SELECTION OF SOME ALFALFA POPULATIOS FOR FORAGE YIELD AND QUALITY USING MODIFIED MASS SELECTION

Mofeeda A. Seiam and M.A. El-Nahrawy

Forage Crops Res. Department, field crop institute, A.R.C, Egypt

ABSTRACT

Modified mass selection method was used to study the gain from selection and compare between the base population and the half-sib families of alfalfa in 2016/2017 season. Selection was practiced among half-sib families for the best eight families (10% intensity of selection). Seeds of selected half-sib families and both modified mass selection cycles C_1 and C_2 were evaluated for forage yield, some yield components and protein percentage. C_1 significantly dominated over the base population as well as C_2 significantly dominated the C_1 for plant height, leaf/stem ratio and forage yield. The realized gains after the two modified mass selection cycles were 6.89, 25.56, 15.87, 19.47 and 0.87% for plant height, leaf/stem ratio, fresh forage yield, dry forage yield, and protein percentage, respectively, over the base population. We may suggest from the results that modified mass selection resulted in a great improvement of forage yield, plant height and leaf/stem ratio, but in small gain for protein percentage. The values of genotypic coefficient of variation (GCV%) and phenotypic coefficient of variation(PCV%) were 5.28% and 7.03% for plant height, 1.30 and 1.79% for leaf/stem ratio, 7.76and 10.26% for fresh forage yield, 8.42 and 11.23% for dry forage yield and 5.53 and 6.55 % for protein percentage, respectively. Broad-sense heritability values for leaf/stem ratio and protein percentage were 72.94% and 71.25% which were higher than those for fresh and dry forage yields and plant height, at 56.47%, 57.07% and 56.15%, respectively.

Key words: *Medicago sativa* **L.**, *Base population, Modified mass selection, Selection cycles, Realized selection gains,* **Heritability, Genotypic and** *phenotypic coefficient of variability.*

INTRODUCTION

Alfalfa is the most important forage crop worldwide. It grows as a green forage for hay, silage or pasture production. Alfalfa plants are characterized with high nutritive value and have a wide adaptability range (Li and Brummer 2012).The presence of large genetic variability in alfalfa leads to create various range of varieties adapted to specific environments and management systems. In order to make selection in alfalfa more efficient, breeders should carefully design and establish breeding programs which will lead to maximize the expected yield. For inclusion in varieties, individual parent plants of alfalfa or other open pollinated perennial forage species are evaluated as clonal materials or according to the performance of their half-sib(HS) progenies, S_1 progenies or, more rarely, full-sib progenies (Poehlman and Sleeper 1995, Casler and Brummer 2008 and Posselt 2010).

Alfalfa breeding programs have long placed minor emphasis on forage quality, as confirmed by negligible rates of genetic gain for its component traits (Annicchiarico*etal*2015).There is limited and somewhat inconsistent information on the possibility to jointly improve leaf/stem ratio and forage yield of alfalfa, despite its selection directed towards increasing frequencies of favorable alleles has improved vigor in alfalfa populations at several levels of inbreeding(Gallais1984 and El-Nahrawy and Bingham 1989) realized gains over the base population were 17.7 and 25.2% for fresh forage yield, 18.7 and 24.8%for dry forage yield and 25.4% for protein yield in the first and second cycles of recurrent selection, respectively (Bakheit and El Nahrawy 1997).The genetic advance of selection for the studied traits ranged from 3.3 to 20.3%(Abdel-Galil 2007).The realized gains after the two mass selection cycles were 14.94, 14.00 and 11.34% for fresh and dry forage yield and crude protein(%), respectively over the base population. Gains from family selection as percentage of base population were 17.24, 16.00and 16.49% for these traits in the same order (Bakheit*et al* 2011). Omara and Hussein (1982) reported that family selection was more rewarding than mass selection for forage yield where the response was 8.66% over the base family mean after one cycle of selection. A significant response to mass selection was obtained after the first cycle of selection which amounted to 20.58 and 5.11% over the base population mean in two successive yield trails. Bakheit (1985) reported that the realized gains of the first and second cycles of mass selection, for the fresh forage yield were 8.43 and 10.7% of the base population, respectively. Bakheit (1986) showed that the expected genetic advance for the best six accessions was 16.10% for plant height, 17.50% for seasonal fresh yield, 20.60% for seasonal dry yield and 21.0% for seasonal protein yield. Bakheit and El-Nahrawy (1997) found that realized gains over the base population were 17.7 and 25.2 for fresh forage yield, 18.7 and 24.8% for dry forage yield and 18.3 and 25.4% for protein yield in the

