

RESPONSE TO THREE METHODS OF RECURRENT SELECTION IN A KHADARAWI BARSEEM (*TRIFOLIUM ALEXANDRINUM* L.) POPULATION

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ABSTRACT

Several studies on response to selection have been completed for Barseem clover, although comparisons of the effectiveness of selection methods have been difficult. The ideal comparison of selection methods would involve selection for the same trait by using different selection methods in a common base population. This type of data are lacking in Barseem. The present study was designed to compare the response to three different selection methods in Khadarawi Barseem population. One cycle of selection was conducted for each of the following methods: half-sib with S_1 as recombiners (H.S), S_1 -families (S_1) and S_2 -families selection. Selection for all programs was based on protein yield (ton-fad⁻¹). A 20% selection intensity was common in the three methods. Response to selection was measured for protein yield and correlated responses on fresh forage, dry forage, seed yield and leaves / stems ratio. All selection methods were successful in improving significantly the population performance for protein yield. S_2 family selection had the largest magnitude of response of 0.346 ton.fad⁻¹. cycle⁻¹ (37.32%), which was insignificantly different from the realized response for S_1 family selection of 0.322 ton.fad⁻¹. cycle⁻¹ (34.74%). H.S family selection gave the lowest gain of 0.157 ton.fad⁻¹. cycle⁻¹ (16.94%). Taking into account both cost. unit⁻¹ gain and length of time required, S_1 families selection had the highest rate of gain. Season⁻¹ with the greatest return on investment.

Key words: Khadarawi Barseem clover, recurrent selection, H.S families, S_1 families, S_2 families, response to selection, relative economic gain.

INTRODUCTION

Recurrent selection methods have been used to improve Barseem clover populations. Recurrent selection includes; a) Development of progenies, (b) Evaluation of progenies and (c) Recombination of selected families or progenies. Recurrent selection methods differ in the type and number of progenies evaluated, size of selected population, parental control and the type of progenies intermated (Hallauer and Miranda, 1988). The flexibility of different types of recurrent selection methods allow for the use of wide range of recurrent selection methods for population improvement with wide range of responses to selection, regardless of the type of recurrent selection method. The common objectives are: (a) Increasing the mean performance of the population and (b) Maintaining genetic diversity to enable long-term improvement.

Many workers studied the effect of different recurrent selection methods in improving yield and other characters of Barseem population. Koriem *et al.* (1980) reported 20.5% gain from one cycle of recurrent selection, based on general combining ability in Meskawi population of over two locations. Mikhiel (1987) recorded a positive response of 22% in forage yield after one cycle of half-sib selection. Bakheit and Mahdy (1988) tested the efficiency of pedigree selection in improving fresh forage yield of Meskawi population and recorded an improvement of 14.14%. Bakheit (1989a) reported realized gains of 13.9 and 21.7% for fresh forage yield, 14.8 and 23.8% for dry forage yield and 14.0 and 22.9% for protein yield from the first and second cycles of recurrent selection in Meskawi population, respectively. Bakheit (1989b), in a Fahl population of Barseem, scored a realized gain from modified mass selection for seed yield of 6.03

and 9.31% for fresh forage, 5.57 and 10.86% for protein yield and 13.23 and 16.19 for seed yield in cycles 1 and 2, respectively, over the base population. Ahmed (1992) concluded that maternal-line selection with S_1 , as recombiners, was superior to both half-sibs and controlled mass selection in Meskawi. The realized gain from that study was 22% in both green and dry forage. Ahmed (2000) obtained a realized gain from recurrent selection for total green forage yield in a Meskawi population *via* combining ability test of 6.6, 6.0, 4.0 and 10.3% for total green forage, dry forage and protein and seed yields.

These studies indicated that recurrent selection methods were effective for improving Barseem population productivity, but it was not clear which of the recurrent selection methods was the most efficient. Several studies on response to selection have been completed for Barseem, although comparisons of the effectiveness of selection methods have been difficult because, in many instances, different selection methods were used with different populations for the same traits; The same method was used in different populations for the same traits or the same method was used in the same population, but for different traits. The ideal comparison among selection methods would involve selection for the same trait by using different selection in a common base population. However, these types of data are lacking in Barseem. The objectives of the recent study were: (i) to compare response to selection for three intra-population recurrent selection methods, including half-sib (H.S), S_1 - family (S_1) and S_2 - family (S_2) in one base population and (ii) to determine the most effective and efficient method for improving Barseem germplasm.

