

SEED YIELD AND SEED YIELD COMPONENTS VARIABILITY IN
THE HELALY POPULATION OF BARSEEM CLOVER
"Trifolium alexandrinum, L"

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ABSTRACT : Variability in Helaly barseem gene pool had determined through driving two types of families. These were half- sib (H.S) and first selfing generation (S_1). Those two types of families had evaluated in two different experiments. In most seed yield and seed yield component characters, among families mean squares were of larger magnitude for S_1 than half-sib families, meanwhile the within families mean squares were generally of opposite order. Additive genetic variance estimates (σ^2A) were positive for all studied seed yield and seed yield component characters. In addition, the ratio of σ^2A / σ^2G , indicated that additive genetic variance was more effective in controlling seed yield and seed yield components. Reduction in mean values associated with S_1 families relative to H.S families reached, 5.38, 1.73, 4.11, 6.78, 3.64 and 3.38% for seed yield, seeds/inflorescence, flowers/ inflorescence, % seed setting, seed index and inflorescence / plant, respectively. Genotypic variation among half- sib families were less than 20% of the studied seed yield and seed yield component mean values, except for seed setting percentage, that had amounted to 23% of the character mean value. While, genotypic variations among S_1 families were more than 20% of the recorded mean values. Phenotypic coefficients of variation for seed yield and seeds/ inflorescence were of larger magnitude for estimates from S_1 families, meanwhile, were about the same for the rest of the studied characters, irrespective of the type of family. Seed yield expressed the least estimate of heritability (0.55 and 0.62) for H.S and S_1 families, respectively. This might indicate the influence of environment in the expression of that character. Expected gain from selection in units was the lowest for seed index (0.549 and 0.477g/cycle) for H.S and S_1 family selection, respectively. Whereas, gain was the highest for the number of flowers / inflorescence (14.24 and 15.09 flowers) for H.S and S_1 family selection, respectively. Relative to the overall mean of character, gain from H.S selection ranged between 26.41% for percent seed setting to 18.12% for number of seeds/ inflorescence. While, gain percent from S_1 family selection ranged between 16.60% for seed index to 29.36 % for number of seeds/ inflorescence.

Key words: Barseem clover, genotypic and phenotypic variation, heritability, gain from selection, seed yield, seed yield components.

INTRODUCTION

In Egypt, forages are the backbone of sustainable agriculture and environmental regeneration. Leguminous forages play a major role in providing high quality feed for the economic production of meat and milk. Also, it is important in soil conservation and environmental protection, as they add organic matter and fixed nitrogen.

Barseem clover "*Trifolium alexandrinum*, L." is an annual legume, well adapted to Mediterranean, central Europe. India and Southern USA, for soiling, hay production and grazing. While the heritability of a

population provides a measure of its genetic potential to response to a generation of selection, the magnitude of h^2 only provides information on the potential over a few generations. As allele frequencies change, so does heritability. A population showing a high h^2 value may have heritability erode to zero very quickly, while another population with a much smaller h^2 value may actually have heritability increase during selection as rare favorable alleles become more frequent. Hence, heritability is a completely unreliable predictor for long-term response although it is generally a good to excellent

predictor of short-term response. Large genetic variability has been found for seed yield and seed yield components. Recorded estimates for seed yield heritability reached 0.63 (Bakheit, 1989-b), 0.97 (Ahmed, 1992), 0.50 (Martiniello and Lannucci, 1998) and 0.595 (Rajab, 2010). Farid *et al.*, (1972) found that seed setting percentage was responsible for most of seed yield variations rather than 1000 seed weight. Phenotypic variation in seed yield amounted to 27% of obtained mean yield (Ahmed, 1992), 19.0% (Martiniello and Lannucci, 1998), 27.3% (Ahmed, 2000) and 12.7% (Rady, 2008).