first and second cycles of recurrent selection, respectively. Hamd Alla *et al* (2012) revealed that one cycle of mass selection for root characteristics was effective in increasing fresh forage yield/plot by 9.9 and 22.9% and dry forage by 11.9 and 22.9% overall cuts in selections from local and exotic populations, respectively (Bakheit and Ali 2013).Realized gains from C_1 and C_2 of mass selection were 4.9 and 14.4% for fresh forage and 5.3 and 13.2% for dry forage yield over the base population. Bakheit *et al* (2016) found that the realized gains of the recurrent selections were 18.6, 11.7, 14.6 and 24.1% for leaf/stem ratio, fresh and dry forage and protein yields, respectively, over the base population.

The success of selection programs for forage yield and its components depend mainly on large genetic variability that has been found for morphological traits along with forage yield. The heritability of the selected traits, the nature of correlations between different characters and the intensity of selection applied are also important for the success of selection (Abdel Galil 2007, Veronesi *et al* 2010, Bakheit *et al* 2011, Hamd Alla *et al* 2012, Annicchiarico 2015 and Badawy 2017).

Abdel-Galil (2007) indicated that there was relative variation among the tested genotypes. The environmental variation ranged from 2.4 to 30.5%.The values of genotypic coefficient of variation for fresh and dry forage yields revealed relative variations among the cultivars under study which were less influenced by environment. Rajab (2010) observed that the highest phenotypic coefficient of variation value (P.C.V.) was recorded for fresh forage yield as 5.075%, 9.036% and 6.792% in the first, second and third seasons. Badawy (2017) estimated genetic parameters for fresh yield, dry yield, plant height and dry leaf/stem ratio. P.C.V. values were 4.75, 4.65, 1.224 and 3.07% and G.C.V. values were 3.21, 3.72, 0.774 and 2.24%, respectively.

Badawy (2013) reported that fresh forage yield expressed the highest estimates of heritability while, the obtained values for dry forage yield were of lower magnitude. Abd El- Naby et *al* (2014) found that broad- sense

619

heritability was 0.90 and 0.84 for plant height and total fresh weight plant^{-1}, respectively. Ahmed *et al* (2015) estimated broad- sense heritability on berseem clover, the highest values obtained for fresh forage yield, dry forage yield and leaf/stem ratio were 98.23 , 98.7 and 100%respectively. Badawy (2017) found that heritability for fresh forage yield reached 69.56%.

The objectives of this study were, i): studying the effect of two cycles of selection for forage yield in alfalfa ecotypes. ii): estimating genetic variability among selected genotypes, heritability and genetic improvement for forage yield, its components and quality, and iii): identifying the promising genotypes and their use in further breeding programs.

MATERIALS AND METHODS

Field trials were conducted in Nubaria Agricultural Research Station (North West of Nile delta, Egypt) The first trial was conducted to evaluate five hundred and twenty five populations during two years from 2009 to2011.The seed lots were collected from Dakhla, Kharga, Elbharei and Siwa oasis and one French population (non-winter dormant). In 2011, twenty five populations (5% intensity of selection) were selected depending on stability of fresh and dry forage yields and quality using modified mass selection method. Equal seeds from each selected genotype were bulked to form C_1seed. The same time, seeds of the twenty- five genotypes were sown as half-sib families. Each family consisted of 200 plants. Cultural practices were applied at optimum levels to realize high alfalfa productivity. In 2011-2014 selected entries (25 populations) were evaluated and selection was practiced among half-sib families for the best 30% families (Eight families).The best twenty fresh forage producing plants from the best eight families were selected and transplanted in an isolated plot to avoid cross pollination with unselected plants. Seeds were harvested from each selected plant separately and mixed to from the first cycle of family selection (C_2).

