Indian J. Genet., **65**(4): 257-260 (2005)

Efficiency of half-sib, full-sib and S_1 progeny recurrent selection methods for improvement in grain and dry fodder yield in pearl millet [*Pennisetum glaucum* (L.) R. Br.]

Yagya Dutt and K. S. Nirania

Department of Plant Breeding, CCS Haryana Agricultural University, Hisar 125 004

(Received: December 2004; Revised: November 2005; Accepted: November 2005)

Abstract

The major aim of pearl millet breeder is to develop stable, high-yielding varieties/hybrids. The improved composite/ population provides base for the development of high-yielding stable varieties/hybrids. The present study was conducted to compare the efficiency of half-sib (HS), full-sib (FS) and selfed progeny (S_1) recurrent selection methods for improvement in yield: and to improve the per se performance of the EC91 PCV5 pearl millet composite. Half sib progeny selection method showed 3.17% realized genetic gain, whereas full-sib progeny selection method showed 11.49% and S_1 progeny selection method showed 31.6% realized genetic gain for grain yield on pooled basis. Thus, S_1 progeny selection method recorded highest realized genetic gain for grain yield as compared to half-sib and full-sib progeny selection methods. Similar trend was also observed for other yield contributing traits. For effective tillers per plant the realized genetic gain was 12.55% for half-sib, 25.11% for full-sib and 28.14% for S_1 progeny selection method. It was 0.61% (HS), 3.55% (FS), 7.69% (S_1) and 0.16 % (HS), 16.06% (FS) 28.04% (S_1) for threshing percentage and harvest index, respectively on pooled basis. Thus, it was revealed that the S_1 progeny selection method is most efficient for improvement in grain yield and its contributing traits in pearl millet. The increase in grain yield in S_1 progeny selection method is correlated with increase in panicle surface area, effective tillers per plant threshing percentage and harvest index. On the other hand, for dry fodder yield, only half-sib progeny selection recorded significant realized genetic gain. This increase in dry fodder yield is correlated with the tallness and lateness.

Key words: Pearl millet, recurrent progeny selection, selection strategy

Introduction

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] is one of the most extensively cultivated cereals in arid and semi arid regions of the world. It is a principal food cereal cultivated on 25 million ha of the drought prone semi arid regions of Africa and Indian subcontinent and has also been grown as a forage crop in the USA, Australia. South Africa and South America [1-2].

Attention must also be given to the yield stability of improved pearl millet populations due to the threats of severe moisture deficits [3]. In recent year's major advances in India and elsewhere in the world in pearl millet has been made in the development of hybrids using male-sterile lines. Although there is a wealth of genetic variability present in this genus [4], even then, a systematic population improvement programme has so far been limited in pearl millet. Increasing grain yield and yield stability have therefore been major breeding objectives (or improving pearl millet. Increasing pearl millet production through recurrent selection should be possible due to pearl millet's tremendous variability [5-6]. Population breeding can effectively utilize the enormous genetic variability present in this species, which holds better prospects for combining stable resistance to various biotic and abiotic stresses with better yield using diverse germplasm [7]. The present study was. therefore, conducted (i) to determine the relative efficiency of three recurrent selection methods *viz.*, half-sib. full-sib and selfed progeny (S_1) selection for use in population improvement (ii) to improve the *per se* performance of composite EC 91PCV5 for its further exploitation in population/hybrid breeding programme.

Materials and methods

Development of progenies: The material for the present study was developed from the composite EC91PCV5. The base population (C_O) of the composite EC91PCV5 was planted in *kharif* 1998. Three types of progenies *viz.* half-sib, full-sib and S_1 were developed from the base composite (C_O). (i) HS progenies were developed by pollinating the selected plants by bulk pollen in the base population (C_O). (ii) Full-sib progenies were generated by crossing selected single plants (with each other) in the base population (C_O). (iii) S_1 progenies were generated by selfing ear-heads of selected plants in base population (C_O).

Evaluation of progenies: The 55 HS, 55 FS and 55 S_1 progenies generated from HC91PCV5 base population (c_0) during *kharif* 1998 were evaluated in replicated trial during *kharif* 1999 at Chaudhary Charan Singh, Haryana Agricultural University, Hisar. The 169 entries with respect to 165 progenies (55 HS, 55 FS and 55 S_1), one base population and three checks were grown in a simple lattice design (13 × 13) with two replications. Each entry was planted in two rows of 4 meter length. All the entries were grown with a hand-operated plough keeping row to row distances of 50 cm and plant to plant distances of 10 cm. Recommended package of practices was followed to raise a good crop. The data were recorded for grain yield (kg), dry fodder yield (kg), panicle length (cm) and panicle girth (cm). Panicle surface area (cm^2) was calculated as per the formula ($\pi \times$ panicle length $\times$ panicle girth). Data on panicle characters was recorded on ten randomly selected competitive plants, whereas, for remaining traits, data were recorded on per plot basis and later converted into per plant by dividing the plot yield with total number of plants in a plot.