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MATERIALS AND METHODS

Parental materials:

The base population under study comprised 37 farmers and market seed lots of Khadarawi multi-cut Barseem clover. In 2000-2001 season, seeds of the base population were sown in 400 rows, 20 cm apart and 4.0 m. long, at the rate of 31.4 kg. ha⁻¹. Cultural practices were applied as recommended for optimum Barseem productivity. Six cuts were taken before adjusting spacing within row to 10 cm among plants through uprooting small-tagged plants.

Half-sib family selection:

In 2000-2001, 400 plants were visually selected before flowering, depending on crown size and general performance. Those selected plants were marked by woodsticks tagged "OP" to indicate the collection of their open pollinated seeds. The highest seed producing 100 plants were saved as half-sib families. In 2001-2002 season, the 100 half-sib families were evaluated in five sets, each with twenty families. Each set was treated as a randomized complete block experiment to evaluate the twenty families with two blocks. One-row plots of 1.5 m. length and 20 cm apart were used. Seeding rate was 31.4 kg.ha⁻¹ (1.03 g. plot⁻¹). Each plot was guarded by two rows planted with base population seeds. Green forage yield was determined from the middle meter of each plot (0.2 m²) from six cuts taken after 60, 100, 135, 195 and 225 days from sowing. A seventh cut was taken after thirty days from the last, but was not included in the evaluation. Dry matter percentage was determined in each cut from random samples of about 100 g., placed in an oven at 70 °c until weight constancy, then presented as a seasonal average. Protein yield was estimated from the data of green forage yield, dry matter percentage and crude protein percentage determined by micro-kjeldahl technique, as outlined by A.O.A.C. (1980) from a composite sample, representing cuts. The data of protein yield were transformed to tons/fad before statistical analysis, according to the following model: protein yield = sets, Rep/ sets, families / sets and combined error using SAS program (1988). Variance components for families (σ^2_f) and error (σ^2_e) were estimated from the analysis of variance. According to the family means, the highest yielding five families, in each set, were identified. This resulted in selection intensity of 20%. Values of (σ^2_f) and (h^2) calculated according to Fehr (1987), were used to estimate the expected genetic advance from selection.

Depending on the results of evaluation, the excluded families were uprooted before flowering. Heads of the best plants, in each selected family, were caged in fine translucent paper bages. Hand tripping was practiced to enhance selfing. S₁-seeds were separately harvested for each selected family.

In 2002-2003 season, S₁-seeds of selected families were planted in isolated plots for intercrossing to produce seeds of the first cycle of half-sib family selection, with population as tester, designated as (C₁ H.S).

S₁-family selection:

Progenies were developed for S₁-family selection by selfing about 400 plants in 2000-2001 season's nursery. Those plants were marked by wood sticks tagged S₁. Hand tripping was applied to enhance setting. S₁ seeds were harvested from each selfed plant, separately, to represent S₁-family. One-hundred S₁ families, with sufficient selfed seeds, were saved. Families evaluation was carried out during 2001-2002 season in a similar manner to half-sib families evaluation, where, five sets each of twenty families with two replicates were used. The plot size was one row, 1.0 m long and 20 cm apart, seeded at the rate of 31.4 kg.ha⁻¹(0.69 g. plot⁻¹). Each plot was guarded by two rows planted with base population seeds. Data collection and statistical analysis were applied in a similar manner to that of H.S-families. A selection intensity of 20% was applied. The highest protein yielding five families, in each set, were identified (a total of twenty families). In 2002-2003 season, the remnant seeds of the selected S₁ -families were planted in isolated plots for inter-crossing to produce seeds of the first cycle of S₁-family selection, designated as (C₁ S₁).

S₂-family selection:

S₂-family selection was conducted by selfing 300 plants in the nursery of 2000-2001 season. S₁-seeds were harvested for each plant, separately. One-hundred and forty S₁-families, with adequate seeds were maintained. In 2001-2002 season, a part of each S₁-family seeds was grown by the ear-to-row method. Rows were subjected to normal cutting schedule. Starting from cut five, weak families were discarded. Also, weak plants, in each maintained row, were uprooted. Three to five vigorous plants in each S₁-row were marked by woodsticks tagged (S₂). Heads of marked plants, in each row, were covered by fine paper bags for isolation. Hand tripping was frequently applied to permit seed setting. After seed harvest, 100 S₂-families with enough seeds, each derived from a single plant in a different S₁ line, were selected. In 2002-2003 season, S₂-families were evaluated in a replicated trial similar to that applied in H.S-family evaluation. Selection of 20% intensity was applied within each set. In 2003-2004 season, seeds of S₁-families, corresponded to the selected S₂ -families, were planted isolated plots for intercrossing to produce seeds of the first cycle of S₂-family selection, designated as (C₁ S₂).

