Minufiya J. Agric. Res. Vol.36 No. 4: 933 -951 (2011) "http://www.mujar.net"

ESTIMATION OF GENETIC VARIANCE COMPONENTS FOR YIELD AND PROTEIN CONTENT FOR SOME NEW GENOTYPES IN MAIZE

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(Received: Mar. 8, 2011)

ABSTRACT: *Increasing grain protein concentration in maize (Zea mays L.) has not been a major focus of most breeding programs, which mainly focus on yield, maturity, and resistance to stress. The objectives of this research work are:*

(1) Evaluation of the non selected and selected H.S families(the original 100 H.S tested and the 20 % H.S selected) in two locations i.e., Gemmeiza and Sids Agricultural Research Stations, three maize population's i. e., Pool – 15 – 67 CIMMYT, Composite – 45 and Gemmeiza yellow.

(2) Evaluation of the original populations and the first cycles of selection (C0 and C1) of all studied populations in two sowing dates (early and late) at University of Menoufiya Agriculturally Research Farm.

(3) Determine the efficiency of the modified ear – to – row method for improving the yielding ability and protein content of the three maize populations. Considerable amount of genetic variations existed between all maize families within each studied population. At the same time, the mean squares of Genotype x location interaction were highly significant for all studied traits of each population separate. It indicated that the behavior of all traits were obviously differing from location to another. For all studied maize populations, the estimates of genotypic variances for grain yield/plant and protein content traits represented in the main and major partition of the phenotypic variances which reflected high estimates of heritability in broad senses. Increasing and/or decreasing rates of all studied traits due to selection showed that the Ear – to – row selection method was effective in this concern. The data showed that the improved one cycle in 1st sowing date (C_1D_1) had the highest mean values of all studied traits such as protein content and grain yield/plant traits except the days of 50 % silk trait for all studied maize populations. Generally, the improved half-sib maize families of Gemmeiza Yellow population had the higher mean value of protein content % (13.925), while Composite-45 population during the 1st sowing date had the highest mean value of grain yield / plant compared to the other studied maize populations (232 gm).

Key words: *Maize (Zea Mays L.), Genetic Variance, Genotypes, Phenotypes, Heritability.*

INTRODUCTION

Maize breeding programs have always concentrated efforts on increasing yield. Other traits directly related to yield, such as plant architecture and resistance to pests and diseases have also been prioritized to attend the needs of maize growers. Maize is one of the major cereal crops in Egypt for its important to human food, animal and poultry feed up to 70 %, and in the manufacture of bread 20%, some industries such as extracting glucose, fructose and oil. Therefore, the development of cultivars to supply the needs of the grain industrial chain represents a possibility of adding value to the product. Some of the most important traits of interest in the maize market are those related to the nutritional quality of the grains, especially protein and oil content. The protein content is a quantitative trait and several studies have pointed that there is a great number of genes involved in its control. Dudley & Lambert (1992) estimated that there are 173 genes affecting this trait. In a study of quantitative trait loci (QTLs) involving 80 markers regularly spaced in the maize genome, sixteen markers grouped in eight regions had been associated to the protein content (Berke & Rocheford, 1995). Additive and non-additive effects are important and dominance occurs essentially for the reduction of the trait (East & Jones, 1920; Sreeramulu & Bauman, 1970; Berke & Rocheford, 1995). Significant environment and genotype x environment interaction effects are, in general, detected for protein content (Genter *et al.*, 1956; Berke & Rocheford, 1995). Among the environment factors that influence protein content, temperature and availability of water and nitrogen in the soil are the most important. (East & Jones, 1920; Oikeh *et al.*, 1998). Plant genotypes, except not pollen genotype, are the main determinant for grain protein content (East & Jones, 1920; Letchworth & Lambert, 1998). The existence of genetic variability and the prospect of selection for protein content in maize have been demonstrated in several studies (Dudley *et al.*, 1977; Dudley & Lambert, 1992; Micu *et al.*, 1995). After seventy-six generations of divergent mass selection in Burr's White population, the increase in protein content was 139%, or 20 times the standard deviation of the original population, without the exhaustion of genetic variability (Dudley *et al.*, 1977). After 90 generations of selection, the last 25 cycles were evaluated in the same experiment. The average gain by selection cycle was of 0.13 ± 0.02 percentile points (Dudley & Lambert, 1992).

