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GENETIC IMPROVEMENT FOR PROTEIN CONTENT AND SOME AGRONOMIC TRAITS IN A WHITE MAIZE POPULATION

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ABSTRACT: *This study was carried out at Gemmeiza and Sids Experimental Stations, Agricultural Research Center (ARC), Egypt. During the two- successive seasons from 2011 and 2012. In 2011 summer season, at Gemmeiza Agricultural Research Station, the S_1 recurrent selection procedure was applied in the new improved cycle (C_0) in the white population (AED Pop.). One hundred and twenty one ears with enough seeds were selected and each was divided into two parts, the first one was assigned for evaluating all studied traits and protein analysis. The second part was kept as remnant S_1 seeds for developing the second cycle for each population. In 2012 summer season, at Gemmeiza and Sids Research Stations, one evaluation trial was conducted. The trial was executed Randomize Complete Block Design (RCBD) with three replications. Data were recorded for grain yield its component and protein yield.*

Mean squares of the protein yield (kg/fed), yield components and agronomic characters were highly significant for all studied traits, indicating that the 121 S_1 progenies of the original cycle (C_0) for this population were different in such traits. Mean squares of genotype x location interaction were highly significant for all characters, indicating that the 121 S_1 progenies were differed in their protein yield and the behavior of these progenies were significantly differed from location to another in this respect for this population. Genotypic and phenotypic variances of protein yield (kg/fed) of 121 S_1 progenies were 2921.92 and 3050.52 at Gemmeiza and 5884.95 and 6403.74 at Sids, respectively. Heritability in broad sense and expected gain from selection of protein yield (kg/fed) of 121 S_1 progenies were 95.78 and 65.13 at Gemmeiza and 91.90 and 38.10 at Sids, respectively. Estimates of heritability in broad sense of 121 S_1 progenies were highly vales for protein yield, grain yield and some other traits of yield components at Gemmeiza and Sids, indicating that, S_1 recurrent selection method were effective to improving of these traits. Mean of protein yield (kg/fed) of 121 S_1 progenies in the original cycle (C_0) for the population AED were 143.0±5.02 and 277.4±5.94 at Gemmeiza and Sids, respectively. While, mean of protein yield (kg/fed) of the highest 10% (12 S_1 progenies) in the same cycle (C_0) were 214.3±17.01 and 373.5±12.53 at Gemmeiza and Sids, respectively.

Key words: *Maize, population improvement, protein content.*

INTRODUCTION

Maize (*Zea mays* L.) is one of the most important cereal crops in Egypt. It ranks the third among cereal crops, after wheat and rice. Maize is used as food, feed, and fodder. It also has several industrial uses such as oil extraction, starch, gluten, alcohol, glucose and ethanol production and many more products.

The main advantage of recurrent selection is to increase the frequency of favorable alleles for the quantitative traits with maintenance of the additive genetic variance (amenable to selection) of such traits in the improved population. S_1 recurrent selection is widely used as an easy and highly efficient procedure for intra-population improvement in maize. Selection based on S_1 progeny performance is effective in utilizing the additive genetic variance in a better way than other intra-population improvement methods and presents an opportunity for selection against major deleterious recessive genes that become homozygous with inbreeding

(Tanner and Smith, 1987; Hallauer and Miranda, 1988).

Globally, maize (*Zea mays* L.) contributes 15% of the protein and 20% of the calories derived from food crops in the world's diet (National Research Council, 1988). In many developing countries in Latin America, Africa, and Asia, maize is the staple food and sometimes the only source of protein in diet. Besides using maize grain as human food, it also contributes 70% of animal feed and as an important secondary source for high quality vegetable oil, as well as many industrial purposes. Grain quality is an important objective in corn breeding (Mazur *et al.*, 1999 and Wang and Larkins, 2001). In corn grain, a typical hybrid cultivar contains approximately 4% oil, 9% protein, 73% starch, and14% other constituents (mostly fiber).