Selection of superior progenies: Three selection criterions *viz*., grain yield, panicle surface area and dry fodder yield were adopted to identify the superior progenies for these three respective traits in each of the three types of selection methods. Out of total 55 full-sib progenies. 11 superior full-sib progenies for grain yield, 11 for panicle surface area and 11 for dry fodder yield were selected adopting 20 per cent selection intensity. Similar criterions and selection intensity were used to identify the superior progenies among half-sibs and S_1 progenies. The remnant seeds of identified superior progenies for grain yield, panicle surface area and dry fodder yield were bulked separately in each three type of progeny methods, thereby, forming nine bulks.

Recombination procedure and creation of experimental varieties: These nine experimental bulks were grown in nine separate blocks in off-season nursery (Feb-April) at ICRISAT, Patancheru, Hyderabad for recombination. Each block consisted of 10 rows of five-meter length. For obtaining seed of each experimental variety, artificial bulk pollination was practiced i.e. at the time of flowering, pollens were collected from plants within the block and bulk pollen was used to pollinate 15 plants of that block. At the time of harvesting, seed from each mass pollinated plant was harvested. The seeds harvested from plants within block were mixed together to form experimental varieties.

Evaluation of experimental varieties: Nine experimental varieties obtained by the above manner along with base population were evaluated at two locations i.e. Hisar (rain-fed) and Karnal (irrigated) during *kharif* 2000. The trial was conducted in a randomized block design with three replications at each location. Each entry accommodated four rows of five meter length. At Hisar (Envt. I), the trial was rain fed and a condition of moisture stress/deficit occurred during the grain filling stage whereas, at Karnal (Envt. II) irrigations were given according to the crop requirement. The data was recorded for days to 50 percent flowering, plant height (cm), effective tillers per plant (number), panicle length (cm), panicle girth (cm), threshing percentage (%), grain yield (kg/plot), and harvest index (%). Panicle surface area (cm^2) was calculated as per the formula ($\pi \times$ panicle length $\times$ panicle girth). Data on panicle characters was recorded on ten randomly selected competitive plants, whereas, for remaining traits, data were recorded on per plot basis and later converted into per plant by dividing the plot yield with total number of plants in a plot. Data were pooled from both the environments/locations and analyzed within and across the environments with randomized block design used at each location using SAS programme. The Realized genetic gain (R) was calculated according to the formula given below.

$$R = \frac{(X_p - X_0) \times 100}{X_0}$$

whereas

X_p = Mean of experimental varieties obtained from completion of one cycle of recurrent progeny selection (half-sib, full-sib and S_1)

X_0 = Mean of base population

Results and discussion

Table 1 represents the pooled analysis of variances of nine experimental varieties obtained from composite EC 91 PCV5. The differences between the treatments at both the locations i.e. Hisar (Envt. I) and Karnal (Envt. II) were significant for all the traits. This indicates that there was sufficient genetic variability in the material under study. Interaction of genotype × environment were significant for all the traits.

Table 2 presents the realized genetic gain obtained after one cycle of recurrent selection (half-sib. full-sib and S_1 progeny selection) methods in both the environments as well as on pooled basis. The tables 2 showed that higher values of realized genetic gain were obtained in environment II (optimal moisture condition) as compared to environment 1 (moisture deficit). The revealed that favorable environment showed higher realized genetic gain as compared to stress (moisture deficit) environment. The expression of realized genetic gain in both environments i.e. moisture deficit (rain fed) and optimal moisture environments is

Table 1. Pooled Analysis of variances for nine experimental varieties of composite EC91 PCV5

Source	df	1	2	3	4	5	6	7	8
Environment	1	2632.02**	81978.07**	10.85**	709786**	6666.67**	4711.57**	1525.35**	17.80**
Rep in Env.	4	2.52	44.74	0.08	86418	6.72	94.09	1.13	0.31
Genotype	8	6.88**	379.32**	0.18**	14488**	56.17**	244.50**	68.35**	17.83**
Env. × Genotype	8	7.27	111.82**	0.32	34316**	89.67**	132.74**	124.35**	24.55**
Error	32	1.08	2.93	0.06	1270	0.18	2.18	1.36	0.17

1 = days to 50% flowering, 2 = plant height, 3 = effective tillers per plant, 4 = panicle surface area, 5 = grain yield, 6 = Dry fodder yield, 7 = threshing percentage, 8 = harvest index

particularly encouraging, as pearl millet is particularly grown in rain fed conditions. The results of our study supported the view of Rattunde and Witcombe, 1993 [8] that expression of better yields by the more advance population in both moisture deficit and optimal moisture conditions is particularly encouraging as pearl millet is grown in areas of frequently but unpredictable moisture deficits.