In another study, samples with high protein content (12-15%) have been identified between local populations from Moldova. After 12 years of recurrent selection, lines with up to 23-24% of protein were obtained, without genetic variability being exhausted (Micu *et al.*, 1995).Grain protein quantity and quality have received relatively little attention from breeders although both traits can be manipulated by breeding and information on heritability has been accumulating for many years, particularly about protein quality. This neglect is the consequence of focusing breeding objectives on attributes of immediate concern like yield, maturity and resistance to stresses (Alexander, 1988).

The classical selection experiment for high and low protein maize conducted at the University of Illinois, has provided valuable information on the possibilities and limitations of recurrent selection for this quantitative trait (Dudley *et al* 1974, Dudley and Lambert, 1992). After 90 generation of selections, the Illinois High protein (IHP) strain reached 320gk-1protein and 173 genes were estimated affecting the trait indicating that additional progress should be possible (Dudley and Lambert 1992). Dudley *et al.* (1977), reported a negative correlation between grain yield and protein concentration ($r= -0.70$) and suggested that low protein was dominated to high protein concentration. On the basis of their data, they further proposed selection for intermediate levels of protein content and higher grain yield as appropriate breeding strategy when the target is increasing protein yield per hectare. Boyat *et al.* (1980) crossed the Illinois high protein strain with French germplasm and following pedigree selection developed high protein inbred lines having 20 to 90 gk-1 protein higher than checks. These lines when tested in hybrid combinations had low grain yield , confirming the negative correlation between protein content and grain yield. In contrast, Kauffmann and Dudley (1979) and pollmer *et al.* (1978a) using germplasm with protein quality levels more nearly representative of standard maize , reported low or insignificant genetic and phenotypic correlations between the two traits (pollmer *et al.*, 1978a). These data suggest that simultaneous improvement of both traits should be feasible and the high negative correlation could be pertaining only to the particular Illinois high protein material. The quantitative nature of protein concentration in the grain, along with the evidence that additive genetic variance is of greater importance than the non additive variance, indicate that recurrent selection should be efficient to improve protein quantity and combing ability for yield (pollmer *et al.*, 1978b; Boyat *et al.* ,1980; kaan *et al.*, 1980).

Simultaneous selection for grain yield and protein concentration by maize of half-sib family selection based on desired gain indices in two maize populations over two selection cycles was effective in improving both traits whereas mass selection was as effective as half-sib family selection for increasing protein concentration (Kauffmann and Dudley, 1979). Six cycles of recurrent selection by means of half – sib family index selection for yield and protein concentration or stratified mass selection for grain yield accompanied by block selection for protein concentration resulted in significant gain in both protein and protein yield per hectare with no change in yield. (Alexander, 1988). Pollmer *et al.* (1980), reported that hybrids circularizing high grain yield be developed protein concentration and performance of hybrid combinations between high Ã high or high Ã low protein lines (Pollmer *et al.*, 1978a and Boyat *et al.*,1980).

A new elite populations with both high protein concentration and good combining ability for yield is needed and the appropriate germplasm to develop them exists (Dudley *et al.*, 1996). Such improved populations could be used as source for new inbred lines development and / or improving elite hybrids. Simultaneous improvement of grain yield and protein concentration is feasible and a systematic breeding effort should lead to important new sources of productive and germplasm.