Estimation of additive and dominance variances:

It was assumed that the gene frequency for "Khadarawi" population would be near to one-half and, consequently, the estimates of variance components, for the three types of families, would be used to calculate (σ^2A) and (σ^2D), as follows (Hallauer and Miranda, 1988):

$$\begin{aligned} \sigma^2 H.S &= 1/4 \sigma^2 A \\ \sigma^2 S_1 &= (1) \sigma^2 A + 1/4 \sigma^2 D \\ \sigma^2 S_2 &= 3/2 \sigma^2 A + 3/16 \sigma^2 D \end{aligned}$$

Such equations were expressed in a matrix notation and solved, using the least squares procedure, as illustrated by Bernardo (2002). The estimates of (σ^2A) and (σ^2D) were used for estimating the expected genetic advance from selecting the superior 20% families in each selection program, when appropriate, as indicated by Fehr (1987). Heritability was calculated on mean of plot basis, as indicated by Fehr (1987).

Evaluation of selection methods:

In 2004-2005 season, the first cycle of the selection methods were evaluated in two adjacent experiments. Each experiment included six entries [base population (C_0), C_1 , H.S, C_1 , S_1 , C_1 , S_2 , Minufeia – Khadarawi population(check₁), Sohag – Khadarawi population(check₂)], replicated six times in a randomized complete block design. Experiment 1 was treated by 10 kg of nitrogen fed-cut (a total of 50 Kg. N. fed.-season) in the form of ammonium nitrate (33.5% N), whereas, experiment 2 was treated by 20 kg of nitrogen fed.- cut (a total of 100 kg. N. fed.-season) in the same form as in experiment 1. Each entry –plot was four rows, 20 cm apart and 4.0 m long. Data were recorded for: 1). Green forage yield of six cuts from two random samples of 0.25 m² from each plot, transformed to tons/ fed before analysis, 2). Dry forage yield, estimated from seasonal fresh forage yield and seasonal average dry matter percentage, 3)

Leaves / stems ratio in dry weight basis (determined at the fifth cut, only), 4). Protein yield, estimated from dry forage yield and crude protein percentage and 5). Seed yield, determined from at random 0.25 m² samples from each plot and transformed to kg / fad. before analysis. The two experiments were statistically combined, as given by Steel and Torrie (1980). The tested entries (C_1 – populations, C_0 and the two checks) were considered fixed, while the environments were random.

RESULTS AND DISCUSSION

Families evaluation:

The analysis of variance of Khadarawi Barseem characters for H.S, S_1 and S_2 families is presented in Table 1. The results indicated that the differences among families were highly significant ($P \geq 0.01$) for all measured traits. The among families mean squares were increased from H.S to S_1 to S_2 , while, the within families variances were, generally, of opposite order.

The variance component (σ^2f) for S_1 families was 3.70, 1.12, 5.08 and 3.15 times the corresponding values for H.S families for protein yield, fresh forage yield, dry matter and protein percentage, respectively. Whereas, the variance component for S_2 families was 1.90, 1.36, 1.33 and 1.14 times the corresponding values for S_1 families for protein yield, fresh forage yield, dry matter and protein percentages, respectively. These results are in accordance with reports on other crops. Genter and Alexander (1962) showed that variation among S_1 families was of higher magnitude than their test crosses. Lonquist and Lindsey (1964), also, found that variance component for S_1 family was four times the H.S. family variance. Mota *et al* (1975) and Goulas and Lonquist (1977) found that the genetic variance, among S_1 lines, was three times that among H.S. families.

Table 1: Pertinent mean squares from analysis of variance and estimates of variance components for families (σ^2f) for H.S, S_1 and S_2 families of Khadarawi Barseem.

