RESPONSE OF PEARL MILLET FORAGE YIELD TO THREE CYCLES OF RECURRENT SELECTION

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Abstract

Three cycles of recurrent selection for forage yield were conducted using a broad-based population of pearl millet at Giza Expt. Station ARC, Egypt during 2003 to 2009 seasons for improvement ten families of pearl millet derived from cv. Shandweel 1. The recurrent selection scheme was based on a two-step cycle during two-years. Results showed that recurrent selection was effective in improving cv. Shandweel 1 over the three cycles of selection. Significant differences among the ten families in each cycle of evaluation and the interaction of (cycle x family) were detected. Evaluation at three cycles showed that families 1, 2 and 4 had significantly higher dry yield than the source families, achieving 19.24, 31.82 and 29.27%, respectively. Response to selection was observed for source population, especially in the first cycle. The selection responses for fresh and dry yield, in the first cycle of recurrent selection (C_1) were 37.59 and 40.90%, respectively, over the source families while the second cycle (C_2) responses were 4.00 and 7.60%, respectively over cycle one (C_1). In addition, the selection responses of the third cycle (C3) were 14.62 and 8.58%, respectively over the second cycle (C_2) for the same traits. Broad-sense heritability values estimated from genotypes were 0.97 and 0.94 for total fresh and dry yield, respectively. The estimates of genetic advance for selection showed that three cycles of selection and open pollination for the selected families in each cycle, has shown an increase of 11.44 and 0.44 t fed^{-1}, representing 36.43 and 6.89% over the general average for total fresh and dry yield, respectively. Also, other traits showed the same trend for genetic advance ranging from 0.02 to 16.95% over the general average. These results indicate that application of recurrent selection method in open pollinated populations of pearl millet, with 10% selection intensity was effective. The rapid gain observed in the first cycle of selection, may be due to easily detecting and eliminating, the low-yielding families and consequently improving the population productivity.

Key words:

Recurrent selection, Cycle of selection, S_1 First selfed generation, Source population, h^2 Heritability, Selection response.

INTRODUCTION

Pearl millet, (*Pennisetum glaucum* (L.) R.Br) is mostly grown as a forage crop in many countries. In Egypt, pearl millet plays an important role to fulfill forage demand in summer season. Developing high yielding cultivars characterized with resistance and / or tolerance to biotic and abiotic stresses of forage crops is one of the important activities of the Forage Crops Res. Sec. As the total area cultivated with summer forage crops is limited, it is badly needed to increase the productivity of forage of such area by releasing highly productive new varieties of summer crops (El-Shahawy and Gheit. 1999, Haggag *et. al.*. 2000; El shahawy *et. al.,* 2000; Mohamed, 2000; Bidinger and Raju, 2000 and Abd El-Galil and Oushy 2007).

Recurrent selection methods were used to improve the frequency of desirable genes in a population so increase the opportunities to extract superior genotypes. In recurrent selection, large amount of genetic variability can be readily obtained by hybridization between many parents. Widely-adapted pearl millet variety ICMV 221 was chosen as a source population for two cycles of recurrent selection among full-sib progeny to assess opportunities for improving the forage nutritional quality of open-pollinated cultivars (Witcombe *et. al.* 1997). Four recurrent selection methods were compared for grain yield, in which 100 S_1 lines from pearl millet cv. Half sib 1 was selected to produce S_2 material, full-sib material, half-sib material from crosses with bulk pollen of HS_1 and half-sib material from crosses with bulk pollen of WC-C75 composite, in two localities of pearl millet, selection differential, heritability and genetic advance were higher with the S_2 than the full-sib and two half-sib methods (Kapoor et al. 1983).

The population improvement program at ICRISAT uses half-sib and S_1 as the two major methods of selection (Singh *et. al.* 1988a). Four methods of selection were compared in a single composite, with up to 6 cycles of selection. This variability was maintained in a population using recurrent intercross whereas the population was improved by selection. This allows repeated opportunities for selection, recombination and transgressive segregation. Singh *et. al.* (1988b) indicated that the most important aspect of a successful recurrent selection program is the choice of parents to form a source population with large amount of desirable genetic variability.