MATERIALS AND METHODS

Modified ear-to-row selection method was conducted in three maize populations i.e., Pool–15– 67 CIMMYT, Composite – 45 and Gemmeiza yellow, during 2002 to 2006 summer growing seasons (except 2004 season) at three various locations; Gemmeiza, (Lower Egypt), Sids (Middle Egypt) Agricultural Research stations, Agricultural Research Center (A.R.C.) and the University of Menoufiya Agricultural Experimental farm. The name, seed color, pedigree, protein content (%) and origin of all the studied populations are presented in Table (1). In 2002 summer planting season, 50 ears from each population were planted to produce 200 half sib families. 100 good looking ears with enough seeds from each population were chosen and divided into two parts; the 1st part was used for evaluation traits and estimation of protein content. The 2nd part was used for planting the selection replicates. In the summer planting of 2003 season, three yield experiments were practiced. All experiments were arranged in Simple Lattice Design (10 x 10) *with* three replications at two various locations i.e., Gemmeiza and Sids Agricultural Research Stations. Plot size was one row; each row was six meters long and 80 centimeters width. Planting was *practiced* in hills which spaced 25 centimeters apart within the row. Therefore, each row contained 25 hills. Hills were marked before sowing and from 2 to 3 kernels were dropped in each hill. After 21 days *from* sowing plants were thinned to one plant per hill and 116 kg N / acre were applied in two equal doses; before the first and the second irrigation. All normal agricultural practices for maize *production* were done in each location as recommended by National Maize Program. In the same season, seeds from the same families within each population, were planted as ear – to – row technique at *Gemmeiza* Agricultural Research Station in an isolated replicate as female rows. While the male was a balanced composite of the 100 families. This replicate was designed as the selection replicate. Selections of half sib families were based on the data of protein content (was determined using the Micro – Kjeldahl method to estimate total nitrogen percentage per 100 gm of *seeds* and multiplied by 6.25 to calculate protein percentage according to Chapman *et al.* (1961), and grain yield per plant (g) together. The information obtained in the yield experiments make it possible to carry out the first selection among half sib families. The selection intensity was 20% (20 families for each population). The second selection will be carried out in the selection replicate. In the summer of 2005 season, the equal number of seeds from the selected families were carefully bulked from each population and planted in plot as non-replicated at Gemmeiza Agricultural Research Station. The plot size was 25 rows, 6 meters long, 80 centimeters width and 25 centimeters between hills in the row. Before silking, all ear shoots were covered by glysine bags to prevent cross-pollination. At 50% silking, pollen grains were collected and bulked from almost all plants within a given subpopulation. The bulk of pollen grains were used to pollinate the all plants within the same plot. Pollinated ears for each population were covered with paper bags and were harvested, dried and shelled together. The seeds were obtained from each sub-population represented cycle one (C1) seeds. In the summer of 2006 season, two field experiments for each population were carried out at University of Menoufiya Agricultural Research farm in two dates, the first date on 26 May and the second on 16 June in order to evaluate the following genotypes:

1- Pool – 15 – 67 CIMMYT Pop. C0.
2- Pool – 15 – 67 CIMMYT Pop. C1.
3- Composite – 45 C0.
4- Composite – 45 C1.
5- Gemmeiza Yellow Pop. C0.
6- Gemmeiza Yellow Pop. C1.

Table (1): The name, seed color, pedigree, protein content (%) and origin of all studied genotypes

POP. NO.	POPULATIONS	ORIGIN	SEED COLOR	PEDIGREE OF POPULATION	PROTEIN COTENT %
1	Pool - 15 - 67 CIMMYT	CIMMYT	White	unknown	7.12
2	Composite – 45	EGYPT	Yellow	Composite of some selected families from population Amarillo Bajio.	11.33
3	Gemmeiza Yellow pop.	EGYPT	Yellow	Derived from genetic pool 33; population 31, 34, 45 and Biak; synthetic varieties 73, B56 and the subtropical population II TA.	11.74

Mstat – C computer program was used for analyzing the available data for selecting the promising half sib families and cycles evaluations trials. In evaluations trials combined analysis were done in Gemmeiza and Sids locations whenever the homogeneity test was not significant. According to Steel and Torri (1980), and Singh and Chowdhury (1985). the available mean squares data were used to estimate the following genetically parameters for separate and combined data:

(1) Genotypic variance : $\delta^2 g = \delta^2 h.s. - \delta^2 e / r$
(2) Phenotypic variance: $\delta^2 ph = \delta^2 g + \delta^2 E$
(3) Environmental variance: $\delta^2 E = \delta^2 e / r$
(4) Heritability in broad sense: $h^2_b = \delta^2 g / \delta^2 ph * 100$
(5) Expected genetic gain from selection: $\Delta G\% = (K * \delta^2 g / \delta ph) * 100$

Where:

K = is constant value equal 1.4 at selection intensity 20 %.
δph= is the standard deviation of Phenotypic variance.

RESULTS AND DISCUSSION

The obtained results could be summarized as follows:

A–Performances of the selected and unselected half-sib maize families for all studied traits:

Highly significant differences among the half-sib maize families (selected and unselected) were obtained in all studied maize populations for protein content trait (Table 2). All mean squares for half-sib families of grain yield / plant trait for all studied populations at the two locations were highly significant. Considerable amount of genetic variations existed between all maize families within each studied population. At the same time, the mean squares of Genotype x location interaction were highly significant of each population separate (Table 3), indicated that the behavior of trait was markedly differing from location to another and explained that the selection among half-sib maize families would be effective using modified Ear – to – row selection method. Composite-45 Pop. had the highest average for all half-sib families (11.779 + 0.108 gm 100 gm-1) while, Gemmeiza yellow population had the highest mean for the selected 20 % maize families (12.910 + 0.049 gm 100gm-1). On the other hand, Pool–15–67 CIMMYT population had lowest average of all 100 half-sib and the selected 20 % maize families for protein content trait 7.326 + 0.092 and 8.143 + 0.040 gm 100gm-1, respectively (Table 4).