Breeding of cross-pollinated, sexual, forages generally aims at the development of superior synthetic cultivars and improved heterogeneous populations. Since seed yield, and most seed yield components traits are quantitatively inherited, selection methods have commonly been to improve breeding populations. Improved breeding populations can be released as an open-pollinated cultivar or be a source of elite parents for synthetic cultivars.

Progeny testing procedures, including half-sibs and selfed generations, which measure general combining ability for synthetic cultivar development, were discussed by Allard (1960). Quantitative genetic information regarding the source populations is needed to plan effective selection programs. It is necessary to obtain information on the extent and nature of genetic variation, heritability, genotype x environment interactions, correlations, and prediction of genetic advance by selection as discussed by Dudley and Moll (1969). Knowledge of the additive genetic variance in relationship to the total genetic variance is important in the breeding of forage species since most breeding methods available make little or no use of the non-additive genetic variance in the source populations (Hill 1977)

The objective of the present study was to evaluate the genetic variability for characters related to seed yield and seed yield components as a step for estimating the

potential toward developing improved population.

MATERIALS AND METHODS

Experimental site

The recent study had carried out at Sakha experimental station, Kafr ElSheikh, Agricultural Research Center, Egypt.

Parental materials

The base population comprised 30 farmers and market seed lots of *Helaly* multi-cut barseem clover. In 2007 – 2008 winter season, seeds of the base population had sown in 300 rows, 20 cm apart and 4.0 m long, at the rate of 36 Kg.ha⁻¹ (2.9 g.row⁻¹). Cultural practices had applied as recommended for optimum barseem productivity. Four cuts were taken before adjusting spacing within row to 10 cm among plants through uprooting small-tagged plants.

Families formulation

In 2007-2008, 300 plants were visually selected before flowering, depending on crown size and general performance. Those selected plants were marked by wood sticks tagged (OP) to indicate the collection of their open pollinated seeds. The highest seed producing 100 plants were saved as half-sib families. S₁- families had developed during 2007 – 2008 season, by isolating 300 plants before flowering by fine translucent cloth. Those plants were marked by wood sticks tagged S₁. Hand tripping had applied to enhance seed setting. S₁ seeds had harvested from each selfed plant, separately, to represent S₁- family. One hundred S₁- families, with sufficient selfed seeds, were saved.

Families evaluation

In 2008- 2009 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 2 m length and 20 cm apart were used. Seeding rate was 36 Kg. ha⁻¹ (1.45 g. plot⁻¹). Each plot was guarded by two rows planted with base

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population seeds. Seed yield, determined from the middle meter of each plot ($\text{g}\cdot\text{plot}^{-1}$). Seed yield components, i.e.; number of heads plant, number of flowers head, number of seeds head and percent seed setting, were determined from five plants in each plot.

S¹- family's evaluation had carried-out during 2008/2009 season in a similar manner to half- sib family's evaluation, where, five sets each of twenty families with two replicates were used. The plot size was 2 m long and 20 cm apart, seeded at the rate of 36 Kg. ha⁻¹ (1.45 g. plot⁻¹). Each plot was guarded by two rows planted with base population seeds.

Data from half- sib and S₁- families evaluation had statistically analyzed according to the following model: measured character = sets, reps sets, families/sets and combined error, using Mstat-c program (1980). Variance components for families (σ^2_F) and error (σ^2_e) were estimated from the analysis of variance. Values of (σ^2_F) and (h^2) calculated according to Fehr (1987) had used to estimate the expected genetic advance from selection. It had assumed that the gene frequency for "Helaly" population would be near to one-half, and consequently, the estimates of variance components, for the two types of families, would be used to calculate (σ^2_A) as follows (Hallauer and Miranda. 1988):

$$\sigma^2_{H.S} = \frac{1}{4} \sigma^2_A$$
$$\sigma^2_{S_1} = (1) (\sigma^2_A + \frac{1}{4} \sigma^2_D)$$

The estimates of σ^2_A and σ^2_D had used for estimating the expected genetic advance from selecting the superior 20 % families in each family type, when appropriate, as indicated by Fehr (1987).