Breeding for improved protein quality in maize began in the mid-1960s with the discovery of mutants, such as opaque-2, that produce enhanced levels of lysine and tryptophan, the two amino acids deficient in maize endosperm proteins. However, adverse pleiotropic effects imposed severe constraints on successful exploitation of these mutants (Prasanna *et al.*, 2001). The International Maize and Wheat Improvement Center (CIMMYT) has developed" Quality Protein Maize" (QPM) that has improved kernel quality characteristics over opaque-2 soft genotypes, by introducing modifier genes and selecting for a hard, vitreous endosperm opaque-2 germplasm (Rodrigues and Chaves, 2002). The biological value of the common maize protein is equivalent to approximately 40% of the biological value of milk protein, while for QPM maize this value is 90% (National Research Council, 1988). The CIMMYT QPM populations, pools, inbreds, and hybrids adapted to subtropical and tropical environments are widely used in the development of high-lysine maize in Brazil, China, Ghana, India, and several Latin American countries (Vasal, 2001).

The main objectives of the present study were to study:

1- The effectiveness of S_1 recurrent selection procedure for improving protein percentage, yield and some of its components and other agronomic characters in two maize populations *i.e.*, A.E.D. white population and G.M.Y. yellow population.
2- The genotypic and phenotypic variance components, beside some of statistical and genetical parameters in the two cycles (C_0 and C_1) of the two populations for different studied traits.

MATREIALS AND METHODS

This study was carried out at two experimental research stations, Gemmeiza and Sids, Agricultural Research Center (ARC), Egypt, during the two - successive seasons started from 2011 and 2012. The name, origin, pedigree and protein percentage of the maize population used in this study are presented in Table 1.

In 2011 summer season, at Gemmeiza Agricultural Research Station, the S_1 recurrent selection procedure was applied in the new improved cycle (C_0) in the AED Population. One hundred and twenty one ears with enough grains were selected and each was divided into two parts, the first one was assigned for evaluating all studied traits and protein analysis. The second part was kept as remnant S_1 grains for developing the second cycle for each population.

Table (1): The name, origin, pedigree and protein percentage of the maize population used in this study.

Population	Origin	Pedigree	Protein%
AED (white)	CIMMYT	Open pollinated exotic population	9.8

In 2012 summer season, at Gemmeiza and Sids Research Stations, one evaluation trial was conducted. The trial experiment was executed in Randomize Complete Block Design (RCBD) with three replications. Data were recorded for grain yield and protein percentage.

The data were recorded on protein yield (Kg/fed.), grain yield (ard/fed), ear length, ear diameter, number of rows/ear, number of kernels/row, 100- kernel weight, plant height, ear height, ear position%, days to 50% tassling, days to 50% silking and resistance of late wilt%.

According to Singh and Chaudhary (1977), the available MS was used to estimate the following genetical parameters for separate and combined data.

Estimation of σ^2g, σ^2gl and σ^2ph were calculated for the yield evaluation of S_1 families of C_0 and these values were to calculate, heritability of S_1 families (h^2 b) and consequently expected genetic advance per cycle from the following equation as given by Singh and Chaudhary (1977):

1- Genotypic variance (σ^2_g) s and (σ^2_g) c and genotypic variance x location interaction ($\sigma^2_{g\,x\,L}$).
2- Phenotypic variance (σ^2_{ph}) s and (σ^2_{ph})c and Phenotypic variance x location interaction (σ^2_{ph} x L)
3- Heritability in broad sense
$h^2_b = \sigma^2_g / \sigma^2_{ph} \times 100$
4- Expected genetic gain from selection
$\Sigma G\ \% = 100\ K\ h^2\ \sigma ph / X$
Where: K =selection intensity for (10 %) = 1.76, h^2 = heritability of S_1 family, σ ph = phenotypic standard deviation, and x = mean performances

RESULTS AND DISCUSSION

Protein yield and yield components :

1-Analysis of variance and genetic parameters for 121 S_1 progenies:

Analysis of variance for protein yield (kg/fed), grain yield (ard/fed) and its components traits for 121 S_1 progenies for cycle (C_1) at the two locations Gemmeiza and Sids for AED population (Tables 2 and 3).

Table (2): Mean squares from analysis of variance for protein yield, grain yield and its components traits for 121 S_1 progenies in the AED population tested at Gemmeiza and Sids in 2012 season.

