

COMPARISON OF SINGLE TRAIT WITH MULTIPLE TRAIT SELECTION IN BARSEEM CLOVER (*Trifolium alexandrinum*, L.)

Ahmed, M. A.

Crop Science Dept., Faculty of Agriculture (EL-Shatby), Alexandria University, Egypt.

ABSTRACT

Comparison of single trait of selection (total green forage yield) via combining ability test, with multiple trait selection (total green forage yield, dry weight of root nodules and seed yield) by using independent culling levels or Index selection for the improvement of barseem clover (*Trifolium alexandrinum*, L.) were obtained from 100 polycrosses isolated from a base population represented the second generation of random mating for a seed synthetic composed from 23 farmer's seed lots of Meskawi (Multi-cut) type. Selection intensity was 10% for the three systems. Selection for multiple trait was significantly much rewarding than single trait selection. A realized gains of 12.20, 17.40, 17.20, 28.50, 14.10, 17.90 and 8.55% from index selection were obtained vs. 6.58, 5.96, 3.79, 10.27, 7.87, 5.05 and 4.47% from single trait recurrent selection for total green forage, dry forage, protein and seed yields, seed index, dry weight of nodules and leaves/stem ratio, relative to the base population. Although index selection gave higher magnitudes of realized gain relative to either the base population or the check varieties, these figures were not significantly different from those obtained with independent culling levels. The amount of effort required for index selection method is somewhat greater beside that, breeder should wait until all observations are recorded to construct an index. These are not essential with independent culling.

INTRODUCTION

Barseem (*Trifolium alexandrinum*, L.) is the most adapted forage crop to Egypt, occupying the largest area (about 0.971 million hectares according to Anonymous (1996) and lasts for about seven months where, consumed in soiling, hay and /or silage or as an open pasture. Barseem exhibits certain biological features which limit the choice of the breeding method such as; inability to make clonal lines, presence of self-incompatibility, small perfect flowers making controlled out-crossing difficult, and insect pollination which renders distal isolation difficult to accomplish and poor seed set. Thus, barseem has received little attention from breeders in so far as selection programs are concerned.

Selection for single trait via different methods was practiced by several workers. Mass selection was found effective in improving yield (Abou-EL-Shawareb 1971, Radwan *et al.*, 1972, Koraiem *et al.* 1980, Bakheit 1989-b and Ahmed 1992). In addition, Omara and Hussein (1982), Mikhiel (1987), Bakheit and Mahdy (1988), Bakheit (1989-a) and Ahmed (1992) found that family selection was more rewarding than mass selection for forage and seed yield in barseem clover.

Selections for more than one trait was practiced in breeding many cross pollinated crops. Alternatives for the selection of several traits are ; Random selection, independent culling levels and index selection. Random selection is practiced for each trait separately until the desired improvement in each character is attained. Independent culling is simultaneous selection for all desired traits in the same generation. Index selection is similar to independent culling, where, selection is simultaneously practiced for all traits, however different weights are given to the different traits in the index. Hazel and Lush (1949) theoretically compared the methods of selection for multiple traits. They showed that index selection was the best followed by independent culling and the least was random selection. So far, the effectiveness of multiple trait selection in barseem clover has not tested.

The present study describes the results of single trait selection (green Forage yield) and multiple trait selection (total green forage yield, dry weight of root nodules and seed yield) using independent culling levels or index selection in barseem clover. Its hoped that the effectiveness of independent culling is found equals to that of index selection, since the former is easier due to avoiding the Con-struction of indices beside, the possibility of selection after measuring each individual character.