RESULTS AND DISCUSSION

The base population for the recent study comprised from 30 farmers and market seed- Lots of *Helaly* multi- cut barseem clover "*Trifolium alexandrinum*, L.". Two types of families had formulated, as a step

before selection for high seed yielding ability. Those were half- sib (H.S Families) and the first generation of self pollination (S₁ Families). Variability in the base population gene pool had estimated depending on variance components of the aforementioned families. Partitioning of variance components had used to estimate phenotypic, genotypic and environmental variances. The estimates of heritability and phenotypic variance had used to calculate the expected genetic advance from selecting the superior 20% families in each selection scheme, when appropriate.

The pertinent mean squares from analysis of variance over sets and estimates of family's variance component for each of half- sib (H.S) and first selfing generation (s₁) families derived from Helaly barseem regarding seed yield and seed yield components had presented in Table1. The analysis revealed highly significant effects ($P \geq 0.01$) of families/ sets for seed yield (g/m^2) and seed yield components (seeds/ inflorescence, flowers/ inflorescence, seed setting %, seed index and number of inflorescences / plant). In most seed yield and seed yield components traits, among families' mean squares were of larger magnitude for S₁ families than half- sib families. Meanwhile the within families mean squares were generally, of opposite order.

Family's variance component for S₁ families was 1.08, 2.01, 1.03, 0.96, 0.74 and 1.56 times the corresponding values for half- sib (H.S) families. Genter and Alexander (1962) Showed that, variation among S₁ families was of higher magnitude than their test crosses. Lindsey *et al.*, (1962), also found that, variance component for S₁ family was four times the H.S family variance. Mota *et al.*, (1975) and Goulas and Lonquist (1976) found that, the genetic variance, among S₁ lines, was three times that among H.S families. Ahmed (2006-a) recorded that, variance component for S₁ families was between 1.12 and 3.7 times the corresponding values for half- sib families of *Khadarwi* barseem clover.

Table (1): Pertinent mean squares from analysis of variance and estimates of family's variance components for half- sib (H.S) and first selfing generation (S₁) Families of *Helaly barseem* seed yield and seed yield components.

Character	Mean squares				σ^2_f	
	Families / Sets		Error			
	H .S	S ₁	H .S	S ₁	H .S	S ₁
Seed yield (g /0.1m ²)	14.42**	14.17**	6.353	5.429	4.034	4.372
Seeds/ inflorescence	83.84**	100.8**	42.07	21.05	19.88	39.89
Flowers / inflorescence	489.4**	460.7**	171.12	131.6	159.1	164.5
Seed setting %	322.3**	283.2**	110.4	79.78	105.9	101.7
Seed index	0.5940**	0.4335**	0.1664	0.1159	0.2138	0.1588
Inflorescences / plant	70.72**	62.31**	27.41	19.47	13.71	21.42

** : Significance at 0.01 level

σ^2_f ; Family's variance component

Hallauer and Miranda (1988) and Falconer (1995), showed that the genetic variance among various types of families was the expectation of $1/4 \sigma^2_A$ for half- sib (H.S) families and $\sigma^2_A + 1/4 \sigma^2_D$ for S₁ families, where; σ^2_A and σ^2_D denotes additive and dominance effects, respectively. The additive and dominance genetic variance components were calculated for the base population, depending upon the two types of evaluated families from the above mentioned equations. The results had presented in Table 2. The estimates of additive variance (σ^2_A) were positive for all studied seed yield and seed yield component characters. While, the estimates of dominance variance (σ^2_D) were negative for all characters, The ratio of σ^2_A / σ^2_G indicated that additive genetic variance was more effective in controlling both seed yield and seed yield component characters. Weyhrich *et al*, (1998) stated that, if additive genetic variance was of greater importance in a population than dominance variance, selection among inbred – progeny might be expected to be superior to other methods under most genetic situations.