Table (2): Analysis of variances for the average of 100 half - sib maize families of Protein content trait for all studied populations

Source of variances	Mean Squares		
	Pool-15-67 CIMMYT Population	Composite – 45 population	Gemmeiza Yellow Population
Replication	0.010	0.0001	0.012
Half Sibs	1.703**	2.332**	5.396**
Error	0.005	0.007	0.009

**: Significant at 0.01 level of probability.

Table (3): Analyses of variances for the average of 100 half sibs of Grain yield trait for all studied populations

SOURCE OF VARIANCES	GRAIN YIELD/PLANT		
	POOL-15-67 CIMMYT POP.	COMPOSITE-45 POPULATION	GEMMEIZA YELLOW POP.
	GEMMEIZA		
Replication	3.498	59.512	3.912
Half sibs	1633.014**	632.124**	2078.587**
Error	335.354	195.816	757.301
	SIDS		
Replication	9.224	27.925	7.463
Half sibs	1754.621**	1004.184**	1862.561*
Error	400.518	231.72	636.931
	COMBINED		
Location	19258.924	11025.264	15329.338
Rep/Loc	7.642	67.301	26.162
Half sibs	2346.322**	1167.684**	2643.902*
Loc x H.S	1041.313*	468.623*	1297.247*
Error	367.936	213.768	697.116

*and **: Significant at 0.05 and 0.01 level of probability.

Table (4): Mean performances of the selected and unselected maize families for protein content (%) trait of all studied maize populations.

MEAN	Pool – 15 - 67CIMMYT	Composite – 45	Gemmeiza Yellow
Mean of 20 % H.S $\pm s\bar{x}$	8.143 ±0.040	12.900 ±0.083	12.910 ±0.049
Mean of all H.S $\pm s\bar{x}$	7.326 ± 0.092	11.779 ± 0.108	11.637 ± 0.164
T - Value	**	**	**

Gemmeiza location had the highest mean value of grain yield / plant for all studied maize populations for 100 H.S and selected maize families (C_1). There were considerable differences between the means of all 100 half-sib and the 20 % selected H.S maize families obtained in all studied maize populations for grain yield/plant trait. These differences explained the possibility of developing yielding abilities in all studied maize populations (Table 5).

Table (5): Mean performances of the selected and unselected maize families for yield of all studied maize populations at two locations and their combined in 2003 season.

Traits	Populations								
	Pool – 15 - 67CIMMYT			Composite – 45			Gemmeiza Yellow		
	Gemm	Sids	Combined	Gemm	Sids	Combined	Gemm	Sids	Combined
20 %H.S	147.045 ±1.857	142.634 ±2.192	144.840 ±2.005	238.725 ±1.854	229.758 ±1.652	234.242 ±1.731	230.625 ± 1.687	214.140 ± 1.862	222.383 ± 1.982
100%H.S	138.215 ± 3.024	131.513 ± 2.112	134.864 ± 2.567	228.184 ±1.897	211.834 ±2.354	220.009 ± 2.007	215.805 ± 2.762	201.564 ± 2.732	208.685 ± 2.937
T-Value	*	*	*	**	**	**	**	*	**

* and ** Significant differences at 0.05 and 0.01 levels of probability.