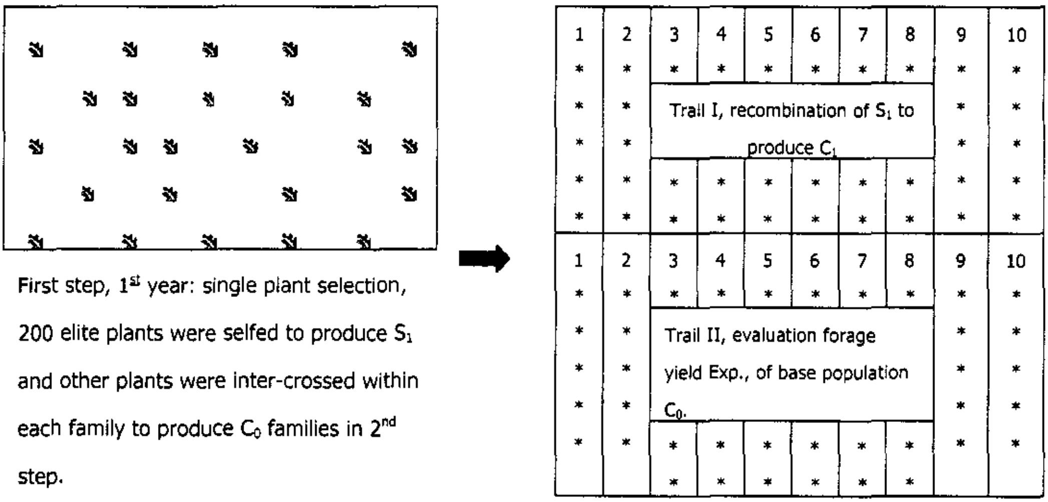
Information on interapopulation and interpopulation variance components and their interactions with locations was derived from S_1, half-sib and reciprocal full-sib families of PSB3 and PSB, random mating population of pearl millet (Zaveri *et. al.*, 1988). Substantial genetic variability was observed for nearly all traits studied. Reciprocal full and half-sib selection were equally effective in improving interpopulation hybrid performance, while S_1 selections through intermating, could be used for interapopulation improvement (Maiti and Wesch-Ebeling 1997).

Heritability can be used with genetic advance to predict advance under selection as mentioned by Johanson *et. al.*, (1955) and Bakheit, (1986). Moreover, the breeder can anticipate improvement from different types and intensities of selection, (Soliman, 1994).

The objective of this research was to improve the pearl millet cv. Shandweel 1 through three cycles of recurrent selection, and to assess changes in forage characteristics in varieties generated by random-mating selected subsets of these families.

MATERIALS AND METHODS

This study was conducted at the Agricultural Experment Res. Stn., ARC, Giza, Egypt during summer seasons of 2003 through 2009. Modified half-sib method is described as an aid to adopt recurrent selection methods in pearl millet (Allard, 1960 and Singh et al. 1988 b) as follows: Ten selected families derived from 100 families due to 100 individual plants from pearl millet cv. Shandweel 1 were used. Each family was visually selected based on phenotypic characteristics, (plant height, stem diameter, no. of tillers, flowering date, plant health, panicle size and shape, and seed weight) and marked with serial numbers. The recurrent selection scheme was based on two-step cycle during two-years (Fig. 1)



First step, 1st year: single plant selection, 200 elite plants were selfed to produce S_1 and other plants were inter-crossed within each family to produce C_0 families in 2nd step.

Second step, 2nd year: recombination of S_1 to produce C_1 & evaluating forage yield Exp., of C_0 base population.

Fig 1. Outline of procedure of recurrent selection in ten pearl millet families in one cycle for improving forage productivity during two years.

Step 1 in the first year, single plant selection:

Single plant selection was conducted within ten typical families (C_0) for improving forage productivity. Selection of superior plants was based on plant architecture and forage yield as follows:

Shandweel 1 cultivar was grown in ten plots during the summer season of 2003. Each plot consisted of 5 rows 4-m long, and 60-cm apart. The crop was sown at a seeding rate of 15 kg fed^{-1} and thinned to a uniform stand, 20 cm among plants along the row. Two hundred elite individual plants were self-pollinated to produce S_1 families and other plants were inter-crossed in each family from source populations to produce C_0. Self-pollinated and intercrossed plants were harvested and separately bulked carefully within each of the ten families.

