ^2_f), environmental variances (σ^2_e) had reduced in S_1 families relative to half-sib families in each measured character. Genotypic variation among half-sib and S_1 families were less than 20% of the studied botanical composition and dry matter partitioning characters mean values, except for cob percentage and husk percentage that had a genotypic variation amount to 24% and 26%, respectively. The estimates of additive variance (δ^2_A) were positive for all studied botanical composition and dry matter partitioning characters. While, the estimates of dominance variance (δ^2_D) were negative for all characters, the ratio of δ^2_A/δ^2_G indicated that additive genetic variance was more effective in controlling all studied botanical composition and dry matter partitioning characters. Estimates of heritability were higher in magnitude when calculated from first selfing generation (S_1) compared to half-sib families, for all studied characters. Stem percentage expressed the least estimate heritability among all studied characters in each family type (0.798 and 0.414 for half-sib and S_1 families, respectively). This might indicate the influence of environment in the expression of that character. Meanwhile husk percentage had highest genetic control expressed on heritability estimates from the two studied types of families.

Keywords: Genotypic variations, Half–sib, S1 families, botanical composition, dry matter partitioning, Heritability.

INTRODUCTION

Maize is one of the most important crops worldwide. Historically breeding efforts in this crop have been primarily focused on the improvement of grain yield and stability and just recently also on the potential utility of maize stover (above ground biomass excluding the grain) as source of biomass for the production of feed, fiber and cellulosic ethanol (Mutton, *et.al*, 2013). Joseph, *et. al.* (2015), demonstrated that, genetic variability of agronomic traits of crops broadens the gene pool of crops. Repeatability and genetic advance determine the effectiveness of selection in breeding program. Phenotypic and genotypic correlations of grain yield with each of days to anthesis, plant height ear height, leaf area and number of ears per plant were positive and significant. Genetic effect for grain yield correlated with that of days to silking, but this was not for phenotypic effect. Any of these traits can be selected for grain yield and the lines studied were considered suitable as gene pool in maize breeding . Path analysis showed that days to silking, leaf area and ear per plant had high positive effect with grain yield of the crop.

Coors (1988) examined the effectiveness of evaluating both half-sib (HS) and selfed (S_1) fami-

lies during selection to improve population per se performance and inbred productivity. Four cycles of combined HS and S_1 selection for increased grain yield and reduced grain moisture were completed in a narrow-based maize population derived from inbred lines, A635, W182 E, and W64A. For each cycle, both HS and S_1 progenies were produced on prolific plants by selfing the bottom ear and exposing the upper ear to random pollen from the population. Half-sib and S_1 progensis were then evaluated in separate trials. Plants with superior HS and S_1 progeny performance, i.e.; above average yield and below average grain moisture in both trials, were selected. Half-sib progeny were used for recombination through the first two cycles. In the third cycle, S_1 progeny were recombined. Both progeny types were recombined to form two subpopulations in the fourth cycle. He showed that, over four selection cycles, yield of the population increased by 3.5%. cycle[1] and grain moisture decreased by 1.5% cycle[-1]. Corresponding increase in yield were not detected in testcrosses with inbred line A554 and W117, but cycle four testcrosses had significantly lower grain moisture than corresponding testcrosses with the initial popula-

tion. The yield of bulked composites from random, self-pollinated plants increased by 209 plant[-1] over four cycles. Broad-sense heritability estimates were 0.34 and 0.76 HS and S_1 families, respectively, for yield and 0.68 and 0.88 for moisture. The genetic covariance of HS and S_1progenies was compared to the variance among HS progenies for grain yield and moisture in order to estimate D1, the covariance of additive and homozygous dominance effects. A large negative value for D1 for yield was obtained. Ullah *et.al*, (2013), evaluated the performance of 196 half-sib families (HSF) derived from *Sarhad* white variety of maize at the research farm of Agricultural university, Peshawar using partially balanced lattice square design with two replications. Results indicated significant differences among HSF for all studied traits (i.e., flowering traits, plant height, ear height, grain moisture and 100-kernel weight), except, grain yield. Maximum heritability estimate (69.17%) was observed for plant height, while, minimum (5.08%) was observed for days to mid-silking.

Obilana and Hallaua (1974), Lothrop *et. al.* (1985) and Million *et. al.* (2012), Ajala *et. al.* (2010), subjected maize population to both full-sib and S_1 recurrent selection schemes to determine the better of the two procedures for improving the population for tolerance to low soil nitrogen. For both schemes, estimated genetic variances were generally large enough for effective selection to take place. Except for ears per plant and stay green under low-N, genetic variances due to S_1 were larger than those due to full-sib selection. Genetic variances under high-N for most traits were also larger for S_1 than for full-sib, Heritability estimates for all the traits except for root lodging under low-N were moderate to high, but the estimates were higher for S_1 than for full-sib family selection under both selection types. Genter and Alexander (1962), Lonnquist (1964), Mota *et.al* (1975) and Goulas and Lonnquist (1976),Coors (1988), examined the effectiveness of evaluating both half-sib (HS) and selfed (S_1) families during selection to improve population per se performance and inbred productivity. Four cycles of combined HS and S_1 selection for increased grain yield and reduced grain moisture were completed in a narrow-based maize population derived from inbred lines, A635, W182 E, and W64A. For each cycle, both HS and S_1 progenies were produced on prolific plants by selfing the bottom ear and exposing the upper ear to random pollen from the population. Half-sib and S_1progenies were then evaluated in separate trials. Plants with superior HS and S_1 progeny performance, i.e., above average yield and below average grain moisture in both trials, were selected. Half-sib progeny was used for recombination through the first two cycles. In the third cycle, S_1 progeny were recombined. Both progeny types were recombined to form two sub-populations in the fourth cycle. they showed that,

over four selection cycles, yield of the population increased by 3.5% cycle1 and grain moisture decreased by 1.5% cycle[-1].Corresponding increase in yield were not detected in testcrosses with inbred line A554 and W117, but cycle four testcrosses had significantly lower grain moisture than corresponding testcrosses with the initial population. Yagya and Nirania (2005), conducted a research to compare the efficiency of half-sib (HS), Full- sib (FS) and selfed progeny (S_1) recurrent selection methods for improvement in yield, and to improve the per se performance of the ECg_1 PCV_5 pearl millet composite. They found that, half-sib progeny selection method showed 3.17% realized genetic gain, whereas, full-sib progeny selection method showed 11.49% and S_1 progeny selection method showed 31.6% realized genetic gain for grain yield on pooled basis. Thus, S_1 progeny selection method recorded highest realized genetic gain for grain yield as compared to half-sib and full-sib progeny selection methods. Thus, it was revealed that the S_1 progeny selection method is most efficient for improvement in grain yield and its contributing traits in pearl millet. EL- Gazzar, *et.al*, (2013), The additive gene effects were more important for silking data, plant height, ear height, grain yield. No. of ears/100-plant and ear diameter. While the non-additive gene effects were important for ear length.

Hallauer and Miranda (1981), Weyhrich *et al.* (1998), Ahmed (2006-a), Bakheit *et.al*, (2001) and Hallauer and Carena (2012), stated that, estimates of the genetic variation among progenies tested (σ_g^2), interactions of progenies with environments (σ_{ge}^2), and experimental error (σ^2) were obtained from the combined analyses of variance for each cycle of selection and then averaged across cycles for each selection program. From the estimates of the components of variance, estimates of heritability (h^2) on a progeny mean basis, the genetic coefficient of variation among progenies tested relative to their mean, (GCV), selection differentials (D), predicted genetic gains (Δ_G), and least significant differences (LSD) were calculated and averaged across cycles of selection. The average estimates of σ_g^2 were largest for inbred progeny selection and smallest for half-sib family selection as expected. Averaged expected genetic gain across all intra-population selection programs was 3.17 ha^{-1}yr^{-1} *vs.* 2.32 q ha^{-1} yr^{-1} for inter-population reciprocal recurrent selection, or 2.64 q ha^{-1} yr^{-1} across all method. On a per cycle and per year basis the differences among types of progeny were relatively small, ranging from (3.75q ha^{-1} yr^{-1} ,1.78 q ha^{-1} cycle[-1]) for half-sib family selection to (9.62 q ha^{-1} yr^{-1} ,3.21 q ha^{-1} yr^{-1}) for S_2inbred progeny selection. Kahriman, *et.al,* (2014), investigated the genetic potential of six maize families for simultaneous selection of oil content and grain yield. Result showed that, there were significant differences among the families and generations for oil content