Character	Mean squares						σ^2f		
	Families			Error			H.S	S_1	S_2
	H.S	S_1	S_2	H.S	S_1	S_2			
Protein yield (ton/fad)	0.1039**	0.3131**	0.5604**	0.0335	0.0505	0.0614	0.0352**	0.1313**	0.2495**
Fresh forage yield(kg/0.2m ²)	0.4990**	0.4837**	0.5671**	0.1809	0.1273	0.0834	0.1590**	0.1782**	0.2419**
Dry matter percentage	4.846**	15.422**	17.89**	2.551	3.7615	2.418	1.148**	5.830**	7.738**
Crude protein percentage	8.177**	18.209**	18.322**	3.717	4.1384	2.308	2.230**	7.035**	8.007**

** Significant at 0.01 level.

Falconer (1967) and Hallauer and Miranda (1988) showed that the genetic variance among various types of families was the expectation of: $1/4 \sigma^2A$ for H.S families, $\sigma^2A + 1/4 \sigma^2D$ for S_1 families and $3/2 \sigma^2A$ and $3/16 \sigma^2D$ for S_2 families, where σ^2A and σ^2D denote additive and dominance effects, respectively. The additive and dominance genetic variance components were calculated for the base population, depending upon the three types of evaluated families from the above mentioned three equations. The results are presented in Table 2. The estimates of σ^2A were positive for the studied characters. Meanwhile, negative estimates of dominance variance (σ^2D) were

detected for both protein and fresh forage yields, indicating the absence of σ^2D . The ratio of σ^2A / σ^2G indicated that additive genetic variance was more effective in controlling both protein and fresh forage yields, whereas, both additive and dominance genetic effects were effective in dry matter and crude protein percentages. Weyhrich *et al* (1998) stated that, if additive genetic variance was of greater importance in a population than dominance variance, selection among inbred – progeny would be expected to be superior to other methods under most genetic situations.

Table 2: Estimates of additive (σ^2A), dominance (σ^2D) and (σ^2A / σ^2G) variances from the three types of families for the studied characters.

Character	σ^2A	σ^2D	σ^2A / σ^2G
Protein yield (ton / fad)	0.1321	- 0.1418	1.00
Fresh forage yield (kg / 0.2m ²)	0.706	- 0.9883	1.00
Dry matter percentage	4.607	5.132	0.47
Crude protein percentage	9.674	1.511	0.86

Heritability estimates of differences among family means (h^2) were higher in magnitude when calculated from S_2 , compared to both S_1 and H.S families for all studied characters (Table 3). Also, S_1 estimates were larger in magnitude than the corresponding figures from H.S families. All estimates of S_1 were more than 0.7, whereas, estimates of S_2 were above 0.8 for all Khadarawi Barseem traits. As for H.S, the h^2 estimates were over 0.6, except for dry matter and crude protein percentages, which scored 0.47 and 0.55 values. So far, there is no literature about the estimates of heritability from different inbreeding levels in Barseem clover, however, the present findings are in accordance with the results of Weyhrich *et al.* (1998), based on data obtained from the Annual Reports of the Cooperative Federal-State Corn Breeding Investigations, Ames, Iowa, USA, (1963) through (1989), where values of heritability estimates ranged from 47.1 (H.S) to 86.7%

(S_2 – progeny). Those figures were consistent with data published by Lamkey and Hallauer (1984). Ahmed (2006) found that heritability estimate, for dry forage yield in Khadarawi population, was larger in magnitude than that of seasonal fresh forage yield. That was true in the present results with protein yield (ton / fad), supposing that variations in protein yield contributed to better estimation of seasonal forage yield. High estimates of h^2 , ranged from 84.1 to 95.2, were reported for Barseem characters by Bakheit and Mahdy (1988), Bakheit (1989), Ahmed (1992), Ahmed (2000) and Ahmed (2006).

Table 3: Estimates of heritability (h^2), expected genetic advance from recurrent selection (G) and relative genetic advance from selection (G%).

Character	h^2			G'					
				H.S		S_1		S_2	
	H.S	S_1	S_2	Units	%	Units	%	Units	%
Protein yield (ton / fad ⁺)	0.6769	0.8358	0.8904	0.4322	47.97	0.4638	51.48	0.6598	73.23
Fresh forage yield (kg / 0.2m ²)	0.6373	0.7366	0.8529	0.8913	42.16	0.5072	23.99	0.6359	30.08
Dry matter percentage	0.4736	0.7560	0.8649	2.065	15.02	2.939	21.38	3.622	26.35
Crude protein percentage	0.5453	0.7730	0.8741	3.088	21.09	3.265	22.30	3.704	25.30

* Calculated according to Fehr (1987).

+ One faddan = 4200m².

Expected genetic advance from selection (Table 3) was the highest for S_2 families, followed by S_1 , and was lowest for H.S families. Protein yield / faddan showed the largest magnitude of relative genetic advance from selection over the three types of families. For fresh forage yield / faddan, the relative advance from H.S selection (42.16%), unexpectedly, was superior to the corresponding values from S_1 (23.99%) or S_2 (30.08%) selection. For H.S selection, the relative advance ranged from 15.02 for dry matter percentage to 47.97 for protein yield / faddan. As for S_1 selection, the relative advance ranged from 21.38 (for dry matter percentage) to 51.48 (for protein yield / faddan). Regarding S_2 selection, the relative advance ranged from 25.3 (for protein percentage) to 73.23 for protein yield.