Step-2, in the second year, recombination & evaluation:

Two trails were sown. In trail I, selected ten S_1 families of first step were grown for recombination for the next cycle (Fig 1), while in trail II ten base families (intercross plants) of the previous cycle (C_0), were planted for evaluating forage yield.

Trail I, the ten S_1 families were intercrossed in separate isolation blocks during the summer season to make all possible intercrosses families for the next cycle of recurrent selection (C_1). Each plot consisted of 5 rows of 4-m long, and 60-cm apart. The crop was sown at a seeding rate of 15 kg fad^{-1}and thinned to a uniform stand, 20 cm among plants along the row. To maximize out-crossing, the ten selected families were planted in isolated plots for open pollination. In addition, the plots were planted in the upwind edge of different sorghum fields to prevent pollen grains from other sources. Equal amounts of 10% selection intensity of seeds from each family population were separately bulked to provide sufficient seeds for the following cycle phase (cycle 1 C_1).

Trail II, the remaining previous cycle (C_0) seeds of the ten families (intercrossed seed) of source population (C_0) were sown at the Agric. Exp. Res. Stn., ARC, Giza, in a RCBD with 4 replications in June. Plots consisted of five rows 3-m long, 60-cm apart with hills spaced 20 cm sown at a seed rate of 20 Kg fad^{-1}. The cultural practices were applied as recommended. Plots were fertilized with 20 kg P_2O_5 fed^{-1} during land preparation, 30 kg N fed^{-1} before the first irrigation and after each cut. Three cuts were taken, (60, 95 and 135 days after sowing) during each season of evaluation. At each cut, the following data were collected at ten guarded plants: plant height, number of stems, stem diameter (cm), leaves/stems ratio %, fresh and dry forage yield. Dry yield was recorded following drying forage sub-samples from each plot.

The same previous procedures were followed as described in Fig. 1 to establish three recurrent selection cycles (C_1), (C_2) and (C_3) in summer 2005, 2007 and 2009, respectively. Selection response was measured for the ten families from C_0, C_1, C_2 and C_3 in summer seasons of 2003, 2005, 2007and 2009, respectively for forage productivity.

The combined analysis of variance was computed for total fresh and total dry weight t fed^{-1} of cycles and families. Broad-sense heritability (h^2) of each trait was estimated using the variance components in the cycle evaluation following the formulae: h^2 (%) = $\delta^2_f / ((\delta^2_f + \delta^2_{fc}/c) / (\delta^2_e/rc))$ where, δ^2_g= estimated genetic variance, δ^2_{fc} = family by cycle interaction variance δ^2_e= error variance, c= number of cycles and r= number of replications (Falconer and Mackay, 1996). Expected genetic advance under selection was estimated as suggested by Allared (1960). Selection response was calculated using the following equation:

Selection response (%) = $((C_1 - C_0) / C_0) * 100$). Where, C_1 and C_0 are means for respective improved and source family, respectively.

RESULTS AND DISCUSSION

The mean performance for three cuts of fresh and dry yields is presented in Table (1). Significant differences were detected among the ten families in each cycle of evaluation and the interaction of (cycle x family), indicating that the families under study were greatly affected by recurrent selection. The total fresh and dry yields ranged from 14.78 to 45.11 t fed^{-1} and, from 2.92 to 9.07 t fed^{-1}, respectively, in different families and cycles.