and grain yield. The variation in oil content in the families was mainly controlled by additive gene actions. Estimated genetic gains were in the range of 0.4% to 4.1 % per cycle for oil content, and 17.7 g to 60.7 g per cycle for grain yield. Abdallah, (2014), conducted a line x tester analysis involving 20 testcrosses generated by 10 elite yellow maize inbred lines with two testers to evaluate grain yield and yield related traits. Analysis of variance indicated significant mean squares due to crosses for ear length ear diameter, number of rows per ear, number of kernels per row, 200 kernels weight, and grain yield. The magnitude of general combining ability variance was much greater than specific combining ability variance for all studied traits, except for ear length and number of kernels per row, indicating the preponderance of additive gene action for these traits. Joseph, $et.al$, (2015), stated that, phenotypic and genotypic variances, genotypic coefficient of variation, repeatability and expected genetic advance were estimated for three flowering and six morphological traits of white kernel low nitrogen donor maize inbred lines. Genotypic and phenotypic variances were equal for floral traits. Thus, gene actions for the traits was additive. Anthesis- silking interval showed high genetic advance with high coefficient of variation suggesting its efficiency for selection. Phenotypic and genotypic correlations of grain yield with each of days to anthesis, plant height ear height, leaf area and number of ears per plant were positive and significant. Genetic effect for grain yield correlated with that of days to silking, but this was not for phenotypic effect. Any of these traits can be selected for grain yield and the lines studied were considered suitable as gene pool in maize breeding for nitrogen stress tolerance.

Ajala $et. al$. (2009), determined the amount of genetic variation present in a maize population, FARZ 23 (096 Ep6), by using full-sib, half –sib and S_1 families. Agronomic and yield data obtained included days to 50% tasseling and silking, plant height, moisture content at harvest, number of ears per plot and grain yield. Heritability estimates were from moderate to large for most traits. The results revealed, direct selection for grain yield is expected to result in favorable increase in other traits except that the selected materials will flower earlier. Since increase in plant height due to selection for grain yield is undesirable, it was concluded that the best selection method for yield improvement that will increase height, the least would be full-sib family selection. Kanagarasu, $et al$, (2010),performed combining ability analysis for yield and its component traits Variance due to SCA was greater than GCA variance for the traits viz., grain yield per plant, cob diameter, cob length, plant height, ear height, leaf length, 100 grain weight, grain rows per cob, days to 50 percent tasseling and days to 50 percent silking. The variance due to SCA was higher than due to GCA

indicating the predominance of non-additive type of gene action in the governance of above-mentioned traits.Yousuf and Saleem (2002), estimated significance of differences among seventy four S_1 families obtained from maize population C-17 grown in triplicated randomized complete block design for number of days taken to tasseling, number of days taken to silking, number of ears per plant, 100-grain weight and grain yield per plant. They observed highly significant difference among S_1 families for all the traits, except for, number of ears per plant where it was non- significant. Genotypic variances were greater than the environmental variances for all the traits, except for, number of ears per plant. Heritability estimates were moderate to high for all the plant traits except for number of ears per plant where they were low in magnitude.

Hallauer and Carena. (2012), stated that, estimates of the genetic variation among progenies tested (σ_g^2), interactions of progenies with environments (σ_{ge}^2), and experimental error (σ_e^2) were obtained from the combined analyses of variance for each cycle of selection and then averaged across cycles for each selection program. From the estimates of the components of variance, estimates of heritability (h^2) on a progeny mean basis, the genetic coefficient of variation among progenies tested relative to their mean, (GCV), selection differentials (D), predicted genetic gains (Δ_G), and least significant differences (LSD) were calculated and averaged across cycles of selection. The average estimates of σ_g^2 were largest for inbred progeny selection and smallest for half-sib family selection as expected. Sardar $et. al$. (2006) computed broad sense heritability estimates, genetic advance and relative expected genetic Advance (REGA) for different fodder yield related traits in two maize populations during Kharif 2002 and 2003.Two maize populations, DRS; developed through recurrent selection and DMS developed through mass selection, were grown in modified RCBD with two replications. They found that, mean squares from the analysis of variance among S1 families for both maize populations indicated highly significant (p≤ 0.01) differences for all the studied traits. Estimates of genetic variances were significant for all traits except stem girth in both populations. Genetic variances in comparison to respective environmental variances were greater for majority of the traits in both populations. Heritability estimates were high and significant for all the traits in both populations. Comparison of two populations revealed that heritability estimates were higher for internode length and fresh fodder yield in the DRS population and for plant height, stem girth, flag leaf area and dry matter content in the DMS population. Genetic advance was higher for internode length, flag leaf area, fresh fodder yield in the DRS population and for plant height, stem girth and dry

matter content in DMS population. REGA% was higher for internode length and fresh fodder yield in DRS population while DMS population attained higher values for plant height, stem girth, flag leaf area and dry matter content. The higher heritability estimates, genetic advance and REGA for fresh fodder yield in DRS population indicates that re-current selection method was comparatively more effective in improving maize population for fodder yield parameters.

The main objectives of the present study were detecting variations in botanical composition and dry matter partitioning in the reference population through studying two types of families i.e., half-sib and S_1-families.

MATERIALS AND METHODS

The present study had carried- out at the Agricultural Experiment Station, Alexandria university, Alexandria, through two successive summer seasons of 2009 and 2010. The base population under study which is a yellow seed synthetic variety of maize were provided by Dr. M. Abd El- Sattar Ahmed, Professor of Crop Science, crop science Department, Faculty of Agriculture, Alexandria, Egypt (Ahmed *et.al*, 2010). In the summer season of 2009, seeds of base population were planted at a plant density of 26000 plant / faddan. Normal practices for maize production were applied as recommended for optimum maize production in the growing region.

In 2009 summer, season, 300 plants were visually selected before flowering, depending on good general performance. Those selected plants were marked by label named (OP) to indicate the collection of their open pollinated seeds. In the meantime, another 300 plants were selfed to produce S_1 seeds. The highest seed producing 100 plants were saved as half- sib families, S_1 – seeds had harvested from each plant, separately, to represent the initial genetic make-up. Progenies were developed for S_1- family selection by selfing 300 plants in the same summer season of 2009. Those plants were marked by label named S_1. S_1 seeds were harvested from each selfed plants, separately, to represent S_1- family. one hundred S_1- Families, with enough selfed seeds, were saved.

In summer season of 2010, each hundred selected half-sib and S_1- Families had evaluated in a trial of five sets, each of twenty families. Each set had treated as a randomized completed block experiment, with two replicates. The plot size was 2.8 m^2 represented by one row, 4.00 m long and 0.7 m. apart. Seeds planted in hills at 0.20 meter within ridge to obtained plant density of 30000 plant / faddan.

The following characters had studied for each type of families:

Botanical composition

A random sample of five plants were taken from each plot for the following measurements:

Leaves percentage (%): Estimated as follow; fresh weight of leaves per plant ∕ fresh weight of whole plant × 100.

Stem percentage (%): Estimated as follow; fresh weight of stem per plant ∕ fresh weight of whole plant × 100.

Ears percentage (%): Estimated as follow; fresh weight of ears per plant ∕ fresh weight of whole plant × 100.

Grain percentage (%): Estimated as follow; weight of grain per plant ∕ weight of ears per plant × 100.

Husks percentage (%): Estimated as follows; weight of husk per ears∕ weight of ears per plant × 100.

Cobs percentage (%): Estimated as follows; weight of cobs/ ears∕ weight of ears/ plant ×100.

Plant dry matter percentage:

Leaves dry matter percentage (Leaves DM%): Determination from a random sample of leaves (about 200 gm) taken at the time of harvest, then dried at 70°C in a forced air dryer to constant weight.

Stem dry matter percentage (Stem DM%): Determined from a random sample of stems (about 500 gm), taken at the time of harvest and dried at 70°C in a forced air dryer to constant weight.