The gain from selection is 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_2 than for S_1 and H.S families for the different studied characters. The expected advance from S_2 was about 1.3 times that from S_1 and 1.23 times that from H.S families, as an average for all the studied characters. The superiority of S_2 over S_1 and H.S families was attributed to the amount of additive genetic variance within each type of families. These results are in agreement with the findings of Hallauer and Miranda (1988) and Weyhrich *et al*, (1998). Ahmed (2000),

with Meskawi population, obtained values for average genetic advance ranging from 30.0 to 41.22% with total green forage and seed yields, respectively. Also, Ahmed (2006), with Khadarawi population, scored values of average advance between 43.46% (for plant height) and 22.14% for dry matter percentage.

C₁- evaluation trial:

The C_1 populations, designated as C_1 . H.S, C_1 S_1 , C_1 S_2 , in addition to C_0 and two Khadarawi check populations were evaluated in two separate experiments, which represented a random environment (Nitrogen level). The data of the two experiments were subjected to combined analysis as a split-plot design, where, the interaction between populations X nitrogen was used to test the significance of the differences between populations (Table 4). Only the effect of populations was found highly significant ($P \geq 0.01$) for all studied traits. Neither the environments (nitrogen levels) nor the populations X environments interaction reached the level of significance for any of the studied characters. Consequently, the average response of populations, over the two environments, was reported.

Table 4: Analysis of variance for green forage yield, dry forage yield, protein yield, leaves / stem ratio and seed yield of Khadarawi Barseem populations under two nitrogen levels.

S.O.V	d.f.	M.S.				
		Green forage yield (ton / fad.)	Dry forage yield (ton / fad.)	Protein yield (ton / fad.)	Leaves / stem ratio	Seed yield (kg / fad.)
Env. (N)	1	65.19 ^{NS}	7.98 ^{NS}	0.572 ^{NS}	370.00 ^{NS}	18365.9 ^{NS}
Rep/env.	5	176.15	13.84	0.375	359.04	9052.9
Populations (P)	5	105.51**	10.78**	0.470**	115.56**	5267.95**
N XP	5	0.539 ^{NS}	0.095 ^{NS}	0.010 ^{NS}	14.61 ^{NS}	915.9 ^{NS}
Combined error	50	23.96	1.016	0.019	20.52	1294.8

N.S: Not significantly different ($P \geq 0.05$).

** : Significantly different at 0.01 level.

Direct response to selection:

The means and percents realized gain in protein yield (ton / fad.) for base, improved and check populations of Khadarawi Barseem, averaged over the two tested environments, are presented in Table 5. The results showed that the improved populations were significantly higher than both the base population C_0 and the two checks. Insignificant difference was obtained between S_1 and S_2 families selection. Meanwhile, both the S_1 and S_2 family selection methods were significantly superior to H.S.

The realized gain per cycle, due to selection, was the highest with S_2 family selection, reaching 0.346 ton / faddan (37.32 and 36.00% relative to base and the average of checks, respectively). The obtained figures, with S_1 family selection, were 0.322 ton / fad. (34.74 and 33.44% relative to the base and the checks average, respectively). As for H.S families selection, the realized gain was 0.157 ton / fad. (16.94 and 15.81 relative the base and the average of checks, respectively).

When the realized gain was calculated on a per year basis, S_1 family selection gave about two times gain / year than H.S family selection (11.15 vs. 5.27%). That gain per year, from S_1 selection was greater than gain from S_2 family selection, (9.00%).

The fact that the additive genetic variance in Khadaeawi population (Table 2) was of greater importance than dominance variance might explain the superiority of inbred-progeny selection. Falconer and Mackay (1996) stated that inbred progeny selection

might not necessarily increase mean performance by directly acting to increase the frequency of favorable alleles, but by directly decreasing the frequency of deleterious recessive alleles.