Response to selection

Recurrent selection between and within families was showed improvement of source populations for the three cuts of fresh and dry yields. Smaller dry forage yield response observed for families 3 and 6 for dry yield (Table 2). Moreover, cycle 1 produced high percentages of 37.59 and 40.90% of fresh and dry forage productivity than cycle (C_0). Generally, the selection response for families 1, 2 and 4 were 4.54, 6.26 and 6.86 t fed^{-1}, respectively, with relative mean performance over the grand mean, 19.24, 31.82 and 29.27%, respectively for total dry yield. Also, data showed that families 7, 8, 9 and 10 were significantly higher in total fresh and dry yields (24.45, 25.60, 33.83 and 38.45 t fad^{-1}) and (5.01, 5.23, 7.00 and 7.69 t fad^{-1}), respectively with relative mean performance over the grand mean 11.23, 11.62, 17.72 and 13.75%, respectively for total dry yield. The trend of the mean values over cycles for fresh and dry yields was similar to trends reported by Burton 1952, Lu and Lambert 1988, Eraky et al. 2003, Bidinger *et. al.* 2006, Badu-Apraku 2007 and Reddii *et. al.* 2010.

The significant improvement in forage yield suggests that recurrent selection was effective in increasing yield of the broad genetic base. Selection in cycle 2 showed that families 1, 4 and 10 had higher dry yield than the source families. Percent increases were 13.68, 12.77 and 10.54%, respectively. Moreover, evaluation at cycle three (C_3), showed that all populations had higher yields than the source population, with enhancement in yield ranged from 3.01 to 20.59 %.

Forage yield response to recurrent selection was determined (Table 3). In the first cycle (C_1), selection responses for fresh and dry yield were 37.59 and 40.90%, respectively over the source family (C_0). However, in the second cycle of recurrent selection (C_2) selection responses were 4.00 and 7.60%, respectively over cycle one (C_1). Moreover, in the third cycle (C_3) selection responses were 14.62 and 8.58%, respectively, over the second cycle (C_2). No significant differences were detected for plant height, stem diameter and leaf/ stem ratio %. After three cycles of selection, all populations showed significant increases in fresh and dry yields within families *per se* and between families. This may be due to the fact on selection was mainly based on forage yield rather than plant height and stem diameter. Selection response to recurrent selection varied from 5.44 to 93.28% per cycle for total dry yield.

The selection response for the first cycle (C_1) of recurrent selection was about 30% as compared to the response obtained from the source population of pearl millet families. The rapid gain observed in the first cycle of selection, may due to that low-yielding families being easily detected and eliminated, resulting in raising the population mean. In addition, accumulation of favorable genes for forage yield and related traits may be played an effective role in increasing yield of populations. In addition, to this dilution effect, genes from the tester may be dominant, epistatic, or complementary, with genes from S_1 genotypes to be evaluated (Burton 1952, Lu and Lambert 1988, Eraky et al. 2003, Bidinger *et. al.* 2006, Badu-Apraku 2007, Reddii *et. al.* 2010. and Younis *et. al.* 2010).

Table 1. Fresh and dry yields (t fed^{-1}) of ten millet families derived from Shandweel 1 cultivar at three cuts and their total cuts in three cycles of recurrent selection.