620

The second trial was sown on Oct. 10th, 2015. A randomized complete block design with four replicates was used. The best plants in each plot based on fresh forage weight (10% selection intensity) were selected. Selections were transplanted in an isolated plot to avoid pollination with unselected plants. Seeds were harvested by hand at seed maturity stage. In 2014/2015 season, equal parts of seeds from each of the selected plants were bulked to form the first cycle of modified mass selection (MMC_1). Similar cultural practices, selection procedure and intensity of selection were adopted as described previously to obtain MMC_2. In 2016/2017 season, to evaluate the response to selection, the base population and two modified mass selection cycles (MMC_1 and $MM C_2$) were tested in a randomized complete block design with four replications. Plot size was 3.0 x4.0 m with rows 20 cm apart. The Seeding rate was 48 kgha^{-1}. Seeds were inoculated with *Rhizobium melolitii* prior to seeding. Starter dose of nitrogen (48 kgha^{-1}) was applied directly after the full establishment. A base dose of Super phosphate (15.5%P_2O_5) at the rate of 360 kgha^{-1} was applied before sowing. 120 kgha^{-1}of Potassium sulphate (46%K_2O) was applied at three equal doses, yearly. Data were recorded at cutting. Nine cuts were taken from each population. The first cut taken at 20 February after 85 days from sowing (15 November 2016). The other cuts were taken at 30-35 day intervals, and the last cut was taken at 26 November 2017. Ten guarded plants were randomly dogged out from each plot to study plant height (cm), leaf/stem ratio (LSR). The plants in each plot were harvested and weighed to determine the forage yield (kg/plot)and a representative sample from each plot was dried at 65˚Ctillconstant weight to determine dry forage yield .Crude protein percentage (%) was determined using standard method (A.O.A.C 1990).

Statistical analysis for all the studied traits were performed according to El-Nakhlawy (2010) using ANOVA procedure of SAS software (2014). The realized gains from selection measured as the

deviation percentage of the overall cycle mean from the base population (Falconer 1989) as follows: Realized gain (%) relative to base population =C1-C0/C0 x 100.

The genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) were calculated according to Burton (1952)

as follows = G.C.V.= σ_G/grand mean x100

P.C.V. = σ_P /grand mean x 100

Where; σ_G: represents genetic standard deviation.

σ_p: represents the phenotypic standard deviation.

Heritability in broad- sense according to Johnson *et al* (1955) as follows;

H = σ^2_G /σ^2_p x 100

Where: σ^2_G is genotypic variance and σ^2_p is phenotypic variance.

RESULTS AND DISCISSIONS

Evaluation of modified mass selection

Analysis of variance (Table 1) shows significant differences among the selected cycles (p ≤0.01) for plant height, leaf/stem ratio, fresh forage yield, dry forage yield and protein percentage.

Table 1. Analysis of variance of plant height, leaf/stem ratio, fresh and dry forage yields and protein percentage of the base population, first (C_1) and second (C_2) of modified mass selection.

SOV	df	MS				
		Plant height	Leaf/stem ratio	Fresh forage yield	Dry forage yield	Protein (%)
Replicates	3	0.30	4.37	3.41	0.22	0.007
Among cycles	2	21.26**	127.92**	20.988**	3.93**	0.037**
Base vs Selected	1	26.04**	18.20*	7.848**	2.02**	0.073**
C_1 vs C_2	1	16.47**	255.83**	34.11**	5.83**	0,001 ns
Error	6	0.28	2.81	1.11	0.10	0.003

Ns: not significant at p ≤ 0.05. *, **: significant at p≤ 0.05 and p ≤0.01, respectively.

Also, significant differences were found between the base population and the two cycles of modified mass selection (p ≤0.01) for all the studied traits. Besides, significant differences were shown between C_2 and C_1 populations (p ≤0.01) for all the studied traits, except protein content. The previous results are in a harmony with those obtained by Wang *et al* (1991), Bakheit and El-Nahrawy (1997), Kimbeng and Bingham (1998), Awad (2001), Bakheit *et al* (2011) and .Bakhiet and Ali (2013).

Means of plant height, leaf/stem ratio, fresh forage yield, dry forage yield and protein percentage of the base population and the selected populations are presented in Table (2).

Table 2. Means of plant height, leaf/stem ratio, fresh and dry forage yield and protein percentage of the base population, first (C_1) and second (C_2) of modified mass selection.