MATERIALS AND METHODS

Parental materials were represented by the second generation of random mating for a seed composite consisting of 23 farmer's seed lots of Meskawi barseem clover. Seeds of Meskawi pool were planted during 1994/1995 season in rows at 20 cm apart and 4.0 m long at the Agricultural Experimental Station of Alexandria University. At flowering, 300 plants with visual satisfactory characters were selected. Heads of selected plants were caged in fine translucent paper pages. Hand tripping was practiced to enhance selfing. Seeds of each plant were harvested separately. The highest seed yielding 100 plants were saved S₁- seeds of the selected plants were parted to be used for intercrossing then for evaluation. In 1995/96 season a polycross mating design with 3 random replicates was planted in isolation. In each replicate, randomly arranged selections (each plant in a row (plot) of 1.0 m long and 20 cm apart) were guarded by one row planted with mixed seeds of all selections. Seeds were mixed with Fahl seed (single-cut cultivar) to preserve a good ground cover of adequate competition during establishment and allow for more branching after the first cut which would result in vigorous flowering. At maturity out-crossed seeds of each polycross were harvested separately. In 1996/97, 100 selected polycrosses were evaluated in a randomized complete block design with three replicates. Each plot was represented by three rows at 20 cm apart and two meters long. Seeding rate was 36 Kg/ha. Each plot was guarded by two rows planted with the commercial Meskawi cultivar. Green forage yield was determined from a random 0.25 m² in each plot for four cuts. Dry weight of active root nodules (g) was determined from random ten plants pulled out after the second cut from each plot. Seed yield was determined from two random 0.25m² samples in each plot.

Phenotypic (P.C.V.) and (G.C.V.) coefficients of variability were calculated according to Burton and De Vance (1953). Genotypic, phenotypic correlation coefficients and heritabilities were calculated from the components of variance and covariance as outlined by Johanson *et al.* (1955).

Depending on the obtained data from the polycrosses evaluation, selection was practiced as follows:

1. Single trait selection :

Depending on results of green forage yield, the best 10% families were recognized. In 1997/98 season, their corresponding S₁-families were planted in isolation for inter-crossing to produce seeds of the first cycle of recurrent selection based on single trait selection. The expected genetic advance from selection of the superior 10% families was estimated as given by Hallauer and Miranda (1981).

2. Independent Culling levels :

Independent culling was practiced for several traits, so that, the best 40% families based on total green forage were selected. From those 40 polycross-families, the best 50% families based on dry weight of effective nodules were selected. The latter group of 20 families was subjected to selection intensity of 50% depending on seed yield, ending by the best 10 S₁ lines. These were planted in an isolated field during 1997/98 season for intercrossing.

3. Index selection :

A classical selection index was used through the application of discriminant function as a base for making selection on several characters simultaneously, where desirable genotypes were discriminated from undesirable genotypes on the basis of their phenotypic performance Smith (1936) defined the genetic worth (H) of an individual as ;

$$H = a_1 G_1 + a_2 G_2 + \dots + a_n G_n$$

Where: G₁, G₂, ... G_n are the genotypic value of individual characters and a₁, a₂, ..., a_n signify their relative economic importance. Equal economic weight was given for the three characters. Another function (I), based on the phenotypic performance of various characters is defined as:

$$I = b_1 p_1 + b_2 p_2 + \dots + b_n P_n$$

Where; b₁, b₂, ..., b_n are to be estimated such that the correlation between H and I, i.e., r_(H,I) becomes maximum.

Data for three characters namely; green forage yield, dry weight of effective root nodules and seed yield were used for obtaining the latter function according to Singh and Chaudary (1979). Depending on the index value, the best 10 % S₁- families were selected, and were planted in isolated block for intermating during 1997/1998 season. Expected genetic gain through selection was predicted by the following equation;

$$G = \frac{(Z/V) \sum \sum a_i b_j G_{ij}}{(\sum \sum b_i b_j P_i)^{1/2}}$$

$$= \frac{(Z/V)W}{(VP)^{1/2}}$$

Where; Z/V is the standardized selection differential (s,) indicating the intensity of selection (i)

- a_i = economic weightage .
- b_i = Regression coefficients.
- G_{ij} = Genotypic variance – covariance matrix .
- P_{ij} = phenotypic variance – covariance matrix.
- Z/V = 1.76 for selection intensity of 10%.