Ear dry matter percentage (Ear DM%): Determined from a random sample of ears (about 2 ears) taken at the time of harvest and dried at 70°C in a forced air dryer to constant weight.

Whole plant dry matter percentage: Calculated as follow ((leaves DM % × leaves % + stem DM% × stem% + Ear DM% × Ear%) / (leaves% + stem% + Ear%).

Grains dry matter percentage: A sample of shelled ears were used to draw two samples each of 100- kernels, weighted immediately then dried in a forced air dryer till weight constancy.

Statistical analysis:

Analysis of variance for the data collected in each set as well as combined analysis over sets was performed as described by Cochran and Cox (1957). According to analysis of variance assumption, numerical data were subjected to square root transformation before analysis. Combined analysis over sets were performed when the assumption of homogeneity of error was not rejected. Forms of analysis of variance for each set and combined analysis over sets had illustrated in Table (1).

Table (1): Forms of analysis of variance for randomized complete block design in each set and combined over sets.

Source of variation	d.f.	M.S.	E.M.S.
(a) Each set			
Replications	(r-1)		
Families	(f-1)	M_1	$\sigma^2_e + r\,\sigma^2_f$
Error	(r-1) (f-1)	M_2	σ^2_e
(b) Over sets			
Sets (S)	(s-1)		
Rep/set	s(r-1)		
Families / sets	s(f-1)	M_1	$\sigma^2_e + r\,\sigma^2_f$
Reps× Families / sets (Eb)	s (r-1) (f-1)	M_2	σ^2_e

Where:

s: number of sets.

σ^2_e: error variance which represent environmental variation.

σ^2_f: Variance component among families and it is a function of the genetic variance.

r: number of replications.

The variance components were calculated from the observed mean squares as follows:

$\sigma^2_f = (M_1 - M_2)/r$

$\sigma^2_e = M_2$

$\sigma^2_{ph} = \sigma^2 f + \sigma^2 e$

Genetic components of variations were estimated as follows:

Heritability (H) = $\sigma^2 f / \sigma^2 ph$ (Hallauer and Miranda, 1981).

Where:

σ^2_f: the genetic variation among families.

σ^2_{ph}: the phenotypic variation.

Predicted selection response was calculated using the formula adapted by Falconer (1989) as follows:

$\Delta G_{\alpha} = K_{\alpha}.\ H.\ \sigma_{ph}$

Where;

K_{α}: The selection differential for α selection intensity ($K_{0.10} = 1.76$).

The percentage of predicted genetic advance under selection response (G%) was calculated as;

G% = $\dfrac{\Delta G}{\overline{X}} \times 100$

Where;

$\overline{X}$ = Overall mean

The Coefficient of variability (C.V.) values for the phenotypic and genotypic variation were calculated as follows:

P.C.V = $\dfrac{\sqrt{\sigma^2_{ph}}}{\overline{X}} \times 100$

G.C.V = $\dfrac{\sqrt{\sigma^2_f}}{\overline{X}} \times 100$ (Burton and De vance, 1953)

Assuming that dominance variance (σ^2_D) is less important than additive genetic variance (σ^2_A),

the estimates of variance components, for the two types of families, would be used to calculate (σ^2_A) and (σ^2_D), as follows (Hallauer and Miranda, 1988):

$\sigma^2 H.S = 1/4\ \sigma^2_A$

$\sigma^2 S_{1} = (1)\ \sigma^2_A + 1/4\ \sigma^2_D$

These two equations were used to drive additive and dominance variances as illustrated by Bernardo, 2002. The estimates of σ^2_A and σ^2_D were used for estimating the expected genetic advance from selecting the superior 10% families in each selection program, when appropriate, as indicated by Fehr, 1987.

RESULTS AND DISCUSSIONS

Forage botanical composition:

Estimates of minimum, mean and maximum values for maize botanical composition characters derived from half-sib (H.S) and first selfing generation (S_1) had presented in **(Table 2).** The range (maximum - minimum) values obtained from half-sib families were of lower magnitude relative to the corresponding values obtained from S_1 families for each studied forage botanical composition characters the estimated figures were, 7.87 *vs.* 12.33, 8.87 *vs.* 10.56, 11.67 *vs.* 14.085, 9.705 *vs.* 12.09 , 7.555 *vs.* 14.68 and 7.285 *vs.* 14.61 for H.S *vs.* S_1 families in leaves%, stem%, ear%, grain%, cob% and husk%, respectively. Also, the mean values recorded from S_1 families were smaller than the corresponding values for half-sib families in all studied characters of botanical composition. Reduction in mean values associated with S_1 families relative to half-sib families reached 0.182, 1.18, 0.98, 3.88, 2.75 and 5.72% for leaves percentage, stem percentage, ear percentage, grain percentage, cob percentage and husk percentage, respectively. This result was in accordance with those reported by Hallauer and Miranda (1988) and Fehr (1987).

Table (2): Estimates of minimum, mean and maximum values, for forage botanical composition of maize (2010 summer season).

Characters	Minimum		Mean		Maximum	
	H. S	S₁	H. S	S₁	H. S	S₁
Forage botanical composition						
Leaves percentage	15.180	13.200	19.188	19.153	23.050	25.530
Stem percentage	30.240	29.330	36.199	35.773	39.115	39.890
Ear percentage	40.765	39.805	45.066	44.625	52.440	53.890
Grain percentage	36.720	34.505	41.903	40.277	46.425	46.595
Cob percentage	11.670	4.450	6.983	6.791	19.225	19.130
Husk percentage	11.860	5.080	15.706	14.807	19.145	19.690

H.S: half-sib families
S_1: First selfing generation families

The pertinent mean square from analysis of variance over sets and estimates of family's variance components for both of half-sib (H.S) and first selfing generation (S_1) families derived from maize regarding botanical composition (2010 summer season) had presented in (Table 3). The analysis revealed highly significant effects (P $\geq$ 0.01) of families/sets for forage botanical composition traits, (leaves%, stem%, ear%, grain%, cob% and husk%). Mean squares among families were larger magnitude for the first selfing generation (S_1) families relative to half-sib families. Meanwhile, within families mean squares took on opposite trend for all studied characters.

Family's variance component for S_1 families were 2.29, 1.19, 2.33, 1.15, 1.07 and 1.27 times the corresponding values for half-sib (H.S) families. The recent results were in accordance to those reported by Genter and Alexander (1962), Lonnquist (1964), Mota *et.al* (1975) and Goulas and Lonnquist (1976). Coors (1988), examined the effectiveness of evaluating both half-sib (HS) and selfed (S_1) families during selection to improve population per se performance and inbred produc-

tivity. Four cycles of combined HS and S_1 selection for increased grain yield and reduced grain moisture were completed in a narrow-based maize population derived from inbred lines, A635, W182 E, and W64A. For each cycle, both HS and S_1 progenies were produced on prolific plants by selfing the bottom ear and exposing the upper ear to random pollen from the population. Half-sib and S_1progenies were then evaluated in separate trials. Plants with superior HS and S_1 progeny performance, i.e., above average yield and below average grain moisture in both trials, were selected. Half-sib progeny was used for recombination through the first two cycles. In the third cycle, S_1 progeny were recombined. Both progeny types were recombined to form two subpopulations in the fourth cycle. They showed that, over four selection cycles, yield of the population increased by 3.5% cycle1 and grain moisture decreased by 1.5% cycle $^{-1}$.Corresponding increase in yield were not detected in testcrosses with inbred line A554 and W117, but cycle four testcrosses had significantly lower grain moisture than corresponding testcrosses with the initial population.

Table(3): pertinent mean squares from analysis of variance and estimates of family's variance components for half-sib (H.S) and first selfing generation (S_1) families of forage botanical composition in maize (2010 summer season).