family	cycle	Fresh forage yield t fed^{-1}				Dry forage yield t fed^{-1}			
		Cut 1	Cut 2	Cut 3	Total cuts	Cut 1	Cut 2	Cut 3	Total cuts
1	C0	6.41	5.84	2.53	14.78	1.12	1.27	0.53	2.92
	C1	9.89	7.85	3.73	21.46	1.88	1.77	0.91	4.56
	C2	10.83	9.12	4.17	24.12	2.10	2.12	0.92	5.14
	C3	13.02	10.34	4.51	27.86	2.43	2.19	0.93	5.55
Mean		**10.04**	**8.29**	**3.73**	**22.05**	**1.88**	**1.84**	**0.82**	**4.54**
2	C0	6.98	6.28	2.76	16.02	1.30	1.33	0.57	3.20
	C1	13.95	10.89	5.44	30.28	2.61	2.35	1.22	6.19
	C2	15.30	12.46	6.08	33.83	2.76	2.96	1.47	7.19
	C3	19.24	15.09	7.25	41.57	3.62	3.25	1.60	8.47
Mean		**13.87**	**11.18**	**5.38**	**30.42**	**2.57**	**2.47**	**1.22**	**6.26**
3	C0	14.02	11.54	5.79	31.35	2.63	2.48	1.28	6.39
	C1	17.38	13.54	6.95	37.77	3.04	2.85	1.55	7.44
	C2	17.37	14.01	6.97	38.35	3.38	3.16	1.68	8.22
	C3	19.85	15.43	7.44	42.72	3.47	3.31	1.57	8.35
Mean		**17.15**	**13.60**	**6.79**	**37.55**	**3.13**	**2.95**	**1.52**	**7.60**
4	C0	8.13	7.14	3.27	18.54	1.42	1.53	0.69	3.64
	C1	16.11	12.50	6.41	35.01	2.91	2.69	1.36	6.96
	C2	16.67	13.49	6.68	36.83	3.17	3.20	1.60	7.96
	C3	21.28	16.51	8.05	45.83	3.65	3.42	1.81	8.88
Mean		**15.55**	**12.41**	**6.10**	**34.05**	**2.79**	**2.71**	**1.36**	**6.86**
5	C0	15.12	12.36	6.26	33.73	2.59	2.55	1.41	6.55
	C1	17.32	13.38	6.92	37.61	3.19	2.85	1.64	7.69
	C2	17.21	13.88	6.90	37.98	3.38	3.21	1.52	8.11
	C3	19.05	14.84	7.09	40.97	3.43	3.12	1.46	8.01
Mean		**17.17**	**13.61**	**6.79**	**37.57**	**3.15**	**2.93**	**1.51**	**7.59**
6	C0	11.09	9.33	4.53	24.95	2.00	1.96	0.94	4.89
	C1	13.83	10.80	5.43	30.05	2.61	2.30	1.18	6.08
	C2	13.67	11.23	5.37	20.27	2.66	2.58	1.23	6.46
	C3	15.98	12.33	5.78	34.09	3.03	2.64	1.24	6.92
Mean		**13.64**	**10.92**	**5.27**	**29.84**	**2.58**	**2.37**	**1.15**	**6.09**
7	C0	8.18	7.17	3.29	18.63	1.58	1.53	0.73	3.84
	C1	11.50	9.06	4.41	24.97	2.11	1.96	1.06	5.13
	C2	11.11	9.32	4.29	24.71	2.16	2.19	1.00	5.35
	C3	13.79	10.89	4.84	29.51	2.38	2.28	1.06	5.72
Mean		**11.14**	**9.11**	**4.20**	**24.45**	**2.06**	**1.99**	**0.96**	**5.01**
8	C0	8.88	7.68	3.59	20.15	1.63	1.66	0.85	4.14
	C1	11.97	9.16	4.62	25.74	2.12	1.96	1.01	5.09
	C2	11.78	9.97	4.64	26.39	2.17	2.21	0.97	5.35
	C3	14.07	11.11	4.93	30.10	2.66	2.48	1.20	6.34
Mean		**11.68**	**9.48**	**4.44**	**25.60**	**2.15**	**2.08**	**1.01**	**5.23**
9	C0	10.28	8.75	4.19	23.21	1.83	1.87	0.92	4.62
	C1	16.28	12.64	6.48	35.39	3.08	2.80	1.54	7.42
	C2	16.53	13.35	6.61	36.48	3.25	2.98	1.54	7.77
	C3	18.71	14.58	6.95	40.23	3.49	3.14	1.56	8.19
Mean		**15.45**	**12.33**	**6.05**	**33.83**	**2.91**	**2.70**	**1.39**	**7.00**
10	C0	12.99	10.78	5.35	29.11	2.24	2.25	1.17	5.66
	C1	17.85	13.81	7.14	38.80	3.29	2.98	1.79	8.06
	C2	18.49	14.85	7.45	40.79	3.19	3.22	1.56	7.97
	C3	20.95	16.27	7.90	45.11	3.82	3.50	1.74	9.07
Mean		**17.57**	**13.92**	**6.96**	**38.45**	**3.14**	**2.99**	**1.57**	**7.69**
Mean Cycle 0 (C0)		10.21	8.68	4.15	23.05	1.83	1.84	0.91	4.58
Mean Cycle 1 (C1)		14.61	11.35	5.75	31.71	2.68	2.45	1.33	6.46
Mean Cycle 2 (C2)		14.90	12.17	5.91	32.97	2.82	2.78	1.35	6.95
Mean Cycle 3 (C3)		17.59	13.74	6.47	37.80	3.20	2.93	1.42	7.55
Grand mean		**14.26**	**11.48**	**5.57**	**31.38**	**2.63**	**2.50**	**1.25**	**6.39**
Lsd. P 0.05 Cycle (C)		0.80	0.66	0.33	1.50	0.15	0.14	0.08	0.30
Lsd. P 0.05 Families (F)		1.26	1.04	0.52	2.37	0.23	0.23	0.13	7.70
Lsd. P 0.05 F x C		2.52	2.09	1.03	4.74	0.46	0.46	0.25	15.39