S. O. V.	d.f	M. S.						
		Protein yield (kg/fed)	Grain yield (ard/fed)	Ear length (cm)	Ear diameter (cm)	No. of rows / ear	No. of kernels/ row	100 kernel weight (g)
Gemmeiza								
Rep.	2	4070.99	21.16	13.09	0.50	5.37	329.09	295.21
Genotypes	120	9151.55**	43.77**	4.61**	0.24**	3.24**	21.64**	12.57**
Error	240	385.78	1.82	1.54	0.08	1.14	9.30	1.41
C.V.%		13.74	13.46	7.53	6.26	7.38	8.81	2.85
Sids								
Rep.	2	2241.35	10.89	3.89	0.06	6.02	24.28	10.71
Genotypes	120	12807.47**	57.84**	5.84**	0.11**	4.48**	14.46**	28.14**
Error	240	1037.57	5.16	0.61	0.02	1.27	3.82	4.52
C.V.%		11.61	11.68	4.42	3.11	7.86	5.19	5.95

** Significant at 0.01 levels of probability.
C.V.% Coefficient of Variability

Table (3): Mean squares from analysis of variance for some agronomic and Resistance to late wilt % traits in 121 S_1 progenies in the AED population tested at Gemmeiza and Sids in 2012 season.

S. O. V.	d.f	M. S.					
		Days to 50 % tassling	Days to 50 % silking	Plant height (cm)	Ear height (cm)	Ear Position %	Resistance to late wilt %
Gemmeiza							
Replications	2	37.10	43.44	4556.20	3125.83	44.04	0.30
Genotypes	120	9.95**	11.80**	728.98**	479.24**	70.05**	95.49**
Error	240	0.84	1.11	161.56	90.72	18.01	13.35
C.V.%		1.51	1.72	6.97	8.39	6.80	3.90
Sids							
Replications	2	6.25	55.57	37.65	6.25	0.05	64.73
Genotypes	120	14.88**	13.95**	708.22**	399.23**	24.03**	187.70**
Error	240	1.52	1.35	90.36	67.40	7.00	34.97
C.V.%		2.16	1.97	4.42	7.42	5.16	6.40

** Significant at 0.01 levels of probability.
C.V.% Coefficient of Variability

Mean squares of the protein yield (kg/fed), grain yield (ard/fed) and its components and agronomic characters were highly significant for all studied traits, indicating that the S_1 progenies of the original cycle (C_0) for this population were different in such traits. At the same time, mean squares of genotype x location interaction were highly significant for all characters, indicating that the 121 S_1 progenies were differed in their protein yield and the behavior of these progenies were significantly differed from location to another.

2- Estimates of genetic parameters for 121 S_1 progenies:

Estimates of genetic parameters for the protein yield (kg/fed) and yield components and agronomic characters in the original cycle (C_0) at the two locations in AED Population (Tables 4 and 5).

Genotypic and phenotypic variances of protein yield (kg/fed) of 121 S_1 progenies were 2921.92 and 3050.52 at Gemmeiza and 5884.95 and 6403.74 at Sids, respectively. Genotypic and phenotypic variances of grain yield (ard/fed) of 121 S_1 progenies were 20.98 and 21.89 at Gemmeiza and 26.34 and 28.92 at Sids, respectively. For ear length (cm), genotypic and phenotypic variances of 121 S_1 progenies were 1.02 and 2.05 at Gemmeiza and 2.62 and 2.92 at Sids, respectively (Table 4).

For ear diameter (cm), genotypic and phenotypic variances of 121 S_1 progenies were 0.08 and 0.12 at Gemmeiza and 0.05 and 0.06 at Sids, respectively. For number of rows/ear, genotypic and phenotypic variances of 121 S_1 progenies were 0.70 and 1.43 at Gemmeiza and 1.61 and 2.24 at Sids, respectively. For number of kernels/rows, genotypic and phenotypic variances of 121 S_1 progenies were 6.17 and 10.82 at Gemmeiza and 5.32 and 7.23 at Sids, respectively. For 100-kerenl weight (g), genotypic and phenotypic variances of 121 S_1 progenies were 3.72 and 6.05 at Gemmeiza and 11.81 and 14.07 at Sids, respectively (Table 4).

Table (4): Estimates of genotypic and phenotypic variance (σ^2g and σ^2ph), heritability in broad sense (h^2_b %) and gain from selection (Δg%) for protein yield (kg/fed) and its components traits in the AED population tested at Gemmeiza and Sids in 2012 season.