The improvement in yield is one of the most important expects in plant breeding. Yield potential is a universal breeding objective. In the present study, among the three progeny recurrent selection methods, half-sib progeny selection method showed 1.17 % realized genetic gain: full-sib progeny selection method showed 11.49 % and S_1 progeny selection method showed 3.17 % realized genetic gain for grain yield on pooled basis. Thus, S_1 progeny selection method gave highest realized genetic gain for grain yield compared with half-sib and full-sib progeny selection methods over the environments. Similar trend was also observed for effective tillers per plant, where, the realized genetic gain was 12.55 % for half-sib. 25.11 % for full-sib and 28.14 % for S_1 progeny selection method.

Panicle surface area is an important selection criterion for improvement in grain yield in pearl millet [18]. S_1 progeny selection method recorded highest realized genetic gain (35.70 %) for this trait followed by full-sib (33.72 %) and half-sib (12.33 %).

The poor sink capacity of traditional millet with 15-20 % harvest index is a basic problem of millet species in itself, causing it to produce low grain yield. This crop has an impressive capacity to produce dry matter that goes to stem and leaves, reducing the harvest index to 15-20 per cent, which is much lower than the percentage in maize and rice [9]. In the present study, except half-sib progeny recurrent selection method, other two progeny selection methods showed realized genetic gain for the harvest index with maximum in S_1 selection method (28.04 %) followed by full-sib (16.06 %). For threshing percentage, the realized genetic gain was recorded maximum in S_1 progeny selection (7.69 %) followed full-sib (3.55 %) and half-sib (0.61%) progeny selection methods.

Earliness is one of the important traits contributing to adaptation to the terminal drought stress [10]. Days to 50 per cent flowering is important trait contributing to the earliness. The reduction in days to 50 per cent flowering was noticed in all three recurrent selection methods. The highest reduction in days to 50 per cent flowering was noticed in S_1 progeny selection (–8.62 %). No significant difference was observed between HS and FS progeny selection methods for this trail. The significant reduction in days to 50 per cent flowering i.e. earliness may be related with the increase in grain yield particularly at rain fed conditions.

Plant height is one of the important traits as the excessive height of many varieties increases the risk

Table 2. Realized genetic gain obtained after completion of one cycle of half-sib, full-sib and S_1 progeny selection methods for yield and its contributing traits in pearl millet

	Days to 50% flowering	Plant height	Effective tiller/plant	Panicle surface area	Grain yield	Dry fodder yield	Threshing percentage	Harvest index
Half-sib								
E1	–4.81	3.72	–9.8	4.17	1.92	6.00	–1.59	1.43
E2	2.54	7.69	21.9	10.98	4.76	8.80	2.96	–2.22
Pool	–5.22	5.72	12.6	12.33	3.17	7.49	0.61	–0.16
Full-sib								
E1	–3.06	–7.69	16.7	32.78	8.95	3.70	1.64	13.90
E2	1.49	–14.42	36.3	35.01	14.60	0.20	5.56	15.70
Pool	–4.87	–11.01	25.1	33.72	11.49	1.85	3.55	16.10
S_1								
E1	–8.32	3.17	15.5	33.14	26.04	1.70	5.53	18.90
E2	–0.96	–3.26	45.0	38.32	35.60	–2.60	9.99	31.50
Pool	–8.62	–6.14	28.1	35.70	31.60	–0.58	7.69	28.00

of lodging and grain loss after storms. On the other hand, tallness has advantage for the varieties especially for fodder purpose. Tall, late-maturing varieties with low harvest index do not respond sufficiently to better management inputs to give much higher returns and hence, they are less suitable for improved and intensive agriculture. In the present experiment, for the plant height, the realized gain recorded in the negative direction on pooled basis in case of S_1 (–6.14 %) and full-sib (–11.01 %) while it is positive direction in half-sib (5.72 %) progeny selection method i.e. experimental varieties obtained from S_1 and full-sib progenies showed dwarfness whereas experimental varieties obtained from half-sib progenies showed tallness over the base population. For dry fodder yield, the significant realized genetic gain was recorded only in half-sib progeny selection method (7.49 %). The benefit of plant height is clearly seen in the experimental varieties developed through half-sib progeny selection method. Thus, the product of half-sib might be suitable for improvement in dry fodder yield.