For all studied maize populations, the estimates of genotypic variances for all studied traits representing the main and major partition of the phenotypic variances which was reflected in high estimates of heritability in broad senses which may allow further improvement through suitable selection method and explained that the selection among half-sib maize families will be effective with modified Ear-to-row method. Kauffmann and Dudley (1979) reported that the genetic variance and covariance estimates from 200 half-sib families were sufficiently accurate to be useful in index development. Abdel-Sabour *et al.* (1989) reported that the genotypic component of variance constituted the major part of the phenotypic variance. Soliman and Sadek, (1999) found that the estimates of phenotypic (δ^2ph) and genotypic (δ^2G) variances were significant for grain yield / plant and indicated that δ^2G was high and constitutes the major part of δ^2ph. Barakat (2003) concluded that the phenotypic (δ^2ph) and genotypic (δ^2g) variances were significant for grain yield trait and genotypic variance (δ^2g) was high and constitutes the major part of phenotypic variance (δ^2ph). In general; heritability estimates in broad sense for all studied traits were high to moderate values obtained for each trait through all studied maize populations at the two locations (Gemmeiza and Sids). This may be due to low estimated (δ^2E) environmental variance. Galal *et al.* (1984) found that the estimate of heritability for grain yield was 92%.The variability parameters; i.e. phenotypic, genotypic and environmental coefficients of variability, took the same trends of phenotypic, genotypic and environmental variances and harmony together. Paterniani (1967) found that the genetic coefficient of variability within each cycle was 15.3, 9.3, 9.1 and 7.0 for the original to the third cycle respectively. For protein content, trait Gemmeiza yellow population had the highest expected gain from selection, as Gs % of mean, which was 19.73% followed by Pool-15-67 CIMMYT population 17.58% and Composite-45 Pop. 12.80%, respectively (Table 6). The expected gain from selection, as ΔGs% of mean, for grain yield/plant trait (Table 7) was higher at Sids location compared to Gemmeiza location and combined data in Pool-15-67, Composite-45 and Gemmeiza yellow populations (19.9, 9.3 and 11.4 %, respectively). Leng(1962) reported that the response from selection in the first ten years was greater than that in any succeeding period.

Table (6): Estimations of Phenotypic, Genotypic and Environmental Variances (δ^2 ph, δ^2 g and δ^2E), heritability in broad sense ($h^2{}_b$), gain from selection (ΔG %), and means for protein content trait in half sib families for all studied populations.

Populations parameters	Pool-15-67	Comp-45	GEMM. Y
Phenotypic Variance(δ^2 pH)	0.852	1.166	2.698
Genotypic Variance (δ^2 g)	0.849	1.163	2.694
Environmental variance (δ^2E)	0.003	0.003	0.004
Plant to plant Variance (δ^2 p L)	0.050	0.070	0.090
Heritability ($h^2{}_b$)	99.65	99.74	99.85
Gain from selection (ΔG %)	17.58	12.80	19.73
Genotypic coefficient of variability	12.58	9.155	14.10
Phenotypic coefficient of variability	12.60	9.167	14.11
Environmental coefficient of variability	0.748	0.465	0.543

Table (7): Estimations of Phenotypic, Genotypic, environmental Variances (δ^2 ph, δ^2 g and δ^2 E), Heritability in broad sense (h^2_b) and Gain from selection (ΔG %) for Grain Yield / Plant trait in 100 half - sib families for all studied population.

Parameters	Grain Yield / Plant								
	Pool – 15 – 67 CIMMYT			Composite - 45			Gemmeiza Yellow		
	Gemmeiza	Sids	Combined	Gemmeiza	Sids	Combined	Gemmeiza	Sids	Combined
Phenotypic Variance (δ^2 ph)	544.338	584.874	340.147	210.708	334.728	187.766	692.862	620.854	456.815
Genotypic Variance (δ^2 g)	432.553	451.368	217.502	145.436	257.488	116.510	440.429	408.544	224.443
Environmental variance (δ^2E)	111.784	133.506	122.645	65.272	77.240	71.256	252.434	212.310	232.372
Plant to plant Variance (δ^2 p L)	3353.5	4005.2	3679.4	1958.2	2317.2	4686.2	7573.0	6369.3	6971.1
Heritability (h^2_b)	79.5	77.2	63.9	69.0	76.9	54.4	63.6	65.8	46.3
Gain from selection (ΔG %)	18.8	19.9	12.2	6.1	9.3	4.3	10.8	11.4	6.5
Genotypic coefficient of variability (G.C.V. %)	15.048	16.155	10.935	5.285	7.575	4.189	9.725	10.028	6.777
Phenotypic coefficient of variability (P.C.V. %)	16.880	18.389	13.675	6.361	8.637	5.681	12.197	12.362	9.965
Environmental coefficient of variability (E.C.V. %)	7.650	8.786	8.212	3.541	4.149	3.837	7.362	7.223	7.305

B – Performances of the first cycle population:

Highly significant differences among genotypes were obtained for all studied traits of the evaluated populations during the two sowing dates (1st and 2nd dates) and their combined data. On the other hand, the Genotypes x Date interactions were not significant in all studied traits. Coefficient of variability was higher in 1st sowing date than 2nd one for protein content trait, while it was higher in 2nd date fot grain yield /plant trait (Tables 8 and 9).