Characters	Mean squares				σ^2_f	
	Families /sets		Error			
	H. S	S₁	H. S	S₁	H.S	S₁
Forage botanical composition						
Leaves percentage	12.960**	25.252**	2.428	1.105	5.266	12.073
Stem percentage	15.078**	15.621**	3.039	1.346	6.019	7.137
Ear percentage	13.805**	26.608**	2.919	1.265	5.443	12.671
Grain percentage	32.273**	34.220**	4.983	2.938	13.645	15.641
Cob percentage	6.441**	6.784**	0.539	0.437	2.951	3.173
Husk percentage	17.877**	22.259**	0.930	0.671	8.473	10.794

**: Significance at 0.01 level.
σ^2_f Family's variance component.

Estimates of genotypic (σ^2_g), environmental (σ^2_e) and phenotypic (σ^2_{ph}) variances along with coefficient of variation at genotypic (G.C.V.) and phenotypic (P.C.V.) levels for maize botanical composition, derived from half-sib and S_1 families had expressed in (Table 4). Genotypic variances among S_1 families was larger in magnitude than the respective value for half-sib families in each measured botanical characters. Meanwhile, within family's variance, (σ^2_f), environmental variances(σ^2_e) had reduced in S_1 families relative to half-sib families in each measured character. These findings match true with those reported by Hallauer and Miranda (1988)and Fehr (1987) and Ahmed (2006 b).

Values of genotypic and phenotypic coefficients of variation, reflects the variation in terms of genetic or phenotypic as a percentage of character mean. Genotypic variation among half-sib and S_1 families were less than 20% of the studied botanical composition characters mean values, except for cob percentage, that had genotypic variation amount to 24%*vs*. 26%, respectively) and for husk percentage among S_1 families had genotypic variation amount to 22%. Phenotypic coefficients of variation were comparable when derived from half-sib and S_1families, for most studied traits with larger magnitude for estimates from S_1 families, irrespective of the type of family (Table 4). The recent results were in accordance to those reported by Obilana and Hallaua (1974), Lothrop *et.al*, (1985) and Million *et. al*. (2012), Ajala *et.al,* (2010), where, maize population was subjected to both full-sib and S_1 recurrent selection schemes to determine the better of the two procedures for improving the population for tolerance to low soil nitrogen. For both schemes, estimated genetic variances were generally large enough for effective selection to take place. Except for ears per plant and stay green under low-N, genetic variances due to S_1 were larger than those due to full-sib selection. Genetic variances under high-N for most traits were also larger for S_1 than for full-sib, Heritability estimates for all the traits except for root lodging under low-N were moderate to high, but the estimates were higher for S_1 than for full-sib family selection under both selection types.

Table (4): Estimates of variance components and coefficient of variation at genetic (G.C.V.) and phenotypic (P.C.V.) levels for forage yield/plot (kg) and forage botanical composition characters in maize (2010 summer season).

Characters	σ^2_g		σ^2_e		σ^2_{ph}		G.C.V.		P.C.V.	
	H. S	S_1	H. S	S_1	H. S	S_1	H. S	S_1	H. S	S_1
Forage botanical composition										
Leaves (%)	5.266	12.073	1.214	0.552	6.480	12.625	11.96	18.14	10.91	18.55
Stem (%)	6.019	7.137	1.519	0.673	7.538	7.810	6.78	7.47	7.58	7.81
Ear (%)	5.443	12.671	1.459	0.632	6.902	13.303	5.18	7.98	5.83	8.17
Grain (%)	13.645	15.641	2.491	1.469	16.136	17.110	8.81	9.82	9.59	10.27
Cob (%)	2.951	3.173	0.269	0.218	3.220	3.391	24.60	26.23	25.70	27.12
Husk (%)	8.473	10.794	0.465	0.335	8.938	11.129	18.53	22.19	19.03	22.53

H.S: half-sib families S_1: First selfing generation families

Additive and dominance genetic variances were calculated for the base population of maize depending upon two types of evaluated families (half-sib and S_1). The results and illustrated in (Table 5).The estimates of additive variance (δ^2_A) were positive for all studied botanical composition characters. While, the estimates of dominance variance (δ^2_D) were negative for all characters, the ratio of δ^2_A/δ^2_G indicated that additive genetic variance was more effective in controlling all studied botanical composition characters.This might indicate the importance of additive genetic variance in maize population, consequently, selection among inbred progeny would be expected to be superior to other methods under most genetic situations (Weyhrich *et al*.,1998).

Table (5): Estimates of additive (σ2$_A$) and dominance (σ^2_D) variance from the two types of forage botanical composition of maize (2010 summer season)

Characters	σ^2_A	σ^2_D	σ^2_A/σ^2_G
Forage botanical composition			
Leaves percentage	21.064	-35.964	unity
Stem percentage	24.076	-67.756	unity
Ear percentage	21.772	-36.404	unity
Grain percentage	54.580	-155.756	unity
Cob percentage	11.804	-34.524	unity
Husk percentage	33.892	-92.392	unity

Heritability estimates for botanical composition characters (h^2) had presented in Table (6). Estimates were higher in magnitude when calculated from first selfing generation (S_1) compared to half-sib families, for all studied characters. Stem percentage expressed the least estimate heritability among all studied characters in each family type (0.798 and 0.414 for half-sib and S_1 families, respectively). This might indicate the influence of environment in the expression of that character. Meanwhile husk percentage had highest genetic control expressed on heritability estimates from the two studied types of families. The present results are in accordance with the results of Weyhrich et al. (1998), Where heritability estimates ranged from 17.1% from half-sibs to 86.7% from S_2-progeny. In the meantime, high estimates of heritability ranged from 48.1 to 95.2 were recorded by Bekheit and Mahdy (1988), Bakheit (1989a), Ahmed (1992) and Ahmed (2000). Ullah et.al, (2013), evaluated the performance of 196 half-sib families (HSF) derived from Sarhad white variety of maize at the research farm of Agricultural university, Peshawar using partially balanced lattice square design with two replications. Results indicated significant differences among HSF for all studied traits (i.e., flowering traits, plant height, ear height, grain moisture and 100-kernel weight), except, grain yield. Maximum heritability estimate (69.17%) was observed for plant height, while, minimum (5.08%) was observed for days to mid-silking.

Expected genetic advance from selecting the superior 10% families, was higher for S_1 relative to half-sib families, for all studied forage botanical composition characters. Expected gain from selection in units were the lowest for cob percentage (2.893 and 3.034 for half-sib and S_1 family selection, respectively). Whereas, gain was the highest for the grain percentage (5.981 and 6.654 for half-sib and S_1 family's selection, respectively). Relative to the overall mean of character, gain from selecting half-sib families ranged between 41.43% for cob percentage to 8.095% for ear percentage. While gain percent from S_1 family selection ranged between 12.57% for stem percentage to 44.68% for cob percentage. Yagya and Nirania (2005), conducted a research to compare the efficiency of half-sib (HS), Full-sib (FS) and selfed progeny (S_1) recurrent selection methods for improvement in yield, and to improve the per se performance of the ECg_1 PCV_5 pearl millet composite. They found that, half-sib progeny selection method showed 3.17% realized genetic gain, whereas, full-sib progeny selection method showed 11.49% and S_1 progeny selection method showed 31.6% realized genetic gain for grain yield on pooled basis. Thus, S_1 progeny selection method recorded highest realized genetic gain for grain yield as compared to half-sib and full-sib progeny selection methods. Thus, it was revealed that the S_1 progeny selection method is most efficient for improvement in grain yield and its contributing traits in pearl millet. EL-Gazzar, et.al. (2013), The additive gene effects were more important for silking data, plant height, ear height, grain yield. No. of ears/100-plant and ear diameter. While the non-additive gene effects were important for ear length.