The selection response was mostly higher in (C_2) than in (C_3). Previous researchers have also reported a higher response of selection based on S_I progeny evaluation in bulked inbred or random-mated populations compared to full-sib reciprocal recurrent. There was a close agreement between predicted and observed response to selection for fresh forage and dry yields (10.26 and 13.07). The obtained results are in line with those reported by El-Shahawy *et. al.*, (2000), Haggag *et. al.*, (2000), and Abdel Galil *et. al.*, (2001) and Abdel Galil and Oushy (2007).

Table 2. Effect of recurrent selection on total fresh and dry yields of ten millet families (derived from c.v Shandweel 1).

Family	Total fresh yield					Total dry yield				
	Cycle 0 %	Cycle 1 %	Cycle 2 %	Cycle 3 %	**Mean %**	Cycle 0 %	Cycle 1 %	Cycle 2 %	Cycle 3 %	**Mean %**
Fam. 1	0.00	45.20*	12.40*	15.50*	**18.27***	0.00	56.13*	12.79*	8.03	**19.24***
Fam. 2	0.00	89.03*	11.72*	22.90*	**30.91**	0.00	93.28*	16.17*	17.85*	**31.82***
Fam. 3	0.00	20.48*	1.52	11.40*	**8.35**	0.00	16.31*	10.52*	1.55	**7.10**
Fam. 4	0.00	88.89*	5.21	24.41*	**29.63***	0.00	91.21*	14.40*	11.46*	**29.27***
Fam. 5	0.00	11.49*	0.99	7.85	**5.08**	0.00	17.37*	5.47	-1.20	**5.41**
Fam. 6	0.00	20.47*	0.73	12.61*	**8.45**	0.00	24.32*	6.25	7.00	**9.39**
Fam. 7	0.00	34.02*	-1.02	19.39*	**13.10***	0.00	33.68*	4.29	6.96	**11.23***
Fam. 8	0.00	27.75*	2.51	14.07*	**11.08**	0.00	22.75*	5.26	18.45*	**11.62***
Fam. 9	0.00	52.50*	3.09	10.28	**16.47***	0.00	60.83*	4.61	5.44	**17.72***
Fam. 10	0.00	33.30*	5.11	10.60	**12.25***	0.00	42.36*	-1.05	13.70*	**13.75***
Mean	**0.00**	**37.59***	**4.00**	**14.62***	**14.05***	**0.00**	**40.90***	**7.60**	**8.58**	**14.27***

* Significant at 0.05 probability

Table 3. Means of cycles of ten families (derived from c.v Shandweel 1) evaluated in three cycles of recurrent selection.

Cycle	Total fresh yield		Total dry yield		Mean of plant height cm		Mean of no. of tillers		Stem diameter cm		Dry leave/stem ratio %	
	Mean t fed $^{-1}$	Res. Selec. %	Mean t fed $^{-1}$	Res. Selec. %	Mean	Res. Selec. %	Mean	Res. Selec. %	Mean	Res. Selec. %	Mean	Res. Selec. %
C 0	23.05	0.00	4.58	0.00	124.30	0.00	4.96	0.00	1.12	0.00	1.03	0.00
C 1	31.71	37.59*	6.46	40.90*	132.03	6.22	7.10	43.15*	0.99	-11.61	1.08	4.85
C 2	32.97	4.00	6.95	7.60	131.40	-0.48	9.64	35.77*	1.08	9.09	1.08	0.00
C 3	37.80	14.62*	7.55	8.58	132.98	1.20	9.45	-1.97	1.07	-0.93	1.10	1.48
mean	**31.38**	**36.17***	**6.39**	**39.29***	**130.18**	**4.73**	**7.79**	**57.06**	**1.02**	**-8.93**	**1.07**	**3.88**