Table (8): Analysis of variance for the C_0 and C_1 cycles and their combined data of Protein content trait for all studied maize populations

S.O.V	Degrees of freedom	Mean squares	Coefficient of variation (%)
DATE (1)			
Replicates	3	1.218	13.4
Genotypes	5	21.621**	
Error	15	2.206	
DATE (2)			
Replicates	3	1.557	12.9
Genotypes	5	22.738**	
Error	15	1.543	
COMBINED			
Dates	1	25.404**	13.2
Rep/Loc	6	1.387	
Genotypes	5	44.252**	
Dates x Genotypes	5	0.106	
Error	30	1.875	

**: Significant at 0.01 level of probability.

Table (9): Analysis of variance for the C_0 and C_1 cycles and their combined data of Grain yield trait for all studied populations

S.O.V	D.F.	Mean Squares
Replicates	3	4.375
Genotypes	5	6456.58**
Error	15	141.575
C.V %		6.0
Replicates	3	53.153
Genotypes	5	5823.18**
Error	15	171.219
C.V %		7.1
Dates	1	2268.75**
Rep/Loc	6	28.764
Genotypes	5	12266.7**
D x G	5	13.050
Error	30	156.397
C.V %		6.5

Increasing and/or decreasing rates of all studied traits due to selection, showed that the Ear – to – row selection method was effective in this concern (Leng, 1962; Paterniani, 1967; Abou- El- Saad *et al.*, 1994). Dudley *et al.* (1974) reported that the mean of protein content in the high protein strain was 26.6% after 70 generations of selection using ear-to-row method representing 244% of the original variety protein content. Significant differences were detected between the two cycles (C_0 and C_1) as shown in Tables (10 and 11) for protein content and grain yield/plant, respectively. Generally, the results showed that the values of half-sib maize families for all studied maize populations of protein content and grain yield / plant traits were higher in the first cycle (C_1) than the original population (C_0). This result was associated with (EL-Agamy *et al.* 1992) for grain yield/plant trait. For all studied maize populations the 1st sowing date had the highest values of protein content (%) compared to the 2nd sowing date and combined data. Significant differences were detected between the two sowing dates using T-test. The data showed that the one cycle improvement in 1st sowing date (C1D1) had the highest mean values of all studied traits such as protein content and grain yield/plant traits. Generally, the improved half-sib maize families of Gemmeiza Yellow population had the higher mean value of protein content % (13.925) as shown in Table (12), while Composite-45 population during the 1st sowing date had the highest mean value for grain yield / plant trait compared to the other studied maize populations (232 gm) in Table (13).

Table (10): Mean performances and increasing and / or decreasing rates of protein content trait for C_0 and C_1 for all maize populations grown in two planting dates.

Dates		Protein content (%)			Increasing p rates (%)		
		Pool-15-67	Com.45	Gem. Y.	Pool-15-67	Com.45	Gem. Y.
Date - 1	C_0	7.915	11.152	11.782	12.2	16.3	18.2
	C_1	8.883	12.975	13.925			
	T – test	*	*	**			
Date - 2	C_0	6.090	9.930	10.523	6.6	9.8	17.3
	C_1	7.558	11.457	12.345			
	T – test	*	*	**			
combined	C_0	7.002	10.541	11.152	9.6	13.2	17.8
	C_1	8.220	12.216	13.135			
	T – test	*	*	**			

* and **: Significant at 0.05 and 0.01 level of probability.

Table (11): Mean performances and increasing and / or decreasing rates of grain yield (gm / plant) trait for C_0 and C_1 of all maize populations grown in two planting dates.

Dates		Grain yield (gm / plant)			Increasing rates (%)		
		Pool-15-67	Com-45	Gemm.Y.	Pool-15-67	Com-45	Gemm.Y
Date - 1	C_0	140.25	221.00	215.00	10.2	5.0	5.8
	C_1	154.50	232.00	227.50			
	T – test	*	*	*			
Date - 2	C_0	129.75	205.50	198.25	10.4	6.6	7.0
	C_1	143.25	219.00	212.25			
	T – test	*	*	*			
combined	C_0	135.00	213.13	206.63	10.3	5.8	6.4
	C_1	148.88	225.50	219.88			
	T – test	*	*	*			

*, significant at 0.05 level of propability.

Table (12): Mean, Rang, Variance, Standard deviation, Standard error and Coefficient of variability of protein content (gm/100gm) trait in all studied populations.