4. Evaluation of selection methods :

In 1998/99 season, seeds of the base population (C_0) and the improved populations through the three different selection schemes i.e.; a) selection for green forage yield only, b) independent culling, and c) index selection, were planted in a randomized complete block design with six replicates. Two checks namely; Serow and Giza 15 were included. Each plot was represented by 5 rows at 0.2 m apart and 3. m long . Data were recorded for; 1) green forage yield for four cuts, (2 random 0.25 m² in each plot), 2) dry matter percentage (determined from samples of about 200g. placed in an oven at 70^oc until weight constancy was reached). Values of dry matter percentage were used for estimating dry forage yield, 3) leaves/stem ratio (determined at the third cut only), 4) Protein yield, which was estimated by using the data of dry forage yield and crude protein percentage determined by the micro-Kjeldahl technique as outlined by A.O.A.C (1980), 5) seed yield was determined from two random 0.25 m² samples from each plot, 6) seed index (g/1000 seeds) and 7) dry weight of nodules (g/plant). Data were statistically analyzed. according to Steel and Torrie (1980).

RESULTS AND DISCUSSION

Polycross evaluation:

The analysis of variance for total green forage yield (kg/0.25m²), dry weight of root modules and seed yield of the tested 100 poly- crosses is presented in Table (1). Highly significant differences among the tested polycrosses were detected for all the studied characters.

Table (1): Analysis of variance for total green forage yield (four cuts), dry weight of root nodules and seed yield of the 100 polycrosses of barseem clover.

S.O.V.	d.f.	Green forage (kg /0.25 m²)	Dry weight of nodules(g/plant)	Seed yield (g/0.25m²)
Replications	2	0.0770	0.00043	1.555
Polycrosses	99	0.3750**	0.00843**	24.498**
Error	198	0.0098	0.00014	1.2877

** Significance at the 0.01 level of probability.

Table (2) , shows the phenotypic variance (δ^2p), genotypic variance (δ^2g), coefficients of variability (C.V) and heritability (h^2) estimates. The values of genotypic variance relative to the environmental variance ($\delta^2p - \delta^2g$)

was high for the three studied traits. The environmental variation ranged from 4.76 % for dry weight of nodules to 14.27 % for seed yield. The phenotypic and genotypic coefficients of variation were descending from seed yield to dry weight of nodules to total green forage yield. These results were reflected in the obtained estimates of broad sense heritability, which took the same pattern. The incidence of high percentage of genetic variabilities indicates that selection based on the studied characters would be fruitful. Radwan, (1969), EL-Nehrawy (1980), Rammah *et al.* (1984), Mikhiel (1987) and Bakheit and Mahdy (1988) reported about the existence of genetic variability in green and seed yield of barseem entries. The high magnitude of that obtained heritability estimates was probably due to under estimate of environmental variance. Bakheit and Mahdy, 1988, obtained heritability estimates for green forage yield of barseem ranging from 44.8% to 81.4%. Bakheit (1989-a) reported that heritability estimate in barseem clover for green forage yield was as light as 91.24%. Ahmed (1992) published a range of 84.1% to 91.5% for heritability of green forage of barseem estimated from single year analysis, meanwhile an estimate of 69.4% for that character was obtained from combined analysis of two years. Also, high estimates of heritability for seed yield was reported by that author, mean while, Bakheit (1989-b) obtained lower value for seed yield heritability of 63.0%. Relative expected advance from selection (G%) amounted to 29.9, 40.7 and 41.2% of the respective means of total green forage yield, dry weight of nodules and seed yield, respectively. The presence of additive variation should be reflected on the gain from selection. Its magnitude should depend on the magnitude of heritability and some other factors such as selection differential. Accordingly, these results would suggest that selection within the polycrosses would be Promising.

Table (2):Phenotypic variance (δ^2p), genotypic variance (δ^2g), phenotypic coefficient of variation (P.C.V.) genotypic coefficient of variation (G.C.V.), heritability % (h^2) and expected genetic advance (G, G%) for studied characters in 100 polycross of barseem clover.