Table (6): Estimates of heritability (H), genetic advance in absolute (GA) and percent of mean (GA%) for forage botanical composition of maize (2010 summer season)

Characters	H		GA		GA%	
	H. S	S_1	H.S	S_1	H. S	S_1
Forage botanical composition						
Leaves percentage	0.813	0.956	3.642	5.978	18.98	31.21
Stem percentage	0.798	0.914	3.856	4.496	10.65	12.57
Ear percentage	0.789	0.952	3.648	6.111	8.095	13.69
Grain percentage	0.846	0.914	5.981	6.654	14.27	16.52
Cob percentage	0.916	0.936	2.893	3.034	41.43	44.68
Husk percentage	0.948	0.970	4.988	5.695	31.76	38.46

H.S: half-sib families
S_1: First selfing generation families

The gain from selection in influenced, largely, by the presence of additive variation. The magnitude of genetic advance depends on the magnitude of heritability and some other factors such as selection differential. Accordingly, the expected genetic advance from selection should be higher for S_1 than half-sib families for the studied botanical composition characters. The expected advance from selecting S_1 families was about 1.33 times that from half-sib families as an average for all the studied botanical composition characters. The superiority of S_1 to half sib family selection was attributed to the amount of additive genetic variance with each type of families. These results agreed with the findings of Hallauer and Miranda (1988), Weyhrich et al. (1998), Ahmed (2006-a), Bakheit et.al, (2011). Hallauer and Carena.(2012), stated that, estimates of the genetic variation among progenies tested (σ_g^2), interactions of progenies with environments (σ_{ge}^2), and experimental error (σ^2) were obtained from the combined analyses of variance for each cycle of selection and then averaged across cycles for each selection program. From the estimates of the components of variance, estimates of heritability (h^2) on a progeny mean basis, the genetic coefficient of variation among progenies tested relative to their mean, (GCV), selection differentials (D),

predicted genetic gains (Δ_G), and least significant differences (LSD) were calculated and averaged across cycles of selection. The average estimates of σ_g^2 were largest for inbred progeny selection and smallest for half-sib family selection as expected. Averaged expected genetic gain across all intra-population selection programs was 3.17 ha^{-1}yr^{-1} *vs.* 2.32 q ha^{-1} yr^{-1} for inter-population reciprocal recurrent selection, or 2.64 q ha^{-1} yr^{-1} across all method. On a per cycle and per year basis the differences among types of progeny were relatively small, ranging from (3.75q ha^{-1} yr^{-1} ,1.78 q ha^{-1} cycle^{-1}) for half-sib family selection to (9.62 q ha^{-1} yr^{-1} ,3.21 q ha^{-1} yr^{-1}) for S$_2$inbred progeny selection. Kahriman, *et.al,* (2014), investigated the genetic potential of six maize families for simultaneous selection of oil content and grain yield. Result showed that, there were significant differences among the families and generations for oil content and grain yield. The variation in oil content in the families was mainly controlled by additive gene actions. Estimated genetic gains were in the range of 0.4% to 4.1 % per cycle for oil content, and 17.7 g to 60.7 g per cycle for grain yield. Abdallah, (2014), conducteda line x tester analysis involving 20 testcrosses generated by 10 elite yellow maize inbred lines with two testers to evaluate grain yield and yield related traits. Analysis of variance indicated significant mean squares due to crosses for ear length ear diameter, number of rows per ear, number of kernels per row, 200 kernels weight, and grain yield. The magnitude of general combining ability variance was much greater than specific combining ability variance for all studied traits, except for ear length and number of kernels per row, indicating the preponderance of additive gene action for these traits. Joseph, *et.al,* (2015),stated that, phenotypic and genotypic variances, genotypic coefficient of variation, repeatability

and expected genetic advance were estimated for three flowering and six morphological traits of white kernel low nitrogen donor maize inbred lines. Genotypic and phenotypic variances were equal for floral traits. Thus, gene actions for the traits was additive. Anthesis- silking interval showed high genetic advance with high coefficient of variation suggesting its efficiency for selection. Phenotypic and genotypic correlations of grain yield with each of days to anthesis, plant height ear height, leaf area and number of ears per plant were positive and significant. Genetic effect for grain yield correlated with that of days to silking, but this was not for phenotypic effect. Any of these traits can be selected for grain yield and the lines studied were considered suitable as gene pool in maize breeding for nitrogen stress tolerance.

Dry matter partitioning:

Estimates of minimum, mean and maximum values for maize dry matter percentages, derived from half- sib (H.S) and first selfing generation (S$_1$) had summarized in (Table 7). Reduction in mean values of dry matter characters associated with selfing, reached 0.1, 2.41, 1.62, 1.76, 9.19 and 4.15% for leaves dry matter percentage, stem dry matter percentage, ear dry matter percentage, grain dry matter percentage, cob dry matter percentage, and husk dry matter percentage, respectively. Range value (difference between maximum and minimum values) for half- sib families were higher than the corresponding values for S$_1$ families in leaves dry matter percentage and ear dry matter percentage. While an opposite trend had observed for stem dry matter percentage, grain dry matter, cob dry matter, and husk dry matter percentage. These results were in accordance with those reported by Fehr (1987) and Ahmed (2006a).

Table (7): Estimates of minimum, mean and maximum values, for dry matter percentage of maize (2010 summer season)

Characters	Minimum		Mean		Maximum	
	H. S	**S$_1$**	**H. S**	**S$_1$**	**H. S**	**S$_1$**
Dry matter percentage						
Leaves dry matter (%)	9.565	10.455	16.137	16.121	23.995	22.500
Stem dry matter (%)	31.935	30.710	36.851	35.961	43.990	43.180
Ear dry matter (%)	38.860	39.660	47.946	47.168	54.450	53.990
Grain dry matter (%)	44.735	41.335	49.760	48.882	56.310	55.885
Cob dry matter (%)	10.880	8.850	16.244	14.751	21.935	21.130
Husk dry matter (%)	8.005	6.665	11.914	11.420	18.030	17.070

H.S: half-sib families
S$_1$: First selfing generation families

The pertinent mean squares from analysis of variance over sets and estimates of family's variance component for each of half- sib (H.S) and first selfing generation (S$_1$) families derived from maize regarding dry matter portioning (2010 summer season) had presented in (Table 8). The analysis showed highly significant effects (P$\geq$ 0.01) of families / sets for leaves dry matter percentage, stem dry matter, ear dry matter, grain dry matter, cob dry matter and husk dry matter. Mean

squares among families were of larger magnitude for the first selfing generation (S$_1$) families relative to half- sib families. Meanwhile, within families mean squares took an opposite trend for all studied dry matter characters.

Family's variance component from S$_1$ families were 1.57,1.35, 1.22, 1.28, 1.78 and 1.67 times the corresponding values for half- sib (H.S) families for leaves dry matter percentage, stem dry matter percentage, ear dry matter percentage, grain dry

matter percentage, cob dry matter percentage, and husk dry matter percentage. In general variance components for S_1 family exceeded the variance for half-sib family. These results were in accord-

ance with those reported by Genter and Alexander (1962), Mota *et al.* (1975), Goulas and Lonnquist (1976) and Ahmed (2006b).

Table (8): Pertinent mean squares from analysis of variance and estimates of family's variance components for half- sib (H.S) and first selfing generation (S_1) families of maize dry matter percentage in (2010 summer season).

Characters	Mean squares				σ^2_f	
	Families /sets		Error			
	H.S	S_1	H.S	S_1	H.S	S_1
Dry matter percentage						
Leaves dry matter (%)	38.225**	53.587**	9.400	8.420	14.412	22.583
Stem dry matter (%)	89.515**	97.082**	39.246	29.097	25.134	33.992
Ear dry matter (%)	264.431**	275.078**	91.953	64.297	86.239	105.390
Grain dry matter (%)	208.272**	213.236**	89.386	61.170	59.443	76.033
Cob dry matter (%)	19.694**	25.40**	8.549	5.570	5.572	9.915
Husk dry matter (%)	13.092**	17.943**	4.102	2.934	4.495	7.504

**; Significant at 0.01 level
σ^2_f; Family's variance component

Variance components, i.e.; genotypic (σ^2_g), environmental (σ^2_e) and phenotypic (σ^2_{ph}) and co-efficient of variations at genotypic (G.C.V) and phenotypic (P.C.V) levels for maize dry matter percentage from half- sib (H.S) and first selfing generation families had illustrated in Table (9). Values of genotypic variances estimated from S_1 families were of larger magnitude amounted to1.57, 1.35, 1.22, 1.28, 1.78 and 1.67 times the corresponding values for half- sib families in leaves dry matter percentage, stem dry matter per-centage, ear dry matter percentage, grain dry mat-ter percentage, cob dry matter percentage, and husk dry matter percentage. Opposite to that, envi-ronmental variance estimates from S_1 families were 0.55, 0.74, 0.70, 0.68, 0.65 and 0.71 of the respective values from half- sib families in leaves dry matter percentage, stem dry matter percentage, ear dry matter percentage, grain dry matter per-centage, cob dry matter percentage, and husk dry matter percentage, respectively. The present results were in accordance with the publications of Hallauer and Miranda (1988), Fehr (1987), Fal-coner (1989)and Ahmed (2006-b).