Generation	Means				
	Plant height (cm)	Leaf/stem ratio (%)	Fresh forage yield (Kg/plot)	Dry forage yield (Kg/plot)	Protein (%)
Base population (C_0)	**66.14**	**44.24**	**37.172**	**9.916**	**18.40**
First cycle (C_1)	**67.83**	**52.51**	**39.445**	**10.765**	**18.58**
Second cycle (C_2)	**70.70**	**55.55**	**43.072**	**11.847**	**18.56**
RLSD: (0.05)	**0.91**	**2.90**	**1.82**	**0.55**	**0.09**
(0.01)	**1.38**	**4.39**	**2.76**	**0.82**	**0.14**

Means of both C_1 and C_2 were significantly greater than the base population (C_0) for all five studied alfalfa traits. Means of the C_2 were significantly higher than those of the C_1 for plant height, leaf/stem ratio, fresh and dry forage yields at p ≤ 0.05.An insignificant difference was detected between C_1 and C_2 for protein percentage (p ≤ 0.05).These results indicated the positive effects of modified mass election to improve alfalfa forage yield and the other two studied yield components. These results are in agreement with those reported by Wang *et al*(1991), Bakheit and El-Nahrawy (1997), Awad (2001), Bakheit*et al* (2011) and Hamd Alla *et al* (2012).

The realized gains from selection estimated as the percentage deviation of the mean of the base population are shown in Table (3). The results indicated that, direct selection was effective in improving the studied traits after the second cycle of modified mass selection by 6.89% for plant height, 25.56% for leaf/stem ratio, and 15.87% for fresh forage yield, 19.47% for dry forage yield and 0.87% for protein percentage. However, the realized gain from selection after C_1 cycle were 2.55, 19.58, 6.11, 18.56 and 0.98% for the previous traits, respectively.

Table 3. Realized gain (%)from modified mass selection for plant height, leaf/stem ratio, fresh and dry forage yield and protein percentage in the two cycles of selection measured in percentage from the base population.

Base population	Cycle of selection	Plant height (cm)	Leaf/stem ratio (%)	Fresh forage yield, (kg/plot)	Dry forage yield, (kg/plot)	Protein (%))
C_0	C_1	2.55**	19.58**	6.11**	18.56**	0.98**
	C_2	6.89**	25.56**	15.87**	19.47**	0.87**

**: significant at p$\leq$ 0.01

Evaluation of family selection

As for family selection, results of the analysis of variance (Table 4) showed significant differences among families (p $\leq$0.01) for all the studied traits,except for protein percentage. Also, the differences between the eight selected families and the base population were significant (p<0.01), except for protein percentage.

Data of means of plant height, leaf/stem ratio, fresh forage yield, dry forage yield and protein content of the base population and the eight families are presented in Table (5). As for plant height, mean values ranged from 71.40 to 75.60cm for the half-sib (H.S.) families compared with 58.83 cm for the base population. All H.S. families were significantly (p $\leq$0.01) taller than the base population. Considering leaf/stem ratio, it ranged from 52.31 to 57.88 for the H.S. families compared with 52.40 for the base population. Furthermore, six H.S. families were significantly higher than the

base population after one cycle of family selection. Only the families G.6, G.7 and G.8 were not significantly different from the base population for leaf/stem ratio.

Table 4. Analysis of variance of plant height, leaf/stem ratio, fresh and dry forage yield and protein percentage for the base population and eight selected families of alfalfa grown in the 2018/2019 season.

SOV	df	MS				
		Plant height	Leaf/stem ratio	Fresh forage yield	Dry forage yield	Protein (%)
Replicates	3	5.59	124.90	83.14	3.02	1.12
Families	8	106.35**	247.23**	192.89**	7.83**	4.089 ns
Base *vs* selected families	1	330.53**	99.97**	201.05**	6.17**	3.629 ns
Between selected families	7	74.32**	268.27**	191.73**	8.07**	3.50 ns
Error (families)	24	5.59	6.21	4.23	1.65	2.22
Error (selected families)	21	4.62	6.11	4.09	1.47	1.71

Ns: not significant at p ≤ 0.05. *, **: significant at p≤ 0.05 and p ≤0.01, respectively

Table 5. Means of plant height, leaf/stem ratio, fresh and dry forage yield and protein percentage for the base population and eight selected families of alfalfa.