Parameter	trait						
	Protein yield (kg/fed)	Grain yield (ard/fed)	Ear length (cm)	Ear diameter (cm)	No. of rows / ear	No. of kernels / row	100 kernels weight (g)
Gemmeiza							
σ^2g	2921.92	20.98	1.02	0.08	0.70	6.17	3.72
σ^2ph	3050.52	21.89	2.05	0.12	1.43	10.82	6.05
h^2_b %	95.78	95.84	49.96	66.67	48.95	57.02	61.49
Δg %	65.13	64.10	7.63	51.14	7.51	9.05	5.32
Sids							
σ^2g	5884.95	26.34	2.62	0.05	1.61	5.32	11.81
σ^2ph	6403.74	28.92	2.92	0.06	2.24	7.23	14.07
h^2_b %	91.90	91.08	89.55	81.82	71.65	73.58	83.94
Δg %	38.10	36.18	12.49	6.33	10.73	7.53	12.66

Table (5): Estimates of genotypic and phenotypic variance (δ^2g and δ^2ph), heritability in broad sense (h^2_b %) and gain from selection (Δg%) for other agronomic traits in the AED population tested at Gemmeiza and Sids in 2012 season.

Parameter	trait					
	Days to 50 % tassling	Days to 50 % silking	Plant height (cm)	Ear height (cm)	Ear Position %	Resistance to late wilt %
Gemmeiza						
σ^2g	4.56	3.56	283.71	129.51	26.02	27.38
σ^2ph	4.98	5.72	364.49	224.50	35.03	45.52
h^2_b %	91.56	62.35	77.84	57.69	74.29	60.15
Δg %	4.84	3.54	11.71	11.31	10.11	6.38
Sids						
σ^2g	6.68	6.30	308.93	165.92	8.52	76.37
σ^2ph	7.44	6.98	354.11	199.62	12.02	93.85
h^2_b %	89.78	90.32	87.24	83.12	70.87	81.37
Δg %	6.16	5.82	10.96	15.26	6.88	12.27

According days to 50% tassling, (Table 5) genotypic and phenotypic variances of 121 S_1 progenies were 4.56 and 4.98 at Gemmeiza and 6.68 and 7.44 at Sids, respectively. According days to 50% silking, genotypic and phenotypic variances of 121 S_1 progenies were 3.56 and 5.72 at Gemmeiza and 6.30 and 6.98 at Sids, respectively. According plant height (cm), genotypic and phenotypic variances of 121 S_1 progenies were 283.71 and 364.49 at Gemmeiza and 308.93 and 354.11 at Sids, respectively. According ear height (cm), genotypic and phenotypic variances of 121 S_1 progenies were 129.51 and 224.50 at Gemmeiza and 165.92 and 199.62 at Sids, respectively. For ear position%, genotypic and phenotypic variances of 121 S_1 progenies were 26.02 and 35.05 at Gemmeiza and 8.52 and 12.02 at Sids, respectively. For late wilt%, genotypic and phenotypic variances of 121 S_1 progenies were 27.38 and 45.52 at Gemmeiza and 76.37 and 93.85 at Sids, respectively (Table 5).

Estimates of heritability in broad sense (h^2_b) % and gain from selection (Δg %) for the protein yield (kg/fed) and its components and agronomic characters in the original cycle (C_0) at the two locations in AED population are presented in (Tables 4 and 5).

Heritability in broad sense and gain from selection of protein yield (kg/fed) of 121 S_1 progenies were 95.78 and 65.13 at Gemmeiza and 91.90 and 38.10 at Sids, respectively. Heritability in broad sense and gain from selection of 121 S_1 progenies were 95.84 and 64.10 at Gemmeiza and 91.08 and 36.18 at Sids for grain yield (ard/fed), respectively. For ear length (cm), heritability in broad sense and gain from selection of 121 S_1 progenies were 49.96 and 7.63 at Gemmeiza and 89.55 and 12.49 at Sids, respectively. Heritability in broad sense and gain from selection of 121 S_1 progenies were 66.67 and 51.14 at Gemmeiza and 81.82 and 6.33 at Sids for ear diameter (cm), respectively (Table 4).

For number of rows/ear, heritability in broad sense and gain from selection of 121 S_1 progenies were 48.95 and 7.51 at Gemmeiza and 71.65 and 10.73 at Sids, respectively. For number of kernels/rows, Heritability in broad sense and gain from selection of 121 S_1 progenies were 57.02 and 9.05 at Gemmeiza and 73.58 and 7.53 at Sids, respectively. For 100-kerenl weight (g), heritability in broad sense and gain from selection of 121 S_1 progenies were 61.49 and 5.32 at Gemmeiza and 83.94 and 12.66 at Sids, respectively (Table 4).