Values of genotypic and phenotypic coeffi-cients of variation, reflects the variation in terms of genetic or phenotypic as a percentage of the char-acter mean. Genotypic variation among half- sib families were less than 20% of the studied dry matter percentage characters mean values, except for leaves dry matter percentage, that had genotyp-ic variation amount to 23% of the of the character mean value. While, genotypic variations among S_1 families were more than 20% of the recorded mean values for most dry matter characters, except for stem dry matter percentage and grain dry matter percentage that showed less than 20% of the char-acters respective mean values. Phenotypic coeffi-

cients of variation were comparable when derived from half- sib and S_1 families for leaves dry matter percentage, cob dry matter percentage, and husk dry matter percentage, with larger magnitude for estimates from S_1 families. Meanwhile, phenotypic coefficients of variation were about the same for the rest of the studied characters, irrespective of the type of family (Table9). The recent results were in accordance to those reported by Obilana and Hallauer (1974), lothrop *et.al.* (1985) and Mil-lon *et. al.* (2012). Ajala *et.al.* (2009), determined the amount of genetic variation present in a maize population, FARZ 23 (096 Ep6), by using full-sib, half –sib and S_1 families. Agronomic and yield data obtained included days to 50% tasseling and silking, plant height, moisture content at harvest, number of ears per plot and grain yield. Heritabil-ity estimates were from moderate to large for most traits. The results revealed, direct selection for grain yield is expected to result in favorable in-crease in other traits except that the selected mate-rials will flower earlier. Since increase in plant height due to selection for grain yield is undesira-ble, it was concluded that the best selection meth-od for yield improvement that will increase height, the least would be full-sib family selection. Kana-garasu, *et al,* (2010),performed combining ability analysis for yield and its component traits Vari-ance due to SCA was greater than GCA variance for the traits *viz.*, grain yield per plant, cob diame-ter, cob length, plant height, ear height, leaf length, 100 grain weight, grain rows per cob, days to 50 percent tasseling and days to 50 percent silking. The variance due to SCA was higher than due to GCA indicating the predominance of non-additive type of gene action in the governance of above-mentioned traits.

Table (9): Estimates of variance components and coefficient of variation at genetic (G.C.V.) and phenotypic (P.C.V.) levels for dry matter percentage of maize (2010 summer season)

Characters	σ^2_g		σ^2_e		σ^2_{ph}		G.C.V.		P.C.V.	
	H. S	S_1	H. S	S_1	H. S	S_1	H. S	S_1	H. S	S_1
Dry matter percentage										
Leaves dry matter (%)	14.412	22.583	4.700	4.210	19.11	26.793	23.52	29.48	27.09	32.11
Stem dry matter (%)	25.134	33.992	19.623	14.548	44.757	48.54	13.60	16.21	18.15	19.37
Ear dry matter (%)	86.239	105.390	45.976	32.149	132.215	136.539	19.37	21.76	23.98	24.77
Grain dry matter (%)	59.443	76.033	44.693	30.585	104.136	106.618	15.49	17.84	20.51	21.12
Cob dry matter (%)	5.572	9.915	4.275	2.785	9.847	12.700	14.53	21.35	19.32	24.16
Husk dry matter (%)	4.495	7.504	2.051	1.467	6.546	8.971	17.79	23.99	21.47	26.23

H.S: half-sib families

S_1: First selfing generation families

Additive and dominance genetic variances were calculated for the base population of maize depending upon two types of evaluated families (half-sib and S_1). The results had presented in (Table 10). Estimates of additive variance (σ^2_A) were positive for all studied dry matter characters. Meanwhile, the estimates of dominance variance (σ^2_D) were negative for all characters. The ratio of σ^2_A / σ^2_G indicated that, additive genetic variance was more effective in controlling leaves dry matter percentage, stem dry matter percentage, ear dry matter percentage, grain dry matter percentage, cob dry matter percentage, and husk dry matter percentage. This might indicate the importance of additive genetic variance in maize population, consequently, selection among inbred – progeny would be expected to be superior to other methods under most genetic situations (Weyhrich et al., 1998).

Table (10): Estimates of additive (σ^2_A) and dominance (σ^2_D) variance from the two types of maize families for dry matter percentage (2010 summer season).

Characters	σ^2_A	σ^2_D	σ^2_A/σ^2_G
Dry matter percentage			
Leaves dry matter (%)	57.648	- 140.26	unity
Stem dry matter (%)	100.536	- 266.176	unity
Ear dry matter (%)	344.956	- 958.264	unity
Grain dry matter (%)	237.772	- 646.956	unity
Cob dry matter (%)	22.288	- 49.492	unity
Husk dry matter (%)	17.98	- 41.904	unity

Heritability estimates for dry matter characters (H) had presented in (Table 11). Estimates were higher in magnitude when calculated from first selfing generation (S_1) compared to half-sib families for all studied characters. Stem dry matter percentage and grain dry matter percentage expressed the least estimate of heritability among the studied characters in each family type (0.56 vs. 0.70 and 0.57 vs. 0.71 for half-sib and S_1 families, respectively). This might indicate the influence of environment in the expression of that characters. Meanwhile, the rest of dry matter characters had higher genetic control expressed on heritability estimates from the two studied types of families. The present results are in accordance with the results of Weyhrich et al. (1998), where, heritability estimation ranged from 17.1 from half-sibs to 86.7% from S_1 progeny. Yousuf and Saleem (2002), estimated significance of differences among seventy four S_1 families obtained from maize population C-17 grown in triplicated randomized complete block design for number of days taken to tasseling, number of days taken to silking, number of ears per plant, 100-grain weight and grain yield per plant. They observed highly significant difference among S_1 families for all the traits, except for, number of ears per plant where it was non-significant. Genotypic variances were greater than the environmental variances for all the traits, except for, number of ears per plant. Heritability estimates were moderate to high for all the plant traits except for number of ears per plant where they were low in magnitude.

Expected genetic advance from selecting the superior 10% families (Table 11) was higher for S_1 relative to half-sib families for all dry matter char-

acters. Expected gain from selection in units were the lowest for cob dry matter percentage and husk dry matter percentage (3.13 *vs*. 4.90 and 3.09 *vs*. 4.41 for half-sib and S_1 family's selection, respectively). Whereas, gain was the highest for ear dry matter percentage (13.19 *vs*. 15.89 for half- sib and S_1 family's selection, respectively). Relative to the overall mean character, gain from selecting half-sib families ranged between 35.94% for leaves dry matter percentage to 17.96% for stem dry matter percentage. While gain percent from S_1 family selection ranged between 23.86% for stem dry matter percentage to 47.64% for leaves dry matter percentage. Souza *et.al,* (2000), studied the response to selection under small effective population size. Thus, the predicted responses to selection based on these expressions will be smaller than those based on the standard procedures for traits with a high level of dominance such as yield. Response to five cycles of half- sib selection were predicted for maize by both expressions, considering that 100 progenies were evaluated and 10 S_1 progenies were recombined, which corresponds to Ne= 10 for each cycle. The accumulated response to selection estimated with the new expression was about 47 and 28% smaller than that based on the standard expression for yield and plant height, respectively. Thus, the expression usually used overestimates the responses to selection, which agrees with reported results, because it does not consider the effective population size that is generally small in recurrent selection programs.

Table (11) : Estimates of heritability (H), genetic advance in absolute (GA) and percent of mean (GA%) for two types of maize dry matter percentage (2010 summer season).

Characters	H		GA		GA%	
	H. S	S_1	H. S	S_1	H. S	S_1
Dry matter percentage						
Leaves dry matter	0.754	0.843	5.80	7.68	35.94	47.64
Stem dry matter	0.562	0.700	6.62	8.58	17.96	23.86
Ear dry matter	0.652	0.772	13.19	15.89	27.51	33.69
Grain dry matter	0.571	0.713	10.25	12.96	20.60	26.51
Cob dry matter	0.566	0.781	3.13	4.90	19.27	33.22
Husk dry matter	0.687	0.836	3.09	4.41	25.94	38.62

H.S; half-sib families.