* Significant at 0.05 probability

Heritability, genotypic and phenotypic of variability and genetic advance

Estimates of broad-sense heritability from the ten families during three cycle of seletion are shown in (Table 4). Broad-sense heritability values were high for total fresh and dry yields in three cuts, plant height, no of tillers stem diameter and leaf/ stem ratio, respectively, indicating that studied traits were less affected by environment and largely influenced by the additive effects of genes and improvement may be achieved through phenotypic selection, as mentioned by Johanson *et. al.*, (1955) bakheit (1986) and Younis *et. al.* (2010).

Table 4. Estimate of variance, heritability and expected genetic advance for ten millet families (derived from c.v Shandweel 1) at three cycles of recurrent selection.

Trait		Mean	δ^2_g	δ^2_p	δ^2_e	h^2	Genetic advance	Genetic advance %
Fresh yield t fed^{-1}	Cut 1	14.33	114.60	117.84	3.238	0.97	2.43	16.95
	Cut 2	11.48	64.31	66.53	2.220	0.96	1.37	11.93
	Cut 3	5.57	21.05	21.60	0.543	0.96	0.44	7.98
	Total	31.38	543.87	555.32	75.09	0.97	11.44	36.43
Dry yield t fed^{-1}	Cut 1	2.64	3.51	3.62	0.108	0.94	0.07	2.83
	Cut 2	2.50	2.80	2.90	0.106	0.95	0.06	2.39
	Cut 3	1.25	1.05	1.09	0.032	0.94	0.02	1.79
	Total	6.39	20.88	21.35	0.466	0.97	0.44	6.89
Plant height cm	Mean	130.67	164.82	286.56	121.74	0.57	5.90	4.52
No. of tillers	Mean	6.70	2.89	3.21	0.321	0.90	0.07	0.99
Stem diameter cm	Mean	1.02	0.04	0.08	0.035	0.55	0.00	0.16
Leave\stem %	Mean	1.02	0.04	0.08	0.002	0.78	0.00	0.02

δ^2_g, Genetic variance, δ^2_p, phenotypic variance δ^2_e, Error variance, h^2 Heritability

The moderate to high heritability estimates obtained from Shandweel 1 families indicated that selection carried out in the population should be able to isolate favorable genes to be recombined in the new genetic background.

Number of superior recombinant families was better than source populations of Shandweel 1 over three cycles, indicating the accumulation of favorable genes for forage yield by adopting recurrent selection method. The estimates of genetic advance for selection showed that three cycles of selection and open pollination for the selected families in each cycle, has shown increases of 11.44 and 0.44 t fed^{-1}, which represents 36.43 and 6.89% over the general average for total fresh and dry yields, respectively. Also, other traits showed the same trend for genetic advance ranging from 0.02 to 16.95% over the general average. The obtained results agreed with those reported by El-Shahawy *et. al.*, (2000), Haggag *et. al.*, (2000), Abdel Galil *et. al.*, (2001) and Abdel Galil, Oushy (2007) and Younis *et. al.* (2010).

These results indicated that the application of recurrent selection in the open pollinated Shandweel 1 cv., with 10% selection intensity is effective for improving forage yield. Furthermore, these findings suggest that millet breeders can utilize recurrent selection method for development of higher yielding varieties with broad genetic base. The results are in agreement with the finding of Bidinger and Raju (2000) who reported an increase in individual grain mass in the modern open-pollinated millet ICMS 7703, by two cycles of recurrent selection. Also, Guzman and Kendall (2000) reported that, recurrent selection is designed to improve population performance and maintain genetic variability for continued selection. In addition results was supported by Bakheit and El-Nahrawy (1997) who found that, comparison between the source populations and populations developed by recurrent selection showed significant response to selection for forage yield in alfalfa for each cycle.