According days to 50% tassling, heritability in broad sense and gain from selection of 121 S_1 progenies were 91.56 and 4.84 at Gemmeiza and 89.78 and 6.16 at Sids, respectively. According days to 50% silking, heritability in broad sense and gain from selection of 121 S_1 progenies were 62.35 and 3.54 at Gemmeiza and 90.32 and 5.82 at Sids, respectively. According plant height (cm), heritability in broad sense and gain from selection of 121 S_1 progenies were 77.84 and 11.71 at Gemmeiza and 87.24 and 10.96 at Sids, respectively. According ear height (cm), heritability in broad sense and gain from selection of 121 S_1 progenies were 57.69 and 11.31 at Gemmeiza and 83.12 and 15.26 at Sids, respectively. For ear position%, heritability in broad sense and gain from selection of 121 S_1 progenies were 74.29 and 10.11 at Gemmeiza and 70.87 and 6.88 at Sids, respectively. For late wilt%, heritability in broad sense and gain from selection of 121 S_1 progenies were 60.15 and 6.38 at Gemmeiza and 81.37 and 12.27 at Sids, respectively (Table 5).

Sadek *et al.* (1986) found that heritability estimates in broad sense in AED were 49.2, 22.9, 32.8, 42.2, 25.0, 13.6 and 23.4% for silking date, plant height, late wilt resistance, grain yield, 100-kernels weight, number of rows/ear and ear length, respectively. While, in Gemmeiza-7421 population, heritability estimates were 55.0, 57.9, 37.3, 75.2, 66.0, 61.0 55.2 and 45.3 for the same traits, respectively. Singh *et al.* (1989) found that the expected genetic gain was higher in the spring season. Coors (1988) showed that heritability estimates in broad sense were 76% for S_1 family for grain yield. Nawar *et al.* (1995) found that the highest estimates of

the expected genetic advance from different selection methods obtained from full-sib family selection either based on S_1 or S_2. Soliman *et al.* (1999) indicated that the expected genetic gain from selection of the best 10% families were 31.70 and 7.41% for grain yield and late wilt resistance, respectively. Barakat (2003) found that the expected genetic gain from selection of the best 10% families was high and in the better direction for all studied traits.

Generally, estimates of heritability in broad sense of 121 S_1 progenies were highly vales for protein yield, grain yield and some other traits of yield components at Gemmeiza and Sids indicating that, S_1 recurrent selection method were effective to improving of these traits.

3- Mean performances of 121 S_1 and 12 S_1 progenies of AED Population:

Mean of the protein yield (kg/fed) and its components and agronomic characters for 121 S_1 progenies and the highest selected 10 % (12 S_1 progenies) in the original cycle (C_0) for the AED population at two locations are presented in (Table 6).

Mean of protein yield (kg/fed) of 121 S_1 progenies in the original cycle (C_0) were 143.0±5.02 and 277.4±5.94 at Gemmeiza and Sids, respectively. While, mean of protein yield (kg/fed) of the highest 10% (12 S_1 progenies) in the same cycle (C_0) were 214.3±17.01 and 373.5±12.53 at Gemmeiza and Sids, respectively. Mean of grain yield (ard/fed) of 121 S_1 progenies in the original cycle (C_0) were 10.0±0.35 and 19.5±0.40 at Gemmeiza and Sids, respectively. While, mean of grain yield (ard/fed) of the highest 10% (12 S_1 progenies) in the same cycle (C_0) were 14.7±1.31 and 26.1±1.04 at Gemmeiza and Sids, respectively.

Mean of ear length (cm) of 121 S_1 progenies in the original cycle (C_0) were 16.5±0.11 and 17.7±0.13 at Gemmeiza and Sids, respectively. While, mean of ear length (cm) of the highest 10% (12 S_1 progenies) in the same cycle (C_0) were 17.2±0.37 and 19.0±0.37 at Gemmeiza and Sids, respectively. Mean of ear diameter (cm) of 121 S_1 progenies in the original cycle (C_0) were 4.7±0.03 and 4.6±0.02 at Gemmeiza and Sids, respectively. While, mean of ear diameter (cm) of the highest 10% (12 S_1 progenies) in the same cycle (C_0) were 4.3±0.08 and 4.4±0.03 at Gemmeiza and Sids, respectively. Mean of number of rows/ear for 121 S_1 progenies in the original cycle (C_0) were 14.5±0.09 and 14.3±0.11 at Gemmeiza and Sids, respectively. While, mean of number of rows/ear for the highest 10% (12 S_1 progenies) in the same cycle (C_0) were 14.9±0.30 and 14.7±0.19 at Gemmeiza and Sids, respectively.

