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Improvement of Single Cut Egyptian Clover (*Trifolium alexandrinum* L.) By Mass and Family Selection Methods

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ABSTRACT

The aim of this study was to compare response to mass and family selection methods for improving Fahl population of berseem. Thereby two cycles of modified mass (C₁ and C₂) and one cycle of family selection were applied on a population of the Fahl variety of Egyptian clover. Plants selected for C₁ were also raised as half sib families in second season and selection was practiced between and within families for the best 10 families. Seeds of selected half-sib families and both modified mass selection cycles C₁ and C₂ along with the base population were evaluated for forage and seed yields in third season. Gains realized from C₁ and C₂ mass selection, respectively were 13.6 and 8.5% for seed yield, 4.9 and 14.4% for fresh forage yield, 5.3 and 13.2% for dry forage yield and 9.1 and 13.2% for 1000-seed weight over the base population. While, gains from family selection as% of base population were 18.5, 8.9, 9.9 and 3.8% for these traits in order. Broad sense heritability among half-sib families were 76.8, 76.1, 98.2 and 84.3% for these traits, respectively. All studied traits were positively correlated but the correlation between seed yield and forage yield were weak. However, one half-sib family was 30.1% higher than base population in seed yield, 34.2% in fresh forage yield, 35.8% in dry forage yield and 16.4% heavier in seed weight. Results suggest that family selection may be more effective for improving seed yield than modified mass selection.

Key words: Berseem, *Trifolium alexandrinum*, mass selection, family selection, forage breeding

INTRODUCTION

The single-cut Fahl variety of berseem clover (Egyptian clover) is widely grown in Egypt as a catch crop preceding major summer crops. It has high nutritional value and is very palatable in addition to being highly productive. In Egypt, very little attention has been given to the improvement of seed or forage production potential of berseem compared to other crops. This may be due to difficult artificial hybridization and high self sterility. Therefore breeders have used mainly the selection procedures for improving forage and seed yield in this crop.

The success of any program of selection to improve seed yield will depend on the genetic variation existing within the initial population, heritability of seed yield, the nature of correlations between seed yield and other traits especially forage yield and the intensity of selection applied. Most of breeders have selected directly for seed yield to improve it.

Koraïem *et al.* (1980), Omara and Hussein (1982), Radwan *et al.* (1983), Bakheit (1985), Younis *et al.* (1986) and Mikhiel (1987) reported that mass selection was effective for improvement

of forage yield in multi-cut Egyptian clover varieties. Family selection was more rewarding than mass selection for in improving forage yield in Meskawi Egyptian clover (Omara and Hussein, 1982). Bakheit (1989) found that both modified mass and family selection were effective for improvement of seed yield of the Fahl variety of berseem clover. In contrast, Radwan *et al.* (1971) stated that visual selection was ineffective for improvement of forage yield in three sets of progenies and the check variety Giza 1 inspite of the wide range in progeny performance and the relatively large heritability estimates for it. No significant response to mass selection for annual forage yield in Miskawi berseem clover was observed by Radwan *et al.* (1972). Selection applied was not effective for increasing seed yield among maternal half-sib populations of berseem clover (Martiniello and Iannucci, 1998). Ahmed (1992) concluded that maternal-line selection with S_1 , as recombiners, was superior to both half-sibs and controlled mass selection in Meskawi population. The realized gain from that study was 22% in both green and dry forage. Also, Ahmed (2006a) reported that all selection methods were successful in improving significantly the population performance for protein yield.

The present work describes the results of two different methods of phenotypic directional selection (mass and family selection) for seed yield and related forage yield traits in Fahl Egyptian clover.

MATERIALS AND METHODS

This investigation was conducted at Qena Agric. Res. Farm, South Valley Univ., Egypt during three successive seasons. The base material for this investigation was a random seed sample of Fahl population obtained from the Forage Crops Section, Field Crops Res. Institute, A.R.C. During first season, the base population was sown on 17th September in a non-replicated nursery (200 rows 3.15 m long, 20 cm apart and 15 cm between hills within row). After seedling establishment the plants were thinned to one plant per hill. The cultural practices were applied at optimum level for maximum productivity. The best plants in each row plot for seed yield/plant (200 plants = 5% selection intensity) were selected as parents to produce the next cycle.