The discrepancy, however, between predicted (Table 3) and realized gain (Table 5) was not unique to the present. Possible reasons for this discrepancy involved the overestimation of heritability in the families evaluation trial. Lamkey and Hallauer (1987) showed that, when heritability was estimated from the variance among families in the selection trials, heritability might be biased upwards and represented an upper bound of the heritability for certain progeny type. Likewise, heritability based on single-year data, such as the case in selection trials, was biased upwards because of genotype X year interaction being confounded in the numerator (Comstock and Moll, 1963). Another possible reason for the lack of relationship between predicted and realized gain was the potential for the genotype X environment interactions, experienced in the selection environment not to be representative of the genotype X environment interactions that occurred in multi-year evaluation trials (Comstock and Moll, 1963). In the calculation of σ^2A and σ^2D , it was assumed that gene frequency with the base population equalled 1/2. The difference between the actual gene frequency and the assumed could be the reason for the discrepancy of the results.

Table 5: Population means and realized gain(%) from selection for protein yield (ton / fad.) in Khadarawi Barsoem averaged over two environments.

Population and selection method	Mean	Realized gain (%)			
		Per cycle		Per year	
		C ₀	Checks	C ₀	Checks
Khadarawi "C ₀ "	0.927c ⁺				
H.S selection	1.084 b	16.94	15.81	5.65	5.27
S ₁ selection	1.249 a	34.74	33.44	11.58	11.15
S ₂ selection	1.273 a	37.32	36.00	9.33	9.00
Checks					
Check population ₁	0.934 c				
Check population ₂	0.938 c				
Average	0.936				

* Realized gain% relative to base = $C_1 - C_0 / C_0 \times 100$.
relative to checks = $C_1 - \text{check average yield} / \text{check average} \times 100$
+ Means followed by a similar letter are not significantly different at 0.05 level

Correlated response to selection:

Selection based on protein yield, resulted in significant changes in other studied characters (Table 4). Fresh forage yield was significantly improved with all three methods of selection (Table 6). The realized gain per cycle, due to H.S reached, 3.1 ton / fad. (7.14 and 5.66% relative to base population and the average of checks, respectively). A more realized correlated gain of 5.19 ton / fad. (11.96 and 10.40%) resulted with S₁ selection (relative to the base and the checks,

respectively). Corresponding values for S₂ selection were insignificantly different from S₁ selection, were 5.75 ton / fad (13.25 and 11.68%, respectively). On per year basis, the realized gain from S1 family selection was the highest as 1.73 ton / fad. (3.99 and 3.47% of base population and checks, respectively).

Table 6: Correlated responses in fresh forage yield (ton / fad.), dry forage yield, leaves / stems ratio and seed yield (kg / fad.) for base, improved and check populations of Khadarawi Barsecm averaged over the two environments.

Population and selection method	Mean	Green forage yield (ton / fad)				Mean	Dry forage yield (ton / fad)			
		Realized gain (%)					Realized gain (%)			
		Per cycle		Per year			Per cycle		Per year	
		C ₀	Checks	C ₀	Checks		C ₀	Checks	C ₀	Checks
Khadarawi "C ₀ "	43.41 c					5.113 d				
H.S. selection	46.51 b	7.14	5.66	2.38	1.89	5.975 c	16.86	12.99	5.62	4.33
S ₁ selection	48.60 a	11.96	10.40	3.99	3.47	6.834 b	33.66	29.24	11.22	9.75
S ₂ selection	49.16 a	13.25	11.68	3.31	2.92	7.487 a	46.43	41.58	11.61	10.40
Checks										
Check population ₁	44.20 c					5.206 d				
Check population ₂	43.83 c					5.370 d				
Average	44.02					5.288				
Population and selection method	Mean	Leaves / stems ratio				Mean	Seed yield (Kg / fad)			
		Realized gain (%)					Realized gain (%)			
		Per cycle		Per year			Per cycle		Per year	
		C ₀	Checks	C ₀	Checks		C ₀	Checks	C ₀	Checks
Khadarawi "C ₀ "	43.19 b					500.1 c				
H.S. selection	48.94 a	13.39	11.03	4.46	3.68	574.0 b	14.78	21.79	4.93	7.26
S ₁ selection	50.41 a	16.80	14.36	5.60	4.79	626.2 a	25.22	32.87	8.41	10.96
S ₂ selection	51.44 a	19.18	16.70	4.80	4.18	635.7 a	27.12	34.88	6.78	8.72
Checks										
Check population ₁	43.76 b					472.50 c				
Check population ₂	44.40 b					470.10 c				
Average	44.08					471.30				

* Realized gain (%) relative to base = $C_1 - C_0 / C_0 \times 100$.
relative to checks = $C_1 - \text{check average yield} / \text{check average} \times 100$.

+ Means followed by a similar letters are not significantly different at 0.05 level.