Mean of number of kernels/row for 121 S_1 progenies in the original cycle (C_0) were 34.6±0.24, and 37.7±0.20 at Gemmeiza and Sids, respectively. While, mean of number of kernels/row for the highest 10% (12 S_1 progenies) in the same cycle (C_0) were 36.5±0.83 and 38.8±0.38 at Gemmeiza, and Sids, respectively. Mean of 100-kernels weight (g) of 121 S_1 progenies in the original cycle (C_0) for the population (A) were 41.7±0.19 and 35.7±0.28 at Gemmeiza and Sids, respectively. While, mean of 100-kernels weight (g) of the highest 10% (12 S_1 progenies) in the same cycle (C_0) were 40.5±0.62 and 36.6±0.60 at Gemmeiza and Sids, respectively.

Mean of days to 50% tassling, days to 50% silking, plant height (cm), ear height (cm), ear position% and resistance of late wilt % of 121 S_1 progenies in the original cycle (C_0) for the AED population 60.6±0.17, 61.4±0.18, 182.3±1.42, 113.5±1.15, 62.5±0.44 and 93.7±0.51 at Gemmeiza and 57.2±0.20, 59.0±0.20, 215.1±1.40, 110.6±1.05, 51.3±0.26 and 92.4±0.72 at Sids, respectively. While, mean of the same traits of the highest 10% (12 S_1 progenies) in the same cycle (C_0) were59.3±0.50, 59.8±0.49, 186.9±5.02, 117.3±4.19, 117.3±4.19 and 95.4±2.24 at Gemmeiza and 56.0±0.49, 57.4±0.40, 225.2±3.98, 115.8±3.68, 63.2±1.62 and 96.0±1.06 at Sids, respectively.

Table (6): Mean per formances of some characteristics of the highest 12 S_1 progenies in first cycle of the Pop. A.

Trait	Loc.	Pedigree												Mean ± Sx	Mean of all progenies ± Sx	t-Value
		2	18	115	35	4	85	11	60	9	92	107	46			
Protein yield/ (kg/fed)	Gem.	353.0	288.9	227.2	236.7	165.1	137.5	205.6	196.9	218.0	200.9	175.8	165.8	214.3±17.01	143.0±5.02	**
	Sids	399.7	426.5	352.7	422.4	367.2	411.4	282.4	389.4	370.0	317.8	396.4	346.2	373.5±12.53	277.4±5.94	**
Grain yield/ (ard/fed)	Gem.	25.2	20.0	13.9	16.6	9.2	9.4	13.4	13.0	16.9	12.6	14.0	11.6	14.7±1.31	10.0±0.35	*
	Sids	28.5	30.0	22.8	28.7	23.1	29.4	20.4	26.4	25.7	21.6	31.5	24.9	26.1±1.04	19.5±0.40	*
Ear length (cm)	Gem.	20.0	17.5	17.2	16.2	18.0	14.9	16.5	18.3	18.0	17.0	16.6	16.7	17.2±0.37	16.5±0.11	*
	Sids	20.3	20.8	17.9	18.7	17.7	18.2	18.3	21.0	17.8	18.2	20.5	18.2	19.0±0.37	17.7±0.13	*
Ear diameter (cm)	Gem.	5.2	4.4	4.5	4.8	4.8	4.3	4.7	4.9	5	4.4	4.5	4.7	4.3±0.08	4.7±0.03	**
	Sids	4.9	4.6	4.8	4.8	4.8	4.7	4.8	4.6	4.7	4.8	4.8	4.9	4.4±0.03	4.6±0.02	**
No. of rows/ ear	Gem.	16.4	14.6	13.0	14.6	15.4	15.4	15.4	15.8	15.6	14.0	13.2	14.8	14.9±0.30	14.5±0.09	N.S
	Sids	15.2	14.2	14.2	15.2	14.8	15.8	15.0	14.0	15.4	15.0	13.6	14.4	14.7±0.19	14.3±0.11	N.S
No. of kernels/ row	Gem.	42.5	40.5	33.9	34.5	32.8	38.2	33.3	36.9	35.9	36.6	36.6	35.8	36.5±0.83	34.6±0.24	N.S
	Sids	40.5	38.7	37.7	39.0	38.0	37.6	39.8	40.5	38.9	36.1	39.1	39.9	38.8±0.38	37.7±0.20	N.S
100-kernels weight (g)	Gem.	38.6	36.3	42.1	42.7	40.3	38.5	38.5	42.3	43.2	42.2	40.2	40.6	40.5±0.62	41.7±0.19	N.S
	Sids	40.3	36.8	39.9	35.0	36.5	35.4	37.5	37.1	33.8	35.9	37.3	33.6	36.6±0.60	35.7±0.28	N.S