Modified mass selection procedure: In second growing season, equal parts of seeds from each of the 200 selected plants were bulked together to form the first cycle of modified mass selection (C_1). Seeds of C_1 were sown on 19th September. The spacing distances, cultural practices, selection procedure and intensity of selection were applied as in the first season and equal parts of seeds from each of the selected plants were bulked together again to form the second cycle (C_2).

In third growing season, base population and two cycles of mass selection (C_1 and C_2) were planted on 19th September for estimating the response to selection. A randomized complete block design with six replications, three of them for forage yield traits and the other three replications for seed yield traits was used. Each plot consisted of four square meters with seeds sown by hand in rows, 20 cm apart, at a seeding rate of 4000 seeds plot⁻¹ (36 kg ha⁻¹). The culture practices were carried out as recommended. Ninety days from sowing the plots for forage yield were clipped by hand sickle. Data were recorded on fresh forage yield/plot and converted into tona gram/hectare. Dry matter percentage was estimated from plot samples of about 300 g of fresh forage dried at 70°C. The micro-kjeldahl method as described by AOAC (1980) was used to determine forage N content in the dried ground forage Nitrogen percentage was multiplied by 6.25 to obtain crude protein content. At seed maturity plots left for seed production evaluation were harvested and data were recorded on seed yield/plant and were converted to yield/ha.

Family selection procedure: In second season, the seeds of plants selected for C₁ were established as half-sib families. Each family consisted of 22 spaced plants. The best ten plants in seed yield from the best ten families were selected out (first cycle of family selection C₁).

In third season, base population and the selected ten families were evaluated in a randomized complete block design with six replications, three of them for forage yield traits and the other three replications for seed yield traits. Each plot consisted of a half square meter (1 m x ½ m). Seeds were sown by hand in rows, 20 cm apart, at a seeding rate of 500 seeds for each replicate equivalent to 36 kg ha⁻¹. Data were recorded on forage and seed yield traits as outlined for mass selection.

Statistical analysis: The analysis of variance and the expected mean squares for all studied traits were performed according to Gomez and Gomez (1984). The phenotypic (δ^2p) and genotypic (δ^2g) variances were computed as outlined by Al-Jiboluri *et al.* (1958). Phenotypic (PCV) and genotypic (GCV) coefficients of variability were calculated according to Burton (1952). Heritability (broad sense) was calculated as: $h^2 = \delta^2g/\delta^2ph \times 100$. Phenotypic (r_{ph}) and genotypic (r_g) correlation coefficients were computed from the components of variance and covariance according to Johnson *et al.* (1955).

The predicted response from selection of the superior 5% plants in C₁ families was estimated as $i \delta ph^2$ whereas, the correlated response in trait (y) when selection is applied to seed yield (x) is $CR_y = i h_x h_y r_g \delta p_y$ according to Falconer (1960), where CR_y = the correlated response of the trait (y), i = the intensity of selection = 2.063, h_x = the square root of the heritability of the trait (x), h_y = the square root of the heritability of trait (y), r_g = the genetic correlation between (x) and (y) traits and δp_y = the phenotypic standard deviation of trait (y).

RESULTS

Mass selection: The analysis of variance and mean values of forage and seed yields of the base population, first (C₁) and second (C₂) cycles of mass selection populations are illustrated in Table 1 and 2. No significant differences between the base population and the mass selected populations for forage yields were observed (Table 1). Although, in the first (C₁) and second (C₂) cycles increases were detected of 4.94 and 14.38% in fresh forage yield, 5.32 and 13.22% in dry forage yield, 4.05 and 11.56% in protein yield and 9.12 and 13.21% in seed index over the base population, respectively. Comparison of the seed yield of the base and selected C₁ populations shows a significant response to selection. However, no significant differences between the first (C₁) and second (C₂) generations of selection were observed. The genetic advance calculated as a percentage

Table 1: Mean squares from analysis of variance of forage and seed yields of the base population, first (C₁) and second (C₂) cycles of mass selection of the Fahl variety of berseem clover

SOV	df	Mean squares				
		Forage yields			Seed yields	
		Fresh (ton ha ⁻¹)	Dry (ton ha ⁻¹)	Protein yield (ton ha ⁻¹)	Seed yield (ton ha ⁻¹)	Seed index (1000-seed g)
Replication	2	3.25	0.12	0.04	0.045*	0.404
Base vs. selection	1	18.81	0.82	0.04	0.053*	0.250
C ₁ vs. C ₂	1	13.44	0.45	0.03	0.004	0.027
Error	4	7.81	0.19	0.01	0.003	0.424