Estimates of minimum mean and maximum values for Helaly barseem's seed yield and seed yield components derived from half- sib (H.S) and first- selfing generation (S₁) had summarized in Table 3. The range (maximum- minimum) values obtained from half- sib families were of lower magnitude relative to the corresponding values obtained from S₁ families for each studied seed yield and seed yield component characters. The estimated figures were, 1.15 vs. 4.0, 9.05 vs. 14.6, 6.7 vs. 11.55, 14.3 vs. 14.85, 0.22 vs. 0.30 and 4.75 vs. 5.25 for H.S vs. S₁ families in seed yield (g/0.1m²), seed index and number of inflorescence /plant, respectively. Also, the mean values recorded from S₁ families were smaller than the corresponding values for half- sib families in all seed yield and seed yield component characters Reduction in mean values associated with S₁ families relative to half-sib families reached 15.38, 1.73, 4.11, 6.78, 3.64 and 3.38% for seed yield (g/0.1 m²), seeds/ inflorescence, flowers/ inflorescence, % seed setting, seed index and inflorescences/ plant, respectively. These results are in accordance with those reported by Fehr (1987) and Hallauer and Miranda (1988).

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Table (2): Estimates of additive (σ^2_A) and dominance (σ^2_D) variances from the two types of *Helaly* barseem families for seed yield and seed yield component characters.

Character	σ^2_A	σ^2_D	σ^2_A / σ^2_G
Seed yield (g/ 0.1 m ²)	16.14	- 51.07	1
Seed / inflorescence	79.52	- 158.5	1
Flowers / inflorescence	636.4	- 1889.6	1
Seed setting %	406.8	- 1220.4	1
Seed index	0.8552	- 2.786	1
Inflorescences	87.00	- 262.3	1

Table (3): Estimates of minimum, mean and maximum values, for *Helaly* barseem's seed yield and seed yield components.

Character	Minimum		Mean		Maximum	
	H.S	S ₁	H.S	S ₁	H.S	S ₁
Seed yield (g /0.1m ²)	7.90	7.00	11.28	9.545	9.050	11.00
Seeds/ inflorescence	21.00	20.40	27.21	26.74	30.05	35.00
Flowers / inflorescence	61.00	58.20	66.47	63.74	67.70	69.75
Seed setting %	32.30	31.95	44.23	41.23	46.95	46.80
Seed index	2.775	2.680	2.775	2.674	2.995	2.980
Inflorescences / plant	24.25	25.25	28.07	27.12	29.00	30.50

Estimates of genotypic (σ^2_g), environmental (σ^2_e) and phenotypic (σ^2_{ph}) variances along with coefficient of variation at genotypic (G.C.V) and phenotypic (P.C.V) levels for *Helaly* barseem seed yield and seed yield components, derived from half-sib and S₁ families had expressed in Table 4. Genotypic variance among S₁Families was larger in magnitude than the respective value for half- sib families in seed yield and seed yield, number of seeds/inflorescence and number of flowers/inflorescence. Meanwhile, within families variance (environmental variance (σ^2_e)) had reduced in S₁families relative to half- sib families in each measured character. These finding matches true with those reported by Fehr (1987), Hallauer and Miranda (1988), Falconer (1995) and Ahmed (2006-b).

Values of genotypic and phenotypic coefficients of variation, reflects the variation in terms of genetic or phenotypic as a percentage of the character mean. Genotypic variation among half- sib families

were less than 20% of the studied seed yield and seed yield component characters mean values, except for seed setting percentage, that had genotypic variation amount to 23% of the character mean value. While, genotypic variations among S₁families were more than 20% of the recorded mean values for most seed yield and seed yield component characters, except for seed index and number of inflorescences / plant, that showed, genotypic variation less than 20% of the characters respective mean values. Phenotypic coefficients of variation were comparable when derived from half-sib and S₁ families, for seed yield and seeds/ inflorescence, with larger magnitude for estimates from S₁families. Meanwhile, phenotypic coefficients of variation were about the same for the rest of the studied characters, irrespective of the type of family. (Table 4). The recent results are in accordance to those reported by Obilana and Hallauer (1974), Lothrop *et al*, (1985) and million *et al*, (2012).