Estimate	Total green forage yield kg/0.25m ²	Dry weight of nodules g/plant	Seed yield G/ 0.25m ²
δ^2p	0.13152	0.002902	9.0245
δ^2G	0.12174	0.002764	7.7368
P.C.V.	18.37	24.27	27.32
G.C.V.	17.67	23.68	25.29
$h^2\%$	92.56	95.24	85.73
ΔG	0.59	0.090	4.533
$^1G\%$	29.93	40.67	41.22
G from index selection = 12.519			

¹ G% for single triat selection.

Phenotypic and genotypic correlation coefficients as well as coheritability between pairs of the three attributes are presented in Table (3). The expected advance was high and it is higher than anticipated. This is due to the overestimation of heritability. Genotype x environment interaction

would cause an increase in the estimates of genetic variance as the experiment was planted in one year and one location. The result would suggest good association between green yield and dry weight of nodules. The other correlation coefficients were low indicating that these characters are independent. High estimates of co-heritability among pairs of the three attributes were detected. These co-heritabilities suggested that there was an inherent relationship between the characters in question. The present results concerning association between traits of barseem are in general agreement with those obtained by EL-Hattab *et al.* (1969), Rammah (1969), Ali (1971), Hassan (1974), Jatasra *et al.*(1980), Beri (1983), Bakheit (1989b) and Ahmed (1992).

Table (3):Phenotypic (r_p), genotypic (r_g) correlation coefficients and coheritability among the studied characters of barseem polycrosses.

Trait	Estimate	Green forage yield	Dry weight of nodules	Seed yield
Green forage Yield	r_p		0.6975	0.1065
	r_g		0.5266	0.1165
	Coheritability		0.7087	0.9515
Dry weight of nodules	r_p			0.2496
	r_g			0.1733
	Coheritability			0.6272

1; Coheritability = $\delta g_1 g_2 / \delta p_1 p_2$

Selection Methods :

Selected polycrosses of barseem under the three practiced selection schemes, i.e., a) recurrent selection for single trait (total green forage yield), b) independent culling, and c) index selection, regarded with means of selection trait (s) are shown in Table (4). Half of the selected families were common among the three selection schemes. These were 25, 32, 48, 65 and 82. Only one family (number 88) was common between the single trait selection and independent culling. Also, independent culling had a common family (Family number 10) with index selection.

Means and realized gain (%) in total green forage yield (t/ha), dry forage yield (t/ha), protein yield (t/ha), seed yield (kg/ha.) seed index (g/1000 seed), dry weight of nodules (g/plant) and leaves/stem ratio for the base population, improved populations and check varieties are presented in Table (5). Improved population significantly surpassed the base population as well as the average of the check varieties in total green, dry and protein yields. Selection for multiple traits through independent culling levels or depending

Table (4): Means of different traits of selected polycrosses of barseem clover under the different studied selection methods.