*Significant at the 5% level of probability

Table 2: Mean and realized gain (%) of forage and seed yields for two cycles of mass selection of the Fahl variety of berseem clover grown in the third season

Generations	Forage yields			Seed yields	
	Fresh (ton ha ⁻¹)	Dry (ton ha ⁻¹)	Protein yield (ton ha ⁻¹)	Seed yield (ton ha ⁻¹)	Seed index (1000-seed g)
Base population	31.77 ^a	6.96 ^a	1.73 ^a	1.03 ^a	3.18 ^a
First cycle of mass selection	33.34 ^a	7.33 ^a	1.80 ^a	1.17 ^b	3.47 ^a
Second cycle of mass selection	36.34 ^a	7.88 ^a	1.93 ^a	1.22 ^b	3.60 ^a
Realized gain (%)					
Cycle 1 ⁺	4.94	5.32	4.05	13.59	9.12
Cycle 2 ⁺	14.38	13.22	11.56	18.45	13.21

Means followed by the same letter in the same column are not significantly different at the 5% probability level as determined by Duncan's Multiple Range test, \bar{C}_0 : Mean base population, ⁺ Realized gain (%): $\bar{C}_1 = \bar{C}_1 - \bar{C}_0 / \bar{C}_0 \times 100$, $\bar{C}_2 = \bar{C}_2 - \bar{C}_0 / \bar{C}_0 \times 100$

Table 3: Analysis of variance of forage and seed yields for the base population and ten selected families of the Fahl variety of berseem clover grown in the third season

		Mean squares				
		Forage yields			Seed yields	
SOV	df	Fresh (ton ha ⁻¹)	Dry (ton ha ⁻¹)	Protein (ton ha ⁻¹)	Seed yield (ton ha ⁻¹)	Seed index (1000-seed g)
Replication	2	15.01	0.53	0.010	0.01	0.05
Families	10	99.00**	6.26**	0.434	0.045**	0.23**
Base vs. selected fam.	1	21.68	1.31**	0.110**	0.090**	0.04
Between families	9	107.59**	6.81**	0.470**	0.039**	0.25**
Error	20	25.72	0.11	0.005	0.010	0.04

**Significant at the 1% level of probability

of the mean of the base population was 13.59 and 18.45% after the first (C_1) and second (C_2) cycles of phenotypic directional selection for seed yield, respectively. But no significant gains were detected for forage yield from mass selection for seed yield. So, after the first cycle of mass selection for seed yield was obtained significant response to selection.

Family selection: The analysis of variance of the forage and seed yields of the selected families and their base population are presented in Table 3. Highly significant differences among families for the traits measured were detected. Highly significant differences between the base population and the selected families for all studied traits, except fresh forage yield and seed index were also observed.

Table 4 shows means of forage and seed yields for the base population and the selected families. The average estimated fresh forage yield of the selected families ranged from 23.27 to 42.62 ton ha⁻¹ with an average of 34.59. One family was significantly higher than the base population after one cycle of family selection. With respect to dry forage yield and protein yield, it ranged from 4.93 to 9.45 ton ha⁻¹ with an average of 7.65 and from 1.25 to 2.36 ton ha⁻¹ with an average of 1.93, respectively. Furthermore, four families i.e., No. 1, 4, 7 and 9 for dry forage yield and five families (No. 1, 4, 7, 8 and 10) for protein yield were significantly higher than the base population after one cycle of family selection. In addition, seed yield for the ten selected families ranged from 1.02 to 1.36 ton ha⁻¹ with an average of 1.22 ton, while 1000-seed weight ranged from

Table 4: Means of forage and seed yields for the base population and the ten selected families of the Fahl variety of berseem clover