CONCLUSION

A high genetic advance was noticed for source population, especially in the first cycle. These may be due to the heterogeneity of cv. Shandweel 1. The rapid gains observed in the first cycle of selection, could be attributed to that low-yielding families were easily detected and eliminated, raising the population mean. Considering the progress achieved and remaining genetic variability in population, it is reasonable to expect that recurrent selection in pearl millet may result in a rapid yield improvement. Also, synthetic would be tested against the commercial varieties and it may be needed to carry out further cycles of selection to raise its productivity.

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إستجابة محصول دخن العلف لثلاث دورات من الإنتخاب التكراري

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الهدف الرئيسي للانتخاب المتكرر هو تحسين العشيرة عن طريق تجميع الجينات المرغوبة في عشيرة متفوقة حيث يؤدي الاخصاب الذاتي والتهجين الى كسر الروابط بين الجينات. تم تنفيذ ثلاث دورات من الانتخاب المتكرر لتحسين انتاجية العلف لمحصول الدخن صنف شندويل ١ في محطة بحوث التجارب الزراعية بالجيزة خلال صيف ٢٠٠٣ الى ٢٠٠٩ . استخدمت ثلاث دورات انتخابية على عشرة عائلات مبشرة من صنف شندويل ١ . وارتكزت دورة الانتخاب المتكررالواحدة على مرحلتين خلال سنتين. من خلال النتائج كان تاثير الانتخاب المتكرر خلال ثلاث دورات انتخابية واضحا في تحسين صنف شندويل ١. وقد اظهرت النتائج ان الانتخاب التكراري ذو تاثير معنوي في تحسين عائلات الدخن خلال ثلاث دورات انتخابية. كانت هناك اختلافات معنوية بين عائلات الدخن وبين الدورات الانتخابية وكذلك التفاعل بين الدورات x العائلات. كانت العائلات ١ و٢ و ٤ معنويا أعلى العائلات انتاجية للعلف الجاف مقارنة بالعشيرة الاصلية C_0 بزيادة مقدارها ١٩,٢٤ و ٣١,٨٢ و ٢٩,٢٧% على التوالي. تم قياس استجابة محصول العلف الاخضر والجاف للانتخاب للدورة الحالية مقارنة بالدورة السابقة وظهرأن الإستجابة للانتخاب في دورة الانتخاب الاولى كانت ٣٧,٥٩ و ٤٠,٩٠ % مقارنة بالعشيرة الاصلية. وكانت ٤,٠٠ و ٧,٦٠ % في دورة الانتخاب الثانية مقارنة بالاولى وفي دورة الانتخاب الثالثة بالمقارنة بدورة الانتخاب الثانية كانت ١٤,٦٢ و ٨,٥٨ % على التوالي. كانت القدرة على التوريث في المعنى الواسع مرتفعة (٠,٩٧ و٠,٩٤) بالنسبة للمحصول الكلي الاخضر والجاف على التوالي مما يدل على ألتأثير الوراثي للدورات الانتخابية والتفاعل والعائلات. وأظهرت تقديرات التقدم الوراثي خلال ثلاث دورات انتخاب تكراري زيادة قدرها ٠,٤٤ و ١١,٤٤ طن للفدان بسبة ٣٦,٤٣ و ٦,٨٩ % مقارنه بالمتوسط العام لمحصول العلف الاخضر والجاف على التوالي. كذلك أظهرت الصفات الأخرى نفس الاتجاه في التقدم الوراثي وتراوحت الزيادة من ٠,٠٢ الى ١٦,٩٥% عن المتوسط العام خلال الثلاث دورات. كان تاثير التقدم الوراثي واضحا على العشيرة الأصلية وخاصة في دورة الانتخاب الاولى وقد يرجع ذلك الى heterogeneity وسهولة استبعاد العائلات منخفضة المحصول من الصنف شندويل ١. وهذه النتائج تشير الى أهمية الانتخاب المتكرر مع نسبة انتخاب ١٠% في تحسين الدخن. وقد لوحظ أن الدورة الاولى كان لها أهمية كبيرة في استبعاد التراكيب غير المرغوبة وبالتالي تحسين إنتاجية العشيرة.