Single trait selection		Independent culling levels						Selection index	
		I; upper 40%		II; upper 50% of (I)		III; upper 50% of (II)			
S ₁ line	Green forage (kg/0.25m ²)	S ₁ line	Green forage (kg/0.25m ²)	S ₁ line	Dry weight on noidules (g/plant)	S ₁ line	Seed yield (g/0.25m ²)	S ₁ line	Index value
25	2.717	2	2.367			15	20.40	2	27.184
		6	2.317	6	0.270				
		7	2.83						
32	2.717	10	2.050	15	0.372	25	17.70	8	14.332
		15	2.833						
		21	2.350	25	0.369				
41	2.517	22	2.333			32	15.63	15	20.388
		23	2.050	32	0.293				
		25	2.717						
48	2.817	30	2.083	41	0.322	48	19.43	18	15.442
		31	2.067						
		32	2.717	48	0.325				
62	2.550	35	2.250			59	9.480	25	17.802
		36	2.150	49	0.248				
		38	2.233						
74	2.383	40	2.000	50	0.245	62	16.30	32	16.607
		41	2.517						
		43	2.167	53	0.355				
82	2.883	48	2.817			80	12.60	48	19.894
		48	2.217	55	0.280				
		50	2.350						
88	2.613	53	2.267	59	0.293	82	18.47	62	16.384
		55	2.307						
		58	2.000	62	0.352				
91	2.533	59	2.220			86	10.34	79	14.342
		62	2.550	68	0.317				
		68	2.330						
92	2.2.667	71	2.017	80	0.307	88	9.517	82	18.891
		74	2.383						
		80	2.283	82	0.358				
		82	2.883						
		83	2.383	86	0.275				
		84	2.267						
		86	2.613	88	0.329				
		87	2.267						
		88	2.417	91	0.286				
		91	2.533						
		92	2.667	92	0.342				
93	2.217								
96	2.000	93	0.268						
Mean	2.375		2.336		0.3103		14.987		
Mean of all polycrosses	1.975		1.975		0.222		10.996		11.84

- Index value is; I = (1.923) (green yield) + (-8.336) (dry weight of nodules) + (0.885) (seed yield)

on selections index were much rewarding than selection depending on single trait. Gains due to either independent culling or index selection were not different for the three aforementioned characters. Single trait selection gave a realized gain of 6.58 and 6.30% in total green forage yield 5.96 and 4.07% in dry forage yield, 2.76 and 3.95% relative to the base population and the average of the two tested checks (Serow and Giza15), respectively Multiple traits selection via independent culling levels increased total green forage yield by 9.67 and 9.27 % dry forage yield by 10.37 and 8.4 % and protein yield by 12.41 and 13.71 % relative to the base population and the average of the checks, respectively. Although the realized gains due to index selection method, were not significantly different from those obtained with independent culling system, it exhibited higher magnitude for all forage yield characters, where, ranged between 12.16 % for total green forage yield, 17.16 % for protein yield relative to the base population and from 11.01 % for dry forage yield to 18.50 % for protein yield relative to the average of the checks.

As for seed yield, significant improvement due to selection methods was recorded, where, realized gain due to single trait selection was 10.27 and 25.09 % relative to the base population and the checks, respectively. This gain was only significant from the average of the checks. Although, the magnitude of gains due to the other multi - trait selection methods shown variable, it had not fail within the limits of significance. Correlated improvement in seed index due to selection methods were ascending as; index selection with gains of 14.31 and 6.92%, independent culling levels with gains of 11.21 and 4.99% then single trait selection with gains of 7.87 and 1.84% relative to the base population and the checks, respectively. Independent culling levels resulted in the highest significant improvement in dry weight of nodules, with 64.7 and 47.7% gain relative to the base population and the checks were obtained. On the same time, lower correlated realized gain due to selection of the top green forage yielding families of 55.1 and 39.1% relative to base population and checks were obtained. The least significant gain was recorded from index selection reaching only 17.9 and 5.8 % relative to the base population and the checks. The superiority of single trait selection is probably due to the high magnitude of coheritability values between dry weight of nodules and total green forage yield (Table 3). Correlated realized gain in leaves/stem ratio was attained due to selection methods. This gain was not significantly different among the different methods. That improvement ranged between 4.47 for single trait selection to 8.55 % for index selection relative to the base population, whereas, was from 3.17 for single trait selection to 7.20 % for index selection relative to the checks. Ahmed (1992) found that the improvement in leaves/stem ratio due to S_1 -line, half-sib or controlled mass selection was not significantly different. He added that, the magnitude of realized gain in that character was relatively smaller than other correlated responses.