Family	Forage yields			Seed yields	
	Fresh (ton ha ⁻¹)	Dry (ton ha ⁻¹)	Protein (ton ha ⁻¹)	Seed yield (ton ha ⁻¹)	Seed index (1000-seed g)
1	42.6 ^a	9.45 ^f	2.36 ^f	1.34 ^d	3.70 ^e
2	30.3 ^{abc}	6.66 ^{bc}	1.64 ^{bc}	1.02 ^a	3.50 ^{cde}
3	32.0 ^{abcd}	6.83 ^{cd}	1.67 ^c	1.07 ^a	2.90 ^{ab}
4	40.5 ^{de}	9.40 ^f	2.34 ^f	1.36 ^d	3.60 ^{de}
5	29.4 ^{ab}	6.21 ^b	1.54 ^b	1.20 ^{abcd}	3.20 ^{bc}
6	33.6 ^{bcde}	7.35 ^d	1.82 ^d	1.13 ^{abc}	3.30 ^{cd}
7	37.6 ^{bcde}	8.45 ^e	2.19 ^e	1.24 ^{bcd}	3.40 ^{cde}
8	37.0 ^{bcde}	8.21 ^e	2.20 ^{ef}	1.24 ^{bcd}	2.80 ^a
9	23.3 ^a	4.93 ^a	1.25 ^a	1.27 ^{cd}	3.40 ^{cde}
10	39.8 ^{cde}	9.04 ^{cd}	2.31 ^{ef}	1.31 ^d	3.20 ^{bc}
Base population	31.8 ^{abcd}	6.96 ^{bcd}	1.73 ^{cd}	1.03 ^a	3.18 ^{bc}
Select. fam. mean	34.6	7.65	1.93	1.22	3.30

Means followed by the same letter in the same column are not significantly different at the 5% probability level as determined by Duncan's Multiple Range test

2.80 to 3.70 g with an average of 3.30 g. Furthermore, six families, namely, no. 1, 4, 7, 8, 9 and 10 for seed yield and two families (No. 1 and 4) for 1000-seed weight were significantly higher than the base population after one cycle of family selection.

It is of interest to note that the overall family mean after one cycle of family selection exceeded the mean of the base population for all studied traits. However, the families which outyielded the base population in seed yield were not higher in fresh forage yield, except family no. 1 which was higher than the base population in both forage and seed yields. These results reflect the weak correlation between forage and seed yields. In addition, family no. 1 could be considered the best selected family which showed 30.10% increase in seed yield and was higher than the base population by 34.15% in fresh forage yield, 35.78% in dry forage yield, 36.42% in protein yield and had 16.35 heavier seeds.

Estimates of phenotypic (δ^2_p) and genotypic (δ^2_g) variances, phenotypic (PCV%) and genotypic (GCV%) coefficients of variability and heritability (h^2) for forage and seed yields for the selected families are shown in Table 5. The phenotypic and genotypic variances expressed as PCV% and GCV% were 17.31 and 15.10% for fresh forage yield, 19.69 and 19.54% for dry forage yield, 20.51 and 20.40% for protein yield, 9.35 and 8.06% for seed yield and 8.73 and 8.02% for 1000-seed weight, respectively.

Broad-sense heritability (Table 5) was high in magnitude for dry forage yield (98.24%), protein yield (98.73%) and 1000-seed weight (84.34%). However, heritability of fresh forage yield and seed yield was smaller than dry yield.

Expected and realized gains from direct selection for seed yield and correlated responses in forage and protein yields and 1000-seed weight are presented in Table 5. The results indicated that after one cycle of family selection, the realized gain for seed yield reached 18.45% from the base population. Likewise, the expected gain from selection based on the superior 5% plants in C_1 family selection was 17.48%. Furthermore, favourable increase in fresh forage yield (8.88%), dry forage yield (9.91%), protein yield (11.56%) and (3.77%) in 1000-seed weight were obtained (Table 5).

The results of phenotypic (r_{ph}) and genotypic (r_{pg}) correlations between each pair of the five traits (Table 6) showed that the genotypic correlation coefficients between traits related to forage

Table 5: Phenotypic variance (δ^2_p) and genotypic (δ^2_g) variances, phenotypic (PCV%) and genotypic (GCV%) coefficients of variability, heritability% (h^2) and realized response for various characters in ten selected families of the Fahl variety of berseem clover