The correlated response of dry forage yield (ton / fad.) to S_2 family selection surpassed the two other methods, resulting in a realized gain per cycle of 2.377 ton / fad (46.43 and 41.58% relative to base population and the checks, respectively). The per year corresponding figures were 11.61 and 10.40% (0.594 ton / fad). A significantly lower gain per cycle of 1.724 ton / fad (33.66 and 29.24 relative to C_0 and the checks, respectively) were obtained with S_1 families selection. The per year corresponding gain maintained the same rank as 0.575 ton / fad.(11.22 and 9.75%). The lowest significant gain per cycle resulted with H.S. selection as 0.862 kg / fad. (16.86 and 12.99% relative to C_0 and the checks, respectively). On per year basis, these gains amounted to 0.287 ton / fad. (5.62 and 4.33% relative to C_0 and the checks, respectively). Commonly, the correlated responses in dry forage yield were of similar magnitude to direct responses obtained in protein yield. Bakheit (1988) reported that protein yield was genetically and phenotypically strongly correlated with green forage yield ($r_p = 1.007$ and $r_s = 0.998$). Horner *et al.* (1989) stated that the S_2 progeny method, was theoretically more effective for changing frequencies of genes having additive effects. Although leaves / stems ratio (dry weight basis) positively responded to the three methods of selection, the difference in realized gain per cycle among the tested selection methods had not reached the level of significance. Considering the realized gain per year, S_1 families selection gave the highest values of 7.22% (5.60 and 4.79% relative to C_0 and the checks, respectively).

Seed yield (Kg / fad.) significantly increased with all selection methods. The realized correlated gain, from H.S. method, was 74.0 kg / fad. (14.78 and 21.79% relative to C_0 and the average of checks, respectively). The obtained gains from S_1 or S_2 families selection were significantly superior to the aforementioned method (126.2 and 135.7 kg / fad., respectively relative to C_0 , on per year basis). The gain from S_1 selection was about double the obtained value from H.S. selection and about 1.24 the obtained gain from S_2 selection. When relating the gain per year to the average of checks, S_1 realized gain amounted to 1.5 that of H.S. and about 1.25 the obtained gain from S_2 families selection. Mikhiel (1987) from one cycle of half-sib selection attained a positive response of 22%. Bakheit and Mohdy (1988) reported an increase of 14.14% in fresh forage yield from one cycle of pedigree selection. Bakheit (1989) reached a realized gain of 13.9 and 21.7% for fresh forage yield, 14.8 and 23.8% for dry forage yield and 14.00 and 22.9% for protein yield in C_1 and C_2 of recurrent selection, respectively. Ahmed (1992) concluded that maternal-line selection with S_1 as recombiners, was superior to half-sibs selection. He reached a realized gain from that method as 22 and 15% in green and dry forage yields, respectively.

The success of breeding methods in improving protein yield and other correlated traits of Khadarawi Barseem, in the present study, depended essentially upon genetic diversity of families and the predominance of additive genetic effects. The increased gain from S_1 family selection over H.S family selection method, was due to greater parental control over alleles that were transferred to the improved population (Fehr, 1987). The present results of selection on Barseem were so far, in general agreement with others. (Koriem *et al.*, 1980 and Ahmed (2000.)

Relative economic gain:

In a comparison of selection methods, not only rates of genetic improvement should be compared, but also the cost of the procedure. Estimates of costs presented in Table 7, served only as a guide to the relative costs, of conducting these selection experiments. Estimates of the cost. cycle⁻¹ were completely independent of time for one unit of gain and, likewise, the time to achieve one unit of gain was independent of cost per unit of gain (Weyhrich *et al.*, 1998.). The average cost to conduct a cycle of selection ranged from 3670 L.E. (H.S) to 5684 L.E. (S_2). Average cost year⁻¹ ranged from 1223 L.E. (H.S) to 1421 L.E. (S_2). The cost. year⁻¹ of the S_2 selection method was partly high because of the additional year required to complete the cycle of this method. This increased cost would be expected to be partly offset by the increased gain. cycle⁻¹ that recorded relative to the two other methods.

More important than the cost.cycle⁻¹ is the investment needed to achieve a given amount of gain. In the present study, a one ton.fad⁻¹ increase in protein yield would be equivalent to a 108% increase over the C_0 . The cost.unit⁻¹ gain ranged from 12509 L.E. (S_1) to 23376 L.E. (H.S). The length of time required to achieve one ton.fad⁻¹ increase in protein yield was highest with H.S and the lowest with S_1 families selection. It is clear from the recent results that, although H.S selection in many instances was a desired method, it was costly per unit gain because of its relatively low rate of gain. Taking into account both cost.unit⁻¹ gain and length of time required, S_1 families selection provided the highest rate of gain, with the greatest return on investment.