Cycles	Mean ($\bar{x}$)	Rang (R)	Variance (S^2)	Standard deviation (S)	Standard Error ($S\bar{x}$)	Coefficient of variation (C.V %)
	Pool - 15 – 67 CIMMYT population					
C_0D_1	7.615	3.03	1.689	1.300	0.650	17.1
C_0D_2	6.090	2.04	0.694	0.833	0.416	13.7
C_1D_1	8.883	2.02	0.680	0.825	0.412	9.3
C_1D_2	7.558	3.02	2.275	1.508	0.754	19.9
	Composite – 45					
C_0D_1	11.153	5.01	4.275	2.068	1.034	18.5
C_0D_2	9.430	2.01	1.524	1.235	0.617	12.4
C_1D_1	12.975	4.00	2.066	1.437	0.719	11.1
C_1D_2	11.458	3.01	2.255	1.502	0.751	13.1
	Gemmeiza Yellow population					
C_0D_1	11.783	3.01	2.059	1.435	0.717	12.2
C_0D_2	10.523	2.01	0.918	0.958	0.479	9.1
C_1D_1	13.925	3.99	0.900	0.949	0.474	6.8
C_1D_2	12.345	3.02	1.607	1.268	0.634	10.3

Table (13): Mean, Rang, Variance, Standard deviation, Standard error and Coefficient of variability of Grain yield trait in all studied populations.

Cycles	Mean $(\bar{x})$	Rang (R)	Variance (S^2)	Standard deviation (S)	Standard Error $(S\bar{x})$	Coefficient of variability (C.V %)
	Pool - 15 – 67 CIMMYT population					
C_0D_1	140.25	22.00	82.917	9.106	4.553	6.5
C_0D_2	129.75	23.00	109.583	10.468	5.234	8.1
C_1D_1	154.50	23.00	107.00	10.344	5.172	6.7
C_1D_2	143.25	25.00	115.583	10.751	5.376	7.5
	Composite – 45					
C_0D_1	221.00	27.00	134.000	11.576	5.788	5.2
C_0D_2	205.50	1.000	150.917	12.285	6.142	6.0
C_1D_1	232.00	20.00	78.000	8.832	4.416	3.8
C_1D_2	219.00	2.000	177.333	13.317	6.659	6.1
	Gemmeiza Yellow population					
C_0D_1	215.00	31.00	164.700	12.832	6.416	6.0
C_0D_2	198.25	31.00	128.917	11.354	5.677	5.7
C_1D_1	227.50	29.00	145.667	12.069	6.035	5.3
C_1D_2	212.25	24.00	226.917	15.064	7.532	7.1

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تقدير مكونات التباين الوراثى للمحصول ومحتوى البروتين لبعض التراكيب الوراثية الجديدة في الذرة الشامية

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الملخص العربى

أجرى هذا البحث في أعوام ٢٠٠٢ ، ٢٠٠٣ ، ٢٠٠٥ و ٢٠٠٦ أثناء الموسم الصيفي وذلك في ثلاث مناطق هي الجميزة (منطقة وسط الدلتا) و سدس (منطقة مصر الوسطى) ومزرعة كلية الزراعة – جامعة المنوفية – شبين الكوم. وذلك باستخدام طريقة انتخاب كوز/ خط المعدلة والتي تم تنفيذها على ثلاث عشائر من الذرة الشامية وهى : Pool -15-67 CIMMYT, Composite - 45 and Gemmeiza Yellow Pop بهدف تقييم العائلات الغير منتخبة والمنتخبة والعشائر الأصلية (C_0) والدورات الانتخابية الأولى لها (C_1) وكذلك تحديد كفاءة طريقة انتخاب الكوز/ خط المعدلة في تحسين صفات المحصول ومحتوى البروتين لجميع العشائر المدروسة من الذرة الشامية ويمكن ايجاز اهم النتائج المتحصل عليها فى الاتى:

(١) أظهرت عائلات الذرة الشامية النصف أشقاء (المنتخبة والغير منتخبة) فيما بينها اختلافات عالية المعنوية في كل العشائر المدروسة وهذا يدل على اختلاف العائلات فى محتواها البروتينى بما يفسر أن الانتخاب بين عائلات الذرة النصف أشقاء مؤثراً باستخدام طريقة الانتخاب كوز/ خط المعدلة. حقق الصنف Composite-45 أعلى المتوسطات مقارنة بالعشائر الأخرى المدروسة للعائلات الغير منتخبة (١١,٧٧٩ ±٠,١٠٨جم/ ١٠٠جرام) ومن ناحية أخرى أظهرت العشيرة Pool-15-67CIMMYT أقل المتوسطات فى العائلات

الغير منتخبة والمنتخبة لصفة المحتوى البروتينى (٧,٣٢٦ ±٠,٠٩٢و٨,١٤٣ ± ٠,٠٤٠ جرام/ ١٠٠جرام).