The success of breeding methods in improving yield and other characters of barseem in the present study essentially dependent upon genetic diversity of material and the incidence of additive genetic effects, beside, the increased gain with using S_1 -families for intercrossing which comprises greater parental control over the alleles that are transferred to the

new population. So that, only gametes from the selected individuals are passed to the new population used to produce half – sib seed for testing (Fehr, 1987). The finding of many workers on barseem clover was in general agreement with that recent finding with recurrent selection based on general combining ability. Among those workers, Koriem *et al.* (1980) reached an actual gain from one cycle of recurrent selection over two location (Alexandria and Nubaria) of 20.5%. Mikhiel (1987) obtained a positive response of 22% in forage yield after one cycle of half sib selection. Bakheit and Mahdy (1988) reflected the efficiency of pedigree selection in improving fresh forage yield of barseem by 14.1%. Bakheit (1989-a) recorded a 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 in the first and second cycles of recurrent selection respectively, over the base population. Bakheit (1989-b) published that the realized gain from modified mass selection for seed yield in mono – cut barseem were 6.0 and 9.3% for fresh forage , 5.6 and 10.9% for protein yield and 13.2 and 16.2 % for seed yield in cycles 1 and 2 respectively over the base population. Ahmed (1992) concluded that maternal–line selection with S₁ lines as recombiners was superior to both half–sib family selection and controller mass selection. He reached a realized gain of 22 and 15% over the base population and the check varieties in both green and dry forage due to S₁–line selection.

The purpose of using a multi–trait selection is to simultaneously improve several traits. Index selection increased the values of index constructed characters (green forage yield, seed yield and dry weight of nodules) (direct response). In dependent culling levels gave similar direct response in those three characters, but the magnitude of direct response on dry weight of nodules was significantly better than that of index selection. The magnitude of realized gains due to index selection were higher than those of independent culling levels in most direct and indirect responses even with insignificant superiority over the latter method. Elgin *et al.* (1970) concluded that the most effective method for improving multiple traits in alfalfa (*Medicago sativa* L.) was the base selection index followed by the independent culling. Moll and Stuber (1971) examined direct and correlated responses to index and single trait selection in maize (*Zea mays*, L.) Responses to single trait selection tended to match expected responses more closely than did responses to index selection.

Although, index selection succeeded in improving total green forage (single trait) as well as dry forage yield, protein yield, seed yield, seed index, dry weight of nodules and leaves /stem ration (simultaneous improvement of many traits), this method, however, has some limitations, such as the difficulty in obtaining reliable estimates of phenotypic and genotypic variances and covariances, the problem of assigning the appropriate economic importance to each trait, and the need to wait until measurements are made for all traits. Consequently the use of independent culling levels may match with the goals of barseem breeders, since, it gave similar responses to that of index selection with possibility of selection within the evaluation season after the measurement of each individual character beside, the simplicity of application.

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مقارنة بين الانتخاب لصفة واحدة والانتخاب لصفات متعددة في البرسيم المصري

محمد عبد الستار أحمد

قسم المحاصيل – كلية الزراعة – (الشاطبي) - جامعة الإسكندرية

تمت مقارنة طريقة الانتخاب على أساس التقييم لصفة واحدة (المحصول الإجمالي للعلف الأخضر) من خلال اختبار القدرة على الإنتلاف مع طريقة الانتخاب لصفات متعددة (المحصول الإجمالي للعلف الأخضر والوزن الجاف للعد الجذرية ومحصول البذرة) وذلك باستخدام كل من أسلوب الاستبعاد بمستويات مستقلة عن بعضها وباستخدام دليل الانتخاب وذلك لتحسين البرسيم المصري. أجريت الدراسة بتقييم مانه هجين متعدد ناتجة من عشيرة أساس تمثل الجيل الثاني الناتج من التزاوج العشوائي لصنف تركيبي ناتج من خلط 23 عينة بذور مزارعين لصنف المسقاوى (متعدد الحشوات). وقد استخدمت شدة انتخاب مقدارها 10% في نظم الانتخاب الثلاثة. أوضحت النتائج أن الانتخاب المبني على أساس تقييم صفات عديدة كان معنويا أعلى فعالية مقارنة بالانتخاب على أساس تقييم صفة واحدة.