Table 7: Gain cycle⁻¹ and year⁻¹ for the improved population of Khadarawi Barseem along with cost for a one unit increase in protein yield and number of years needed to achieve this increase.

Selection method	Gain Cycle ⁻¹	Gain year ⁻¹	Average Cost cycle ⁻¹	Average cost year ⁻¹ †	Cost unit ⁻¹ of gain ‡	Time to achieve one unit of gain §	Return on investment ¶
	t.fad ⁻¹	t.fad ⁻¹	L.E.	L.E.	L.E.	Year	Ton.fad ⁻¹ L.E. ⁻¹ x10 ⁵
H.S.	0.157	0.052	3670	1223	23376	19	4.28
S ₁	0.322	0.107	4028	1343	12509	9	7.99
S ₂	0.346	0.087	5684	1421	16428	11	6.08

† Calculated by taking cost.cycle⁻¹ divided by the number of years required to complete one cycle.

‡ One unit of gain is equal to one ton. fad⁻¹ increase in protein yield. Calculated as the cost divided by the gain. Cycle⁻¹.

§ Calculated as the inverse of gain cycle⁻¹ multiplied by the number of years required per cycle.

¶ Calculated by taking gain cycle⁻¹ divided by the total cost. Cycle⁻¹. All calculations were made, assuming a cost of 10 L.E. per nursery row, 10 L.E. per yield trial plot and a cost of an average size isolation plot of 350 L.E.

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المخلص العربي

الاستجابة لثلاث طرق من الانتخاب الدوري في عشيرة البرسيم الخضراوي (*Trifolium alexandrinum*, L.)

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بالرغم من إجراء العديد من الدراسات لتقدير الاستجابة للانتخاب في البرسيم المصري فإن مقارنة كفاءة طرق الانتخاب ما زالت صعبة لأن المقارنة بين طرق الانتخاب يجب أن تتضمن الانتخاب لنفس الصفة باستخدام طرق مختلفة وتطبيقها علي عشيرة أساس مشتركة وهذا ما لم يتم في حالة البرسيم المصري وقد أجريت للدراسة الحالية لمقارنة الاستجابة لثلاث طرق مختلفة من طرق الانتخاب في عشيرة البرسيم الخضراوي وقد نفذت دورة انتخاب واحدة بكل من الطرق التالية:

- انتخاب العائلات نصف الشقيقة وتلقيح عائلات الجيل الأول للتقويح الذاتي الخاصة بها لإنتاج عشيرة الدورة الانتخابية المحسنة (H.S.).
- انتخاب بين عائلات الجيل الذاتي الأول (S₁).
- انتخاب بين عائلات الجيل الذاتي الثاني (S₂).

وتم الانتخاب في الطرق الثلاثة لصفة محصول البروتين (طن / فدان) باستخدام شدة انتخاب قدرها 20%. وقد تم قياس الاستجابة للانتخاب في محصول البروتين بالإضافة إلى الاستجابات المرتبطة في صفات محصول العلف الأخضر ومحصول العلف الجاف ومحصول البذور ونسبة الأوراق إلى السيقان.

وقد أظهرت النتائج أن جميع طرق الانتخاب كانت ناجحة معنويًا في تحسين إنتاجية العشيرة من محصول البروتين. وقد تميزت طريقة انتخاب عائلات الجيل الذاتي الثاني (S₂) بأعلى مستوى استجابة بلغ 0.346 طن / فدان / دورة (37.32%) والتي لم تكن مختلفة معنويًا عن التحسين الناتج من استخدام طريقة انتخاب عائلات الجيل الأول للتقويح الذاتي (S₁) والبالغ 0.322 طن / فدان / دورة (34.74%). أما طريقة انتخاب العائلات نصف الشقيقة مع تلقيح عائلات الجيل الذاتي الأول للمقابلة لها (H.S.) فقد أنتجت أقل استجابة بلغت 0.157 طن / فدان / دورة (16.94%). وباعتبار كل من التكلفة لكل وحدة استجابة للانتخاب وطول الفترة المطلوبة لإتمام الدورة الانتخابية فإن الانتخاب بين عائلات الجيل الذاتي الأول (S₁) فقد أعطت أعلى معدل استجابة للموسم الواحد وتتطلب مستوى معتدل من الاستثمار وتعطي أعلى عقد على الاستثمار.