(٢) تحققت أعلى تقديرات للكفاءة الوراثية لصفة محتوى البروتين فى Gemmeiza yellow ويليه صنف Composite-45 وأخيراً العشيرة Pool-15-67CIMMYT (٩٩,٨٥، ٩٩,٧٤، ٩٩,٦٥ على التوالي)

(٤) أظهرت متوسطات العائلات النصف أشقاء لصفات المحصول ومكوناته لكل العشائر تحت الدراسة وخلال الموقعين الزراعيين (الجميزة – سدس) معنوية عالية كما وجدت اختلافات وراثية بين عائلات الذرة الشامية داخل كل عشيرة من العشائر الثلاثة المدروسة. وفى نفس الوقت كانت متوسطات التفاعل الموقع x التركيب الوراثى عالية المعنوية لكل الصفات المحصولية للعشيرة الواحدة مشيراً إلى اختلاف سلوك الصفات من موقع إلى أخر. حققت منطقة الجميزة أعلى متوسط لصفة محصول الحبوب وكذلك صفات مكونات المحصول مقارنة بمنطقة سدس لكل العائلات النصف أشقاء المنتخبة والغير المنتخبة ماعدا بعض الحالات ، كما وجدت اختلافات بين متوسطات جميع العائلات المنتخبة والغير المنتخبة لكل العشائر ولكل الصفات المدروسة ، هذه التباينات توضح إمكانية تحسين القدرة المحصولية لكل العشائر تحت الدراسة.

(٥) بالنسبة لكل العشائر الثلاثة تحت الدراسة، وجد أن التباينات الوراثية لكل الصفات المحصولية الجزء الهام والأكبر من التباينات المظهرية والتي أعطت فرصة كبيرة للتحسين من خلال طريقة الانتخاب المناسبة كما أظهرت أن الانتخاب بين العائلات النصف أشقاء أكثر كفاءة باستخدام طريقة الانتخاب كوز/ خط .

(٦) بالنسبة لصفات المحصول ومكوناته فإن معاملات الاختلاف المظهري (Ph.C.V) والوراثى (G.C.V) والبيئي (E.C.V) جاءت متجانسة مع النباتات المظهرية والوراثية والبيئية وأظهرت منطقة سدس أعلى قيمة للتحسين من الانتخاب لصفة محصول الحبوب/ نبات مقارنة بالجميزة والتحليل المشترك للعشائر Composite-45 و Gemmeiza yellow (١٨,٠٤ ، ١٣,١٩%) في حين حققت منطقة الجميزة أعلى معدل تحسين للعشيرة Pool -15-67CIMMYT (٢١,٣٢%).

(٧) أظهرت النتائج وجود اختلافات ذات معنوية عالية بين دورات الانتخاب المحسنة والأصلية (C_0 و C_1) لجميع العشائر الثلاثة وتحت ظروف مواعيد الزراعة المختلفة والتحليل المشترك بينهما لصفة محتوى البروتين .

(٨) إن معدلات الزيادة لصفة محتوى البروتين (%) الراجع إلى الانتخاب أظهر كفاءة عالية لاستخدام طريقة الانتخاب كوز/ خط في التحسين .

(٩) كانت متوسطات العائلات لكل العشائر تحت الدراسة ولكل الصفات المحصولية عالية فى الدورة التحسينية الأولى (C_1) مقارنة بالعشيرة الأصلية (C_0)وأيضاً حقق الميعاد الأول للزراعة (D_1) أعلى المتوسطات في جميع العشائر ولكل الصفات المدروسة مقارنة بالميعاد الثاني (D_2) على مستوى دورات التحسين (C_1،C_0) . كما أظهرت النتائج وجود اختلافات معنوية بين مواعيد الزراعة الأول والثاني . وعموماً حققت الدورة الانتخابية الأولى للعشيرة Composite-45 وخلال ميعاد الزراعة الأول أعلى متوسطات المحصول.