Table (4): Estimates of variance components and coefficient of variation at genotypic (G.C.V) and phenotypic (P.C.V) levels for *Helaly* barseem seed yield and seed yield components.

Character	σ^2_g		σ^2_e		σ^2_{ph}		G.C.V		P.C.V	
	H.s	S ₁	H.s	S ₁	H.s	S ₁	H.s	S ₁	H.s	S ₁
Seed yield (g /0.1m ²)	4.034	4.372	3.177	2.715	7.211	7.087	17.81	21.91	23.81	27.89
Seeds/ inflorescence	19.88	39.89	12.04	10.53	31.92	50.42	16.39	23.62	20.76	26.55
Flowers / inflorescence	159.1	164.5	85.56	65.8	244.7	230.3	18.97	20.12	23.53	23.81
Seed setting %	105.9	101.7	55.20	39.89	161.1	141.6	23.27	24.46	28.70	28.86
Seed index	0.2138	0.1588	0.0832	0.0580	0.2970	0.2168	15.44	13.87	18.20	16.20
Inflorescences / plant	21.65	21.42	13.61	9.735	35.36	31.16	16.58	17.07	21.18	20.58

Heritability estimates for seed yield and seed yield components (h^2) had presented in (table 5). Estimates were higher in magnitude when calculated from first selfing generation (S₁) compared to half- sib families, for all studied characters. Seed yield expressed the least estimate of heritability among all studied characters in each family type (0.55 and 0.62) for half- sib and S₁- families, respectively. This might indicate the influence of environment in the expression of that character. Meanwhile, seed yield component characters had higher genetic control expressed on heritability estimates from the two studied types of families. The present results are in accordance with the results of weyhrich *et al.* (1998), where heritability estimates ranged from 17.1 % from half- sibs to 86.7% from S₂ – progeny. Ahmed (2006-a) found that heritability estimates were ascending from half- sib to S₁ to S₂ families. In the mean line, high estimates of heritability ranged from 84.1 to 95.2 were reported by Bakheit and Mahdy (1988), Bakheit (1989-a), Ahmed (1992) and Ahmed (2000).

Expected genetic advance from selecting the superior 20% families, was higher for S₁ relative to half- sib families, for most studied seed yield and seed yield component characters. Expected gain from selection in units was the lowest for seed index (0.549 and 0.477 g/ cycle) for half- sib and S₁ family selection, respectively. Whereas, gain

was the highest for the number of flowers/ inflorescence (14.24 and 15.09 flowers) for half- sib and S₁ families' selection, respectively. Relative to the overall mean of character, gain from selecting half- sib families ranged between 26.41% for percent seed setting to 18.12% for number of seeds/ inflorescence. While gain percent from S₁ family selection ranged between 16.60% for seed index to 29.36% for number of seeds/ inflorescence.

The gain from selection 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 S₁ than half- sib families for the studied seed yield and seed yield component characters. The expected advance from selecting S₁ families was about 1.07 times that from half- sib families, as an average for all the studied seed yield and seed yield component characters. Paradoxically, half- sib family selection was of superior advance to S₁ family selection in seed index and number of inflorescences/ plant. The superiority of S₁ to half- sib family selection was attributed to the amount of additive genetic variance within each type of families. These results are in agreement with the finding of Hallauer and Miranda (1988), Weyhrich *et al.*, (1998), Ahmed (2006-a) and (2006-b).

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Table (5): Estimates of heritability (h^2), genetic advance in absolute (GA) and percent of mean (GA %) for *Helaly* barseem seed yield and seed yield components.