Genotype	Plant height (cm)	Leaf/stem ratio (%)	Fresh forage yield (kg/plot)	Dry forage yield (kg/plot)	Protein percentage (%)
H.S.					
G.1	71.40	54.72	41.549	10.803	18.691
G.2	74.86	55.12	44.824	11.967	18.886
G.3	73.23	57.06	43.810	11.522	18.949
G.4	75.60	56.78	43.740	10.962	18.631
G.5	72.90	57.88	42.662	11.101	18.623
G.6	74.10	55.03	41.040	11.074	18.410
G.7	72.10	52.31	43.527	11.678	18.622
G.8	73.90	53.53	41.429	10.660	18.527
Bass Population	58.83	44.28	38.674	9.258	18.022
RLSD (0.05)	3.45	3.63	3.001	1.672	ns
(0.01)	4.68	4.88	3.980	2.391	ns

As for, fresh forage yield (kg/plot),it ranged from 41.040 kg/plot for G.6to 44.824kg/plot for G.2. Five families were significantly higher than the base population (38.674kg/plot) in fresh forage yield. Dry forage yield for the families ranged from 10.660kg/plot for G. 8 to 11.967 kg/plot for G.2, while the dry yield of base population was 9.258 kg/plot. All families except two families(G.1 and G.8) were significantly higher than the base population in dry forage yield. Insignificant differences were detected among families for protein means. Protein percentage means ranged from 18.022 % for the base population to 18.949% for G.3. Similar results were reported by other investigators (Awad 2001, Bakheit *et al* 2011, Annicchiarico 2015and Bakheit *et al* 2016).

A summary for the main genetic parameters is presented in Table (6). The genotypic and phenotypic variances expressed as GCV% and PCV% were 5.28% and 7.03% for plant height, 1.30 and 1.79% for leaf/stem ratio, 7.76and 10.26% for fresh forage yield, 8.42 and 11.23% for dry forage yield, 5.53 and 6.55% for protein content, respectively.

Table 6. Different genetic parameters for different traits of alfalfa genotypes.

Genetic parameter	Plant height (cm)	Leaf/stem ratio (%)	Fresh forage yield (Kg/plot)	Dry forage yield (Kg/plot)	Protein percentage (%)
Range	58.83-75.60	44.28-57.88	38.674 – 44.824	9.258-11.967	18.022-18.949
Mean	71.87	54.98	42.362	11.12	18.618
σ^2_G	0.144	0.509	10.78	0.876	0.057
σ^2_E	0.836	2.211	30.89	1.135	0.037
σ^2_{GE}	0.293	1.006	16.33	0.612	0.092
σ^2_{Ph}	0.255	0.978	18.89	1.56	0.080
GCV (%)	5.28	1.30	7.76	8.42	5.53
PCV (%)	7.03	1.79	10.26	11.23	6.55
H (%)	56.47	72.94	57.07	56.15	71.25

σ^2_E: environment variance, σ^2_G: genotypic variance.σ^2_{GxE} genotypic x environment variance, σ^2_P: phenotypic variance,
P.C.V.: phenotypic coefficient of variability and G.C.V.: genotypic coefficient of variability, .H: heritability.

These results showed a sufficient genotypic variation among selected families after one cycle of family selection for different traits. Broad-sense heritability values were high for leaf/stem ratio and protein percentage with values of 72.94 and 71.25%, respectively. But, for fresh and dry forage yields, heritability values were medium with values of 57.07 and 56.15%, respectively. Regarding plant height, heritability was 56.47%. The medium heritability values of forage yield and plant height demonstrated more environmental effects on these traits. Similar results were reported by Awad (2001) and Bakheit *et al* (2011 and 2016), Annicchiarico *(*2015) and Badawy (2013 and 2017).

ACKNOWLEDGMENTS

REFERENCES

Abd El-Galil, M.M. (2007). Yield potential, genetic variation, correlation and path Coefficient for two newly developed synthetics and three commercial varieties of alfalfa. Egyptian, J. Plant Breeding, 11 (3):45-54.

Abd EL-Naby, Zeinab, M, Wafaa, W. M. Shafie and M. A. EL-Nahrawy (2014). Genetic analysis and maternal effects in barseem clover. Life. Sci. J. 11 (55):407418.

Ahmed, M. Abd EL-Sattar, M. N. Barakat, and A. M. S. Rady (2015). Genotypic variation in Egyptian gene pool of barseem clover (*Trifolium alexandrinum*, L.). Egypt. J. Plant. Breed. 19(3): 307-326.