وقد بلغ التحسين الفعلي الناتج عن طريقة دليل الانتخاب 12.16 ، 17.44 ، 17.16 ، 28.48 ، 14.31 ، 17.89 و 8.55% في مقابل 6.58 ، 5.96 ، 3.79 ، 10.27 ، 7.87 ، 55.05 و 4.47% من طريقة الانتخاب على أساس تقييم صفة أحده وذلك لصفات محصول العلف الأخضر الكلي ومحصول العلف الجاف ومحصول البروتين ومحصول البذرة ومعامل البذرة والوزن الجاف للعد الجذرية ونسبة الأوراق : السيقان وذلك بالنسبة لعشيرة الأساس. وبالرغم من تفوق قيم التحسن الفعلي الناتج عن طريقة دليل الانتخاب وذلك بالنسبة لعشيرة الأساس أو بالنسبة للأصناف الاختبارية فإن تلك القيم لم تكن مختلفة معنويا عن القيم الناتجة من طريقة الاستبعاد بمستويات مستقلة عن بعضها. ومع الوضع في الاعتبار أن الجهد اللازم لطريقة دليل الانتخاب يعتبر أكبر بالإضافة إلى أن المربي عليه أن ينتظر لحين إتمام تسجيل جميع الصفات حتى يتمكن من صياغة دليل للانتخاب. تلك الترتيبات ليست ضرورية لتنفيذ طريقة الاستبعاد بمستويات مستقلة على محصول البرسيم حيث أنه محصول تمتاز صفاته بأنها قوية الترابط.

Table (5): Means and realized gain (%) of forage yield, seed yield ,dry weight of nodules and leaves /stem ratio for the original and improved cycles of barssem by selection.

Population	Green forage yield (t/ha)			Dry forage yield (t/ha)			Protein yield (t/ha)			Seed yield (kg/ha)		
	*Realized gain (%)			Realized gain (%)			Realized gain (%)			Realized gain (%)		
	Mean	Base	Checks	Mean	Base	Checks	Mean	Base	Checks	Mean	Base	Checks
Base population (C ₀)	101.4 cd			15.43c			3.690b			624.0b		
Selection methods												
Single trait	108.07b	6.58	6.30	16.35b	5.96	4.07	3.792b	2.76	3.95	688.1ab	10.27	25.09
Independent culling	111.2a	9.67	9.27	17.03a	10.37	8.40	4.148a	12.41	13.71	730.5a	17.07	32.79
Index selection	113.73a	12.16	11.75	17.44a	13.03	11.01	4.323a	17.16	18.50	801.7a	28.48	45.74
Check varieties												
Serow	99.60d			15.01c			3.658b			495.3d		
Giza 15	103.93c			16.40c			3.638b			604.9bc		
Average	101.77			15.7			3.648			550.1		

Population	Seed index g/1000 seed			Dry weight of nodules g/plant			Leave/stem ratio		
	Realized gain (%)			Realized gain (%)			Realized gain (%)		
	Mean	Base	Checks	Mean	Base	Checks	Mean	Base	Checks
Base population (C ₀)	2.159f			0.218d			41.43b		
Selection methods									
Single trait	2.329c	7.87	1.84	0.338b	55.05	39.10	43.28a	4.47	3.17
Independent culling	2.401b	11.21	4.99	0.359a	64.68	47.74	44.41a	7.19	5.86
Index selection	2.468a	14.31	7.92	0.257c	17.79	5.76	44.97a	8.55	7.20
Check varieties									
Serow	2.269e			0.232d			42.26ab		
Giza 15	2.304d			0.253c			41.63b		
Average	2.287			0.243			41.95		

Means followed by the same letters in each column are not significantly different at 0.05 level.

*Realized gain % : from base = Selection method mean – base population mean / base population mean x 100.
 from checks = Selection method mean – check varieties mean / check varieties mean x 100.