Estimate	Forage yields			Seed yields	
	Fresh (ton ha ⁻¹)	Dry (ton ha ⁻¹)	Protein (ton ha ⁻¹)	Seed yield (ton ha ⁻¹)	Seed index (1000-seed g)
δ^2_p	35.86	2.27	0.157	0.013	0.083
δ^2_g	27.29	2.23	0.155	0.010	0.070
PCV (%)	17.31	19.69	20.510	9.35	8.730
GCV (%)	15.10	19.54	20.400	8.06	8.020
h^2 (%)	76.10	98.23	98.730	76.82	84.340
Expected response	1.89	0.55	0.170	0.18	0.110
Expected response (%)	5.95	7.90	9.830	17.48	3.460
Realized response	2.80	0.69	0.200	0.19	0.120
Realized response (%)	8.81	9.91	11.560	18.45	3.770

Realized gain was calculated as: $(\bar{C}_1 - \bar{C}_0 - \bar{C}_0 / \bar{C}_0) \times 100$, \bar{C}_0 : Mean base population, \bar{C}_1 : Mean families of cycle 1

Table 6: Phenotypic (above) and genotypic (below diagonal) correlation coefficients among pairs of traits of ten selected families of the Fahl variety of berseem clover

Traits	Forage yields			Seed yields	
	Fresh (ton ha ⁻¹)	Dry (ton ha ⁻¹)	Protein (ton ha ⁻¹)	Seed yield (ton ha ⁻¹)	Seed index (1000-seed g)
Fresh forage yield (ton ha ⁻¹)	-	0.726	0.558	0.430	0.068
Dry forage (ton ha ⁻¹)	1.120	-	0.784	0.501	0.158
Protein yield (ton ha ⁻¹)	1.010	1.07	-	0.597	0.184
Seed yield (ton ha ⁻¹)	0.200	0.202	0.232	-	0.163
1000-seed weight g	0.176	0.200	0.199	0.221	-

yields (fresh, dry and protein yields) were higher than their corresponding phenotypic correlations. Also, high genotypic correlations suggested that there was inherent relationship between the traits in question. On the contrary, results for correlations between seed and forage yields indicated a weak positive correlation between seed yield and forage yield (0.200). These results confirmed those obtained from the analysis of variance of Table 3.

DISCUSSION

The implications of the effect mass selection on improving forage and seed yield in single cut Egyptian clover were studied. The obtained result show that after the first cycle of mass selection for seed yield was obtained significant response to selection such response could be a reflection of the weak reflection of the weak correlation between forage and seed yields. The lack of a more significant response after the first cycle of selection might be due to the inbreeding effect resulting from the high selection intensity. Similar results were obtained by Bakheit (1989), where significant response to mass selection for seed yield was obtained after the first cycle of selection with no significant differences between the first and second cycles of selection. Significant response to mass selection for forage yield after the first cycle of selection was obtained by Omara and Hussein (1982) and Ahmed (2006a).

Otherwise, these results for forage yield are in general agreement with those obtained by Ali (1971), Radwan *et al.* (1972) and Bakheit (1985) in Miskawi berseem clover.

Results from one cycle of family selection it is clear that direct selection for seed yield was effective in improving single cut Egyptian clover variety Fahl. Bakheit (1989) demonstrated that the families which outyielded the base population in forage yield were not the same families which were superior for seed yield, except only one family. Similar results were obtained by Burton and DeVane (1953).

From phenotypic (δ^2p) and genotypic (δ^2g) it is clear that these results revealed sufficient genotypic variability among selected families after one cycle of family selection for seed yield.

High broad sense heritability for dry and protein forage yield and 1000-seed weight indicating that the environmental effects were small compared to the genetic effect but heritability of fresh and seed yield was smaller than dry yield suggesting more environmental influences on fresh and seed yields. Similar results were reported by Bakheit (1989) and Ahmed (2006b).

Comparison of the expected and realized gain from selection shows a quite good agreement between expected and realized gain in seed yield and seed index. But for forage yields, the realized response was higher than the expected one. These results are in line with those reported by Bakheit (1989) and Ahmed (2006a).

Owing to the high phenotypic ($r_{p,h}$) and genotypic ($r_{g,g}$) correlations between each pair related to forage yields suggested that there was inherent relationship between the traits in question. But weak positive correlation between seed and forage yields. These results confirmed with those obtained from the analysis of variance. These results with this respect are in line with those obtained by Schaaf *et al.* (1962), El-Hattab *et al.* (1969), Bakheit (1989) and Ahmed (2006b).

CONCLUSION

The results concluded that family selection more effective for improving seed yield than modified mass selection.

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