*, ** and N.S indicates significant differences at the 0.05, 0.01 and non-significant probability, respectively.

Table (6) : Continued.

Trait	Loc.	Pedigree												Mean ± Sx	Mean of all progenies ± Sx	t-Value
		2	18	115	35	4	85	11	60	9	92	107	46			
Days to 50% tassling	Gem.	57	59	60	58	56	61	62	60	59	59	60	61	59.3±0.50	60.6±0.17	N.S
	Sids	57	57	54	54	55	58	57	56	54	58	54	58	56.0±0.49	57.2±0.20	N.S
Days to 50% silking	Gem.	58	60	60	58	57	62	62	61	58	60	61	61	59.8±0.49	61.4±0.18	N.S
	Sids	58	59	56	56	56	59	58	57	56	59	56	59	57.4±0.40	59.0±0.20	N.S
Plant height (cm)	Gem.	200.0	202.5	175.0	197.5	187.5	152.5	190.0	205.0	182.5	190.0	202.5	157.5	186.9±5.02	182.3±1.42	**
	Sids	210.0	232.5	220.0	257.5	212.5	220.0	220.0	237.5	212.5	217.5	237.5	225.0	225.2±3.98	215.1±1.40	**
Ear height (cm)	Gem.	122.5	122.5	107.5	147.5	115.0	100.0	110.0	120.0	115.0	105.0	140.0	102.5	117.3±4.19	113.5±1.15	*
	Sids	110.0	130.0	107.5	140.0	97.5	115.0	105.0	127.5	102.5	110.0	120.0	125.0	115.8±3.68	110.6±1.05	**
Ear Position %	Gem.	61.7	60.5	61.4	74.7	61.4	65.4	57.6	58.6	63.1	55.3	69.0	70.0	63.2±1.62	62.5±0.44	N.S
	Sids	52.4	55.9	48.9	54.4	45.8	52.3	47.7	53.7	48.3	50.6	50.5	55.6	51.3±0.94	51.3±0.26	N.S
Resistance to late wilt %	Gem.	100.0	97.1	100.0	97.1	100.0	76.5	88.2	100.0	100.0	100.0	100.0	85.3	95.4±2.24	93.7±0.51	N.S
	Sids	93.7	100.0	94.1	94.1	91.2	91.2	100.0	100.0	100.0	100.0	93.8	94.1	96.0±1.06	92.4±0.72	N.S

*, ** and N.S indicates significant differences at the 0.05, 0.01 and non-significant probability, respectively.

Finally, the S_1 *per se* selection method was effective in improvement of the two populations under study. Mittelmann *et al.* (2003) found that genetic gain estimates for protein content varied from 4.07 to 8.97 %. The lowest estimates of genetic gain were observed for oil content. They indicated that estimates of additive variance for protein and oil content in maize populations were significant. Ajala *et al.* (2009), found that the grain yield varied from 1 to 4 t/ha for the S_1 families and 2.5 to 6.6 t/ha for the half-sibs. The means showed that S_1 selection for plant height and grain yield were greatly reduced when compared with the other two methods. Gamea (2010), found that the average increasing rate of grain yield per cycle was 9.7% in the LOCAL Pop. and 6.6% in the Pop-59E. Gupta *et al.* (2013) found that, Vivek Quality Protein Maize (QPM) 9, the improved QPM hybrid, showed 41% increase in tryptophan and 30% increase in lysine over the original hybrid. Okporie *et al.* (2013), found that, genetic gains were 2.1% from protein, 0.1% from lysine, 1.4% from oil, 0.5% for amylpectin and 3.7% from sugar. While, genetic losses of -0.1 days in the number of days to 50% tasseling and -2.5 days in the number of days to 50% silking.