The results of the present investigation revealed that S_1 progeny selection method appeared as the most efficient for improvement in grain yield. A similar trend was also observed for other grain yield components like panicle surface area, effective tillers per plant, threshing percentage and harvest index. S_1 progeny selection method, on the other hand, showed a reduction in plant height and days to 50 per cent flowering. Thus, the gain in grain yield was achieved with the improvement in effective tillers per plant, panicle surface area, threshing percentage, harvest index along with earliness. S_1 progeny selection method also simpler to operate because producing selfed progeny does not involve any crossing work. S_1 selection method also beneficial in the way that it saves time if the selected progenies are to be chanalized into inbred line development. The present results are in conformity to earlier studies [11-14] that revealed that selfed progeny selection methods (S_1) were superior than either full-sib or half-sib progeny selection methods for improvement in grain yield and its contributing traits. The superiority of the S_1 progeny selection method over full-sib and/or half-sib for grain yield might be due to (i) S_1 progeny selection method providing better chances for exposing the deleterious recessives in the populations (ii) It is more effective in unraveling the hidden genetic variability than either half-sib or full-sib [15] (iii) It exploits more of the additive genetic variances, which is the primarily gene effect that improves the general combining ability [9].

The results of this investigation suggest that it is possible to make reasonable progress in increasing the yield with the use of the various progeny recurrent selection methods (half-sib, full-sib and S_1) with maximum gain through S_1 selection method for grain yield and half-sib for dry fodder yield. The material obtained from S_1 and full-sib progeny recurrent selection methods could be utilized in future breeding for improvement in grain yield whereas the material of half-sib progeny selection method could be used for higher fodder yield breeding programme.

References

1. **Kumar A. K. and Andrews D. I.** 1993. Genetics of quantitative traits in pearl millet: a review. Crop Sci., **33**: 1-20.
2. **Burton G. W. and Wilson J. P.** 1995. Identification and heterotic chromosome blocks for forage yield in short-day exotic pearl millet land races. Crop Sci., **35**: 1184-1187.
3. **Bidinger F. R., Mahalakhmi V., Talukdar B. S. and Algarswamy G.** 1982. Improvement of drought resistance in pearl millet. *In*: Drought resistance in crops with emphasis on rice. IRRI, Los Banos, Philippines, pp. 357-377.
4. **Muny B. R., Upadhay M. K., Manchanda P. L.** 1976. Classification and cataloguing of a world collection of genetic stocks pennisetum. Indian J. Genet., **27**: 313-394.
5. **Burton G. w. and Powell J. B.** 1968. Pearl millet breeding and cytogcnetics. Adv. Agron., **20**: 50-89.
6. **Rattunde H. F., Singh P. and Witcombe J. R.** 1989. Feasibility of mass selection in pearl millet. CropSci., **29**: 1423-1427.
7. **Kanwar J. S., Ryan J. G.** 1976. Recent trends in world sorghum and millet production and some possible future development. Hyderabad, ICRISAT.
8. **Rattunde H. F. and Witcombe J. R.** 1993. Recurrent selection for increased grain yield and resistance to downy mildew in pearl millet. Plant Breeding, **110**: 63-72.
9. **Bilquez A. F.** 1975. Improvement of millet in Senegal; analytical summary of the main results obtained during the first four years of work (Fr). Dakar, Senegal, ISRA 79 pp.
10. **Bieler P., Fussell L. K. and Bidinger F. R.** 1993. Grain growth of [*Pennisetum glaucum* (L.) R. Br.]. Under well watered and drought stressed conditions. Field Crop Research, **31**: 41-54.
11. **Khadr F. H.** 1977. Recurrent selection in pearl millet, *Pennisetum typhoides* in north Nigeria. Z. Pfl. Zucht., 79-84.
12. **Kapoor R. L., Singh F., Yadav H. P. and Sain Dass.** 1986. Recurrent selection in pearl millet. Journal of Research, Haryana Agricultural University, **13**: 424-428.
13. **Singh P., Rai K. N., Witcombe J. R., Andrews D. J.** 1988. Population breeding methods in pearl millet improvement. *Pennisetum americanum* L. Agron. Tropicale, **43**: 185-193.
14. **Jindla L. N.** 1981. Components of genetic variability of some quantitative characters in a synthetic population of pearl millet (*Pennisetum typhoides* (Burrn) S&H) Ph.D. Thesis, PAU. Ludhina.
15. **Zaveri P. P., Phul P. S. and Chahal G. S.** 1988. Genetic studies in relation to population improvement in pearl millet. Indian J. Genet., **48**: 175-180.