S_1; First selfing generation families.

The gain from selection in influenced, largely, by the presence of additive variation. The magnitude of genetic advance depends on the magnitude of heritability and some other factors such as selection differential. Accordingly, the expected genetic advance from selection should be higher for S_1 than half- sib families for the studied dry matter characters. The expected advance from selecting S_1 families was about 1.4 times that from half-sib families, as an average for all the studied dry matter characters. These results were in agreement with the findings of Hallauer and Miranda (1988),Weyhrich *et al*. (1998), Ahmed (2006-a) and (Bakheit *et. al.* (2007). Kanagarasu *et. al.* (2010),performed combining ability analysis for yield and its component traits Variance due to SCA was greater than GCAvariance for the traits *viz*., grain yield per plant, cob diameter, cob length, plant height, ear height, leaf length, 100 grain weight, grain rows per cob, days to 50 percent tasseling and days to 50 percent silking. The variance due to SCA was higher than due to GCA indicating the predominance of non-additive type of gene action in the governance of above-mentioned traits. Hallauer and Carena. (2012), stated that. Estimates of the genetic variation among progenies tested (σ_g^2), interactions of progenies with environments (σ_{ge}^2), and experimental error (σ_e^2) were obtained from the combined analyses of variance for each cycle of selec-

tion and then averaged across cycles for each selection program. From the estimates of the components of variance, estimates of heritability (h^2) on a progeny mean basis, the genetic coefficient of variation among progenies tested relative to their mean, (GCV), selection differentials (D), predicted genetic gains (Δ_G), and least significant differences (LSD) were calculated and averaged across cycles of selection. The average estimates of σ_g^2 were largest for inbred progeny selection and smallest for half-sib family selection as expected. Averaged expected genetic gain across all intra-population selection programs was 3.17 ha^{-1}yr^{-1} *vs*. 2.32 q ha^{-1} yr^{-1} for inter-population reciprocal recurrent selection, or 2.64 q ha^{-1} yr^{-1} across all method. On a per cycle and per year basis the differences among types of progeny were relatively small, ranging from (3.75q ha^{-1} yr^{-1} ,1.78 q ha^{-1} cycle^{-1}) for half-sib family selection to (9.62 q ha^{-1} yr^{-1} ,3.21 q ha^{-1} yr^{-1}) for S_2inbred progeny selection.

Conclusion

– Reduction in mean values associated with S_1 families relative to half-sib families reached 0.182, 1.18, 0.98, 3.88, 2.75 and 5.72% for leaves percentage, stem percentage, ear percentage, grain percentage, cob percentage and husk percentage, respectively.

– Genotypic variances among S_1 families was larger in magnitude than the respective value

for half-sib families in each measured botanical characters. Meanwhile, within family's variance, (σ^2_f), environmental variances(σ^2_e) had reduced in S_1 families relative to half-sib families in each measured character.

– Genotypic variation among half-sib and S_1 families were less than 20% of the studied botanical composition characters mean values, except for cob percentage, that had genotypic variation amount to 24% and 26%, respectively.

– The estimates of additive variance (δ^2_A) were positive for all studied botanical composition characters. While, the estimates of dominance variance (δ^2_D) were negative for all characters, the ratio of δ^2_A/δ^2_G indicated that additive genetic variance was more effective in controlling all studied botanical composition and dry matter partitioning characters.

– Estimates of heritability were higher in magnitude when calculated from first selfing generation (S_1) compared to half-sib families, for all studied characters. Stem percentage expressed the least estimate heritability among all studied characters in each family type (0.798 and 0.414 for half-sib and S_1 families, respectively). This might indicate the influence of environment in the expression of that character. Meanwhile husk percentage had highest genetic control expressed on heritability estimates from the two studied types of families.

– Expected genetic advance from selecting the superior 10% familieswas the highest for the grain percentage (5.981 and 6.654for half- sib and S_1 family's selection, respectively).while, expected gain from selection in units were the lowest for cob dry matter percentage and husk dry matter percentage (3.13 *vs*. 4.90 and 3.09 *vs*. 4.41 for half-sib and S_1 family's selection, respectively). Meanwhile, gain was the highest for ear dry matter percentage (13.19 *vs*. 15.89 for half- sib and S_1 family's selection, respectively).

REFERENCES

Abdallah T.A.E. (2014). Combining ability estimates using line x tester analysis to develop high yielding maize hybrids. Egypt. J. Plant Breed. 18 (1): 45-55.

Abreu G. B., M. A. P. Ramalho, F. H. R. B. Toledo, J.C. de Souza. (2010). Strategies to improve mass selection in maize. Maydica 55 (2010): 219-225.

Ahmed, M. Abd El-Satter, (1992).Improvement of barseem clover (*Trifolium alexandrium*, L.) by different methods of selection. Ph. D. Thesis, Fac. Agric.Alex. Univ., Egypt.

Ahmed, M. Abd El-Satter. (2000). Comparison of single trait with multiple trait selection in barseem clover (*Trifoliumalexandrium*, L.)..

J. Agric. Sci. Mansoura Univ., 25: 4601-4613.

Ahmed, M. Abd El-Satter. (2006 a).Variability, correlations and path-coefficient analysis in two populations of multi cut barseem clover. Alex. J. Agric. Res., 51(2): 63-72.

Ahmed, M. Abd El-Satter. (2006 b).Response to three methods of recurrent selection in a Khadarawi barseem (*Trifolium alexandrium*, L.) population. Alex. J. Agric. Res., 51(3): 13-23.

Ahmed, M.Abd EL-Sattar, M.H.EL-Sheikh , Kadria M El-Sayed and Doaa Khamis Abdelmohsen .2010.Combining abilities of forage maize ensilability characters as affected by plant density .Proceeding 2 nd Sci. Conf. Cereals Crops. February 10-11,2010(Alexandria),(1):51-61.

Ajala S.O., C.E. Ago and G. Olaoye, (2009).Comparison of predicted responses to three types of recurrent selection procedures for the improvement of a maize (Zea may, L.) population. Journal of plant breeding and crop science. 1(8): 284-292.

Ajala S.O., J. G. Kling, A. Menkir, and S. O. Alabi.(2010). Full- Sib *vs*. S_1 selection scheme for the improvement of amaize population for tolerance to low soil nitrogen.Maydica 55: 239-248.

Bakheit, B. R. (1989a).The effect of recurrent selection and performance of seed synthetics in barseem clover (*Trifoliumalexandrium*, L.). Forage Res.15:1-7.

Bakheit, B. R. ;M. A. Ali and A.A. Helmy (2011).Effect of selection for crown diameter on forage yield and quality components in alfa alfa (Medicago Sativa L.).Asian, J. of Crop Sci.,3:67-68.

Bakheit, B. R. ;M. A. Ali and A.M. Abdo EL-Wafa (2007).The efficiency of seed yield in the Fahl variety of Egyptian clover (*Trifoliumalexandrium*, L.). J. Agric. Sci., Mansoura Univ., 32(1):11-19.

Bakheit, B. R. and E. E. Mahdy(1988).Improving barseem clover(*Trifoliumalexandrium*, L.)through pedigree selection among and within farmer'sseed lots.Assiut J. Agric. Sci. 19:267-278.

Burton, G. W. and De Vance, E. H. (1953).Estimating heritability in tall Fescue (fescue orundinacea) from replicated clonal material. Agron. J., 45:478-481.

Cochran, W. G. and G. M. Cox.(1957). Experimental Designs.John Wiley & sons.Inc. New York, USA.

Coors, J.G. (1988). Response to four cycles of combined half-sib and S_1 family selection in maize.Crop science 28(6).

EL- Gazzar, I.A.I.; M. A. EL- Ghonemy and S. Th. Mousa.(2013).Evaluation of new inbred lines of white maize via line x tester analysis over three locations. J. plant production, Mansoura Univ. 4(6): 897-906.

Falconer, D. S., (1989). Introduction to quantitative Genetics 3rd Ed., Longman Scientific and Technical, New York, pages: 438.