Annicchiarico, P. (2015). Alfalfa forage yield and leaf/stem ratio: narrow-sense heritability, genetic correlation, and parent selection procedures. Euphytica 205:409–420

Annicchiarico P, B. Barrett, E.C. Brummer, B. Julier, A.H. Marshal (2015). Achievements and challenges in improving temperate perennial forage legumes. Crit Rev Plant Sci;34:327–380.

A.O.A.C. (1990). Official Methods of Analysis. 15th Ed., Association of Official Analytical Chemist, Washington, DC., USA., pp: 56-132.

Awad, I.M.H. (2001). Selection response in berseem (*Trifolum alexandrinum*, L.) and alfalfa (*Medicago sativa*, L.). Ph.D. Thesis, Faculty of Agric., Assiut Univ., Egypt.

Badawy, A. S. M. (2013). Recurrent selection for seed yield in "Helaly" Barseem clover. Ph. D. Thesis, Fac. of Agric. Alex. Univ., Egypt.

627

Badawy, A. S. M. (2017). Variability and potentiality of selection among farmers seed lots of barseem clover "*Trifolium alexandrinum*, L.". Alex. J. Agric Sci., 62(6): 469-476.

Bakheit, B. R. (1985). Effect of mass and family selection on productivity of Egyptian clover (*Trifolium alexandrinum*, L.). Assuit J. Agric. Sci. 16, 35-46.

Bakheit, B. R. (1986). Genetic variability, genotypic and phenotypic correlations and path-coefficient analysis in Egyptian clover (*Trifolium alexandrinum*, L.). J. of Agron. and Crop Sci. 157(1): 58-66.

Bakheit, B. R., A. Abo-Elwafa1; M.M. Abdel-Galil and A.M.A. Abdelmonem (2016). Impacts of recurrent selection and synthetic population on forage and seed yields of mono cut Egyptian clover (*Trifolium alexandrinum*, L.) Assiut J. Agric. Sci., 1: 31-44.

Bakheit, B.R., and M.A. Ali, (2013). Improvement of single cut Egyptian clover (*Trifolium alexandrinum* L.) by mass and family selection methods. *Asian Journal of Crop Science, 5: 304-311.*

Bakheit, B.R. and M.A. El-Nahrawy(1997). Alternative approaches to alfalfa population improvement. Egypt J. Plant Breed., 1: 27-34.

Bakheit, B.R., M.A. Ali and A.A. Helmy (2011). Effect of Selection for Crown Diameter on Forage Yield and Quality Components in Alfalfa (*Medicago sativa*, L.). Asian Journal of Crop Science, 3: 68-76.

Burton, G.W. (1952). Quantitative inheritance in grasses. Proc. 6th Int. Grassland Congr., 1: 277283.

Casler, M.D. and E.C. Brummer (2008). Theoretical expected genetic gains for among- and within- family selection methods in perennial forage crops. Crop Sci 48:890–902.

El-Nahrawy, M.A. and E.T.Bingham (1989). Performance of S_1 alfalfa lines from original and improved populations. Crop Sci; 29:920–923.

El-Nakhlawy, F.S. (2010). Experimental Design and Analysis in the Scientific Research. Sci .Pub. Center, King Abdulaziz UNiversity, Jeddah, Saudi Arabia.

Falconer, D.S.(1989). Introduction to Quantitative Genetics. 3rd Ed., Longman Scientific and Technical, New York, USA Pages: 438.

Gallais, A. (1984). An analysis of heterosis vs. inbreeding effects with an autotetraploid cross-fertilized plant: *Medicago sativa*, L. Genetics 106:123–137.

Johanson, H.W., H.F. Robinson and R.E. Comstock (1955). Estimates of genetic and environmental variability in soybeans. Agron. J. 47: 314318.

Hamd Alla, W. A., B. R. Bakheit , A. Abo- Elwafa and M. A. El-Nahrawy (2012). Effect of mass selection for root characteristics on forage yield and some of its components in alfalfa. Egypt. J. Plant Breed. 3:1 – 18.

Kimbeng, C.A. and E.T. Bingham (1998). Forage yield potential of alfalfa plants of varying crown size from old stands. Plant Breed., 117: 251-254.