Character	h^2		GA		GA%	
	H.S	S ₁	H.S	S ₁	H.S	S ₁
Seed yield (g /0.1m ²)	0.5594	0.6200	2.110	2.31	18.71	24.20
Seeds/ inflorescence	0.6228	0.7900	4.930	7.85	18.12	29.36
Flowers / inflorescence	0.6502	0.7100	14.24	15.09	21.42	23.67
Seed setting %	0.6574	0.7133	11.68	11.87	26.41	28.79
Seed index	0.7199	0.7325	0.5490	0.4770	18.33	16.60
Inflorescences / plant	0.6127	0.6874	16.58	5.370	22.74	19.80

H.S: half- sib families.

S₁: First selfing generation families.

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الإختلافات في محصول البذرة ومكوناته للعشيرة هلالى من البرسيم المصري

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المخلص العربي

تهدف الدراسة الى تقدير الاختلافات في الوعاء الجيني لعشيرة البرسيم المصري "هلالى" من خلال دراسة نوعان من العائلات ; عائلات نصف منسبة half- sib وعائلات الجيل الأول للتلقيح الذاتي (S₁). تم تقييم نوعي العائلات في تجربتان منفصلتان في محطة بحوث سخا بمحافظة كفر الشيخ- مركز البحوث الزراعيه-مصر. في معظم صفات محصول البذرة ومكوناته كان متوسط مربع الانحرافات بين العائلات أكبر في قيمته عند تقديره من عائلات الجيل الأول للتلقيح الذاتي مقارنة بالعائلات النصف منسبة، بينما كان اتجاه متوسط مربع الانحرافات داخل العائلات معاكس لذلك. وقد ظهرت تقديرات موجبة للتباين الإضافي σ^2_A لجميع صفات محصول البذرة ومكوناته المدروسة. أيضاً فقد أظهرت نسبة التباين الإضافي σ^2_A إلى التباين الكلي دوراً فعالاً في التحكم في توريث صفات محصول البذرة ومكوناته. وقد بلغ الانخفاض في قيم متوسطات الصفات في عائلات الجيل الأول

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للتلقيح الذاتي مقارنة بالعائلات النصف منسوبة ٥.٣٨ و ١.٧٣ و ٤.١١ و ٦.٧٨ و ٣.٦٤ و ٣.٣٨ % لصفات محصول البذرة وعدد البذور / نورة و عدد الأزهار / نورة ونسبة عقد البذور ومعامل البذرة وعدد النورات على النبات على الترتيب. من ناحية اخرى كانت الاختلافات الوراثية بين العائلات النصف المنسوبة (H.S) أقل من ٢٠% من متوسط صفات محصول البذرة ومكوناته، فيما عدا صفة نسبة عقد البذور التي وصلت إلى ٢٣% من متوسطها. في المقابل فقد بلغت الاختلافات الوراثية بين عائلات S₁ أكثر من ٢٠% من متوسطات الصفات المدروسة. وكانت قيم معامل الاختلاف المظهري لمحصول البذور وعدد البذور / نورة أكبر عند تقديرها من عائلات S₁ ، بينما كانت التقديرات متماثلة لباقي الصفات المدروسة بغض النظر عن نوع العائلة المدروسة وقد سجلت صفة محصول البذور أقل تقدير لمعامل التوريث (٠.٥٥ و ٠.٦٢ لعائلات H.S و S₁ على الترتيب). وهذا قد يرجح تأثير البيئة على تعبير تلك الصفة. كما سجلت أقل تقديرات للتحسن المتوقع من الانتخاب لصفة معامل البذرة (٠.٥٤٩ و ٠.٤٧٧ جرام / نورة / نورة (١٤.٢٤ و ١٥.٠٩ زهرة لكل نورة) لعائلات H.S و S₁ على الترتيب). ومنسوبة إلى متوسط الصفات، فإن التحسن الناتج عن انتخاب عائلات H.S تراوح بين ٢٦.٤١% لنسبة عقد البذور إلى ١٨.١٢ لصفة عدد البذور / نورة. بينما كانت قيم التحسن المئوي من انتخاب عائلات S₁ يتراوح بين ١٦.٦٠% لصفة معامل البذرة إلى ٢٩.٣٦% لصفة عدد البذور / نورة.