Fehr, W.R. (1987).Principles of cultivar Development Vol. 1.Theory and technique MacMillian pub.Co, N.y, USA 536p.

Genter, C. F and M.W. Alexander (1962).Comparative performance of S_1 progenies and testcrosses of corn. Crop Sci., 2:516-519.

Goulas, C. K and J. H. Lonnquist. (1976). Combined half-sib and S_1 family selection in maize composite population Crop. Sci., 16:461-464.

Hallauer, A. R. and J. B. Miranda (1988).Quantitative Genetics in maize breeding.Iowa State Univ. Press Ames. Iowa, USA.

Hallauer. A. R., M. J. Carena. (2012). Recurrnt selection methods to improve germplasm in maize. Maydica electronic publication 57: 266-283.

Joseph O. D., O. A. Oduwaye, S. A Olakojo, and D. K. Ojo.(2015). Genetic variability, repeatability, traits relationships and path coefficient analysis in low nitrogen donor white inbred lines of maize (zea mays L.).Maydica electronic publication 60 (3): 962-967.

Kahriman, F., C. O. Egesel and I. Onac (2015). A preliminary study for determination of the possibility of simultaneous selection for oil content and grain yield in maize. Maydica 60(3): 1055-1066.

Kanagarasu S., G. Nallathambi and K.N. Ganesan.(2010). Cobining ability analysis for yield and its component traits in maize (Zea mays L.). Electronic journal of plant breeding 1 (4): 915-920 .

Lonnquist, J. H., (1964). Modification of the ear-to row procedure for the improvement of maize populations Crop Sci., 4:277-288.

Lothrop, J.E.,R. E. Atkins and O. S. Smith(1985). Variability yield and yield components in IAPIR grain Sorghum random – mating population . I. Means, variance components and hertiabilites. Crop Sci. 25:235-244.

Million, F.Habtama and N. Alemayehu.(2012). Genetic variability of Ethiopian fenugreek (trigonella foenum- gracum) Landraces. Tornal of plant breeding and crop Sci., 4(3): 93-84.

Mota, M. O., J. R. Zincly and R. Vencovsky.(1975). Performance of half-sib and S_1-progenies of the maize (Zea mays, L.) variety of centralmex. (cited after pl.breed. Abst; 46:431.

Mutton, G., N. P. Rojas, L. Galicia, A. Rosales, K. V Pixley and N. de Leon. (2013). Cell wall composition and biomass digestibility diversity in Mexican maize (Zea mays, L.) Landraces and CIMMYT inbred lines. Maydica electronic publication, 58: 211-33.

Obilana, A. T. and A. R. Hallauer (1974). Estimates of variability of quantitative traits in BSSS by using un selected maize inbred lines .Crop Sci.14:99-103.

Obilana, A. T. and A. R. Hallauer (1974). Estimation of variability of quantitative traits in BSSS by using unselected maize inbred lines Crop Sci., 14: 99-103.

Sardar, A. H., R. S. Shah and G. Hassan, (2006). Estimates of variability, heritability and genetic advance for fodder traits in two maize populations. Pakistan Journal of Biological Sciences, 9: 2618-2623.

Souza Jr. C.L., I. O. Geraldi and R. Vencovsky (2000).Response to Recurrent selection under small effective population size.Genet.Mol. Biol. 23(4).

Ullah.K., H. UR Rahman, M. Noor, M. UR Rahman, M. Iqbal and S. Ullah. (2013). Heritability Estimates and yield performance of half-sib families derived from maize variety Sarhed white. Sarhad J. Agric. 29(1) 29-32.

Weyhrich R.A., K.R. Lamkey and A.R. Hallauer, (1998). Effective population size and response to S_1- progeny selection in the BS11 maize population. Crop Sci. 38: 1149- 1158.

Yagya, D., and K.S. Nirania. (2005). Efficiency of half-sib, full sib and S_1 progeny recurrent selection methods for improvement in grain and dry fooder yield in pearl millet [pennisetumglaucum (L.) R. Sr.].The Indian Journal of Genetics and plant breeding. 65(4): 257-260.

Yousuf, M. and M. Saleem, (2002).Estimates of heritability for some quantitative characters in Maize. International Journal of Agriculture andBiology, 4 (1): 103-104.

تقدير التصنيفات الوراثيه فى عشيرة اساس من الذره الشاميه باستخدام نوعيين من العائلات

٣-التركيب النباتى و توزيع الماده الجافه

محمد عبد الستار احمد , محمد حسن الشيخ , قدرية محمود السيد , دعاء خميس عبد المحسن

قسم المحاصيل – كلية الزراعة (الشاطبي) جامعة الإسكندرية

الملخص

عشيرة الأساس للدراسة الحالية عبارة عن صنف تركيبي من الذرة الشامية أنتجه الأستاذ الدكتور محمد عبد الستار أحمد استاذ المحاصيل بكلية الزراعة جامعة الإسكندرية بمصر. استخدمت عشيرة الاساس لإنتاج نوعان من العائلات كخطوة سابقة للانتحاب على اساس القدرة الإنتاجية. العائلات المنتجة مثلت كل من العائلات نصف الشقيقة وعائلات الجيل الأول للتلقيح الذاتي . وقد تم تقدير الاختلافات في الوعاء الجيني لعشيرة الاساس اعتماداً علي تفصيص مكونات التباين في صفات كلا نوعي العائلات. بلغ الإنخفاض في قيم متوسطات الصفات المسجلة لعائلات الجيل الأول للتلقيح الذاتي ٠,١٨٢ و ١,١٨ و ٠,٩٨ و ٣,٨٨ و ٢,٧٥ و ٥,٧٢% من القيم المسجلة من العائلات النصف المنسبة لصفات نسبة الأوراق ونسبة السيقان ونسبة الكيزان ونسبة الحبوب ونسبة القوالح ونسبة أغلفة الكوز علي الترتيب. كما كان التباين الوراثي بين عائلات الجيل الأول للتلقيح الذاتي أكبر من القيم المناظرة والمقدرة للعائلات النصف المنسبة لجميع صفات التركيب النباتي وتوزيع المادة الجافة. وفي المقابل فإن التباين داخل العائلات ومكون تباين العائلات والتباين البيئي سجلت قيم أقل عند تقديرها من عائلات الجيل الأول للتلقيح الذاتي بالمقارنة بحالة تقديرها من العائلات النصف المنسبة لجميع الصفات المدروسة. وقد بلغت الاختلافات الوراثية بين العائلات النصف المنسبة وعائلات الجيل الأول للتلقيح الذاتي أقل من ٢٠% من متوسطات صفات التركيب النباتي وصفات توزيع المادة الجافة بين الأجزاء النباتية فيماعدا صفة نسبة القوالح ونسبة أغلفة الكوز التي أظهرت اختلافات وراثية بلغت ٢٤% و ٢٦% علي الترتيب. تقديرات التباين المضيف سجلت قيم موجبة لجميع صفات التركيب النباتي وتوزيع المادة الجافة علي الأجزاء النباتية, بينما كانت تقديرات التباين السيادي سالبة لجميع الصفات, كما أن نسبة التباين الإضافي إلي التباين السيادي يشير إلي ان التباين الإضافي كان أكثر فاعلية في التحكم في صفات التركيب النباتي وتوزيع المادة الجافة بين الأجزاء النباتية. تقديرات معامل التوريث أظهرت قيم مرتفعة عند حسابها من بيانات عائلات الجيل الأول للتلقيح الذاتي مقارنة بالعائلات النصف المنسبة لجميع الصفات المدروسة. وقد سجلت صفة نسبة السيقان أقل تقدير لمعامل التوريث بين جميع الصفات المدروسة في كلا نوعي العائلات (٠,٧٩٨ و ٠,٤١٤ للعائلات النصف المنسبة وعائلات الجيل الأول للتلقيح الذاتي, علي الترتيب) وقد يعبر ذلك عن تأثر الصفات بالبيئة, في ذات الوقت أظهرت صفة نسبة أغلفة الكوز أعلي تحكم وراثي والتي عبر عنها تقديرات معامل التوريث من كلا نوعي العائلات.