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التحسين الوراثى لمحتوي البروتين و بعض الصفات المحصولية فى عشيرة بيضاء من الذرة الشامية

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الملخص العربي

أجريت هذه الدراسة في محطتي بحوث الجميزة و سدس بمركز البحوث الزراعية خلال الفترة من٢٠١١-٢٠١٢.

وكانت أهداف الدراسة:-

١ – تقدير كفاءة طريقة الانتخاب المتكرر الـ S_1 في تحسين نسبة البروتين والصفات المحصولية في عشيرة من الذرة الشامية البيضاء الأمريكاني بدري (AED Population).

٢ – تقدير مكونات التباين الوراثي والمظهري في أنسال S_1 في نفس العشيرة لمختلف الصفات.

وقد تم إجراء التلقيحات الذاتية سنة ٢٠١١ في محطة بحوث الجميزة لعدد ٥٠٠ نبات في العشيرة تحت الدراسة لإنتاج أنسال S_1 وذلك لتنفيذ طريقة الانتخاب المتكرر لـ S_1 .

في سنة ٢٠١٢ زرعت أنسال S_1 في تجربة في جهتين (سدس والجميزة) ، ونفذت التجربة في تصميم قطاعات كاملة العشوائية في ثلاث مكررات.

بناء على التحليل الإحصائي لبيانات هذه التجارب تم انتخاب ١٠ % من أنسال S_1 الأعلى في محصول البروتين ومحصول الحبوب لعمل جميع التوليفات الممكنة لكل التراكيب الوراثية .

سجلت القياسات على الصفات التالية :-

محصول البروتين (كجم/فدان) ، نسبة البروتين ، محصول الحبوب (اردب/فدان) ، طول الكوز (سم) ، قطر الكوز (سم) ، عدد الصفوف / كوز ، عدد الحبوب / صف ، وزن ١٠٠ حبة (جم) ، ارتفاع النبات (سم) ، ارتفاع

الكوز (سم)، موضع الكوز ، تاريخ التزهير في النورة المذكرة ، تاريخ التزهير في النورة المؤنثة و نسبة المقاومة لمرض الذبول المتأخر.

و يمكن تلخيص أهم النتائج المتحصل عليها فيما يلي : -

١- كانت هناك اختلافات عالية المعنوية بين أنسال الـ S_1 في قدرتها لمحصول البروتين ومعظم الصفات المدروسة لكل التراكيب الوراثية.

٢ – أظهرت النتائج وجود اختلافات عالية المعنوية لصفة محصول البروتين و الصفات الخضرية الأخري مما يدل علي ان ١٢١ S_1 كانت مختلفة لكل الصفات تحت الدراسة.

٣ – تراوح متوسط محصول البروتين (كجم/ فدان) لأنسال الـ S_1 قبل الإنتخاب بين ١٤٣,٠ ± ٥,٠٢ كجم /فدان بالجميزة ، ومن ٢٧٧,٤ ± ٥,٩٤ كجم/ فدان بسدس ، بينما تراوح المتوسط لهذه الصفة فى نباتات الـ S_1 المنتخبة بين ٢١٤,٣ ± ١٧,٠١ كجم /فدان في الجميزة ، ومن ٣٧٣,٥ ± ١٢,٥٣ كجم /فدان في سدس. هذا المتوسط الأخير كان عاليا ومختلف معنويا عن المتوسط العام لأنسال الـ S_1 قبل الانتخاب.

٤- اختلفت مكونات التباين المظهري اختلافا معنويا لكل التراكيب الوراثية فى العشيرة تحت الدراسة. وكان هناك تباينا واسعا مما شجع على استخدام الانتخاب المتكرر للـ S_1 في تحسين مثل هذه التراكيب الوراثية لمحصول البروتين .

٥ – كانت قيم درجة التوريث بالمعنى الواسع لانسال الـ S_1 لصفة محصول البروتين (كجم/فدان) عالية (٩٥,٧٨ و ٩١,٩٠%) في الجميزة وسدس على الترتيب .

٦ – حقق التحسين المتوقع على أساس انتخاب أفضل ١٠ % من سلالات S_1 لصفة محصول البروتين ارتفاعا بلغ ٢٣,٠٨ % في الجميزة و ١٥,٠٧% في سدس.