Li, X. and E.C. Brummer (2012). Applied genetics and genomics in alfalfa breeding. Agronomy 2:40–61.

Omara, M.K. and M.Y. Hussein (1982). Selection for productivity of green material in berseem clover (*Trifolum alexandrinum* L.). Assiut J. Agric. Sci., 13: 105-116.

Pecetti, L. and E. Piano (2005). Heritability of morphophysiological traits and inbreeding effects in grazing-type lucerne. Plant Breed 124:176–179.

Poehlman, J.M .and D.A. Sleeper (1995). Breeding Field Crops, 4th ed. Iowa State University Press, Ames.

Posselt, U.K. (2010). Breeding methods in cross-pollinated species. In: Boller B, Posselt UK, Veronesi F (eds) Fodder crops and amenity grasses. Handbook of plant breeding. Springer, New York, pp 39–87.

Rajab, M.N. (2010). Studies on breeding of Egyptian clover (*Trifolium alexandrinum,*L.). Ph.D. Dissertation, Fac. Agric. Minia Univ., Egypt. Sci.

SAS (2014). SAS: Business analytics and business intelligence software. SAS Inst. http://www.sas.com/en_us/home.html (accessed 30 Sept. 2014).

Wang, S., M.A. Brick and C.E. Townsend (1991). Response of alfalfa to bidirectional selection for root bark area and xylem vessel diameter. Can. J. Plant Sci., 71: 427-435.

Veronesi, F., E.C. Brummer and C. Huyghe (2010). Alfalfa. In:" B. Boller *et al* (eds.), Fodder crops and Amenity Grasses, Handbook of Plant Breeding, Springer Science + Business Media, P: 395-437.

انتخاب بعض عشائر البرسيم الحجازى للمحصول وجودته بأستخدام طريقة الانتخاب الاجمالى المعدل

مفيدة عبد القادر صيام و محمد ابو زيد النحراوى

قسم بحوث العلف – معهد المحاصيل الحقلية – مركز البحوث الزراعية

تم استخدام طريقة الانتخاب الاجمالى المعدل لدراسة العائد من الانتخاب والمقارنة بين العشيرة الاصلية و العائلات المنتخبه انصاف الأشقاء فى ٢٠١٦ / ٢٠١٧ . تم الأنتخاب بين العائلات انصاف الأشقاء وانتخاب أفضل ثمان عائلات (كثافة الأنتخاب ١٠%) ثم تقييم بذور العائلات انصاف الأشقاء المنتخبة ودورتا الأنتخاب الأجمالى المعدل للمحصول العالى وبعض مكونات المحصول ونسبة البروتين. تفوقت الدورة الأولى بشكل كبير على العشيرة الأصلية وتفوقت الدورة الثانية على الدورة الأولى فى صفة أرتفاع النبات ونسبة الأوراق للسيقان ومحصول العلف. و كان العائد من الانتخاب بعد دورتين انتخاب تحسن بنسب مئوية٦,٨٩و ٢٥,٥٦ و ١٥,٨٧ و ١٩,٤٧ و ٠,٨٧% لارتفاع النبات و نسبة الأوراق للسيقان و محصول العلف الأخضر و محصول العلف الجاف و نسبة البروتين على التوالى مقارنةبالعشيرة الأصلية و تشير النتائج الى ان الانتخاب الاجمالى المعدل أدى الى تحسين كبير فى انتاجية العلف و ارتفاع النبات و نسبة الأوراق للسيقان و لكن العائد من الانتخاب كان منخفض لنسبة البروتين. بلغت نسبة ال GCV%PCV% ٥,٢٨ و ٧,٠٣% لارتفاع النبات و ١,٣٠ , ١,٧٩ لنسبة السيقان للأوراق و ٧,٧٦ و ١٠,٢٦ لمحصول العلف الأخضر و ٨,٤٢ و ١١,٢٣% لمحصول العلف الجاف و ٥,٥٣ و ٦,٥٥% لنسبة البروتين على التوالى. و بلغت قيم كفائة التوريث بمعناه الواسع لارتفاع النبات و نسبة الأوراق للسيقان و محصول العلف الأخضر و محصول العلف الجاف و نسبة البروتين ٥٦,٤٧% و ٧٢,٩٣% و ٧١,٢٥% و ٥٧,٠٧ % و ٥٦,١٥% على التوالى.