



Selection for improved seed set in a Rajasthan pearl millet [*Pennisetum glaucum* (L.) R. Br.] landrace population

F. R. Bidinger and C. T. Hash

International Crops Research Institute for the Semi-Arid Tropics, Patancheru 502 324

(Received: April 2006; Revised: December 2007; Accepted: December 2007)

Incomplete seed set is a common characteristic of many pearl millet landraces of western Rajasthan, although this character is not commonly recorded in germplasm evaluations [1]. Reduced seed set is a common phenomenon in plants heterozygous for certain non-standard chromosome arrangements (e.g., translocations or inversions); as a portion of female (and male) gametes produced during meiosis have lethal duplications or deletions [2]. This effectively reduces genetic recombination in affected genomic regions and thus maintains specific allele combinations. Where such allele combinations confer some advantage, the underlying non-standard chromosome arrangements will be retained in the population — especially in cross-pollinated species such as pearl millet in a stressful environment such as western Rajasthan. It is hypothesized that this phenomenon may have contributed to the substantial restructuring of the pearl millet genome compared to that of other grasses [3].

As grain number per unit area is the major determinant of grain yield in pearl millet [4], reduced seed set may affect grain yield. However, because of the negative relationship between grain number and grain size, an increase in grain size as a result of incomplete grain set may compensate for at least a portion of the potential yield loss from incomplete seed set [5]. In addition, larger seeds may thresh more easily and/or be better retained in the subsequent winnowing processes, enhancing the compensation, and the retention of the incomplete seed set in the population. The objectives of this study were to quantify the effect of incomplete seed set on grain yield and the response to selection for improved seed set in a typical western Rajasthan landrace population.

The experiment was carried out as a part of the breeding of the Barmer Restorer Population from the original Barmer Population [6] by one cycle of S_1 testcross selection for fertility restoration, grain yield and plant type. (The procedure involved making S_1 progeny and testcrossing these to a selected male-sterile

line, evaluating the S_1 testcrosses in replicated trials for fertility restoration and agronomic value, and finally recombining the S_1 progenies with the best testcross performance, using reserve S_1 seed). More than half of the 64 Barmer S_1 testcrossed progenies evaluated in 2000 rainy season were segregating for incomplete seed set. We selected 18 S_1 progenies whose testcrosses had uniformly good seed set, planted reserve seed of these and selfed (to produce S_2 s) and testcrossed (to ICMA 94444) 322 plants from these 18 S_1 rows. Both S_2 s and their testcrosses were grown the following rainy season (2001). Thirty of the 322 S_2 progenies that were visually judged to both have uniformly complete open-pollinated seed set, and to produce testcrosses with uniformly complete open-pollinated seed set were retained. Selfed (S_3) progeny of these 30 selected S_2 s were random-mated by hand pollination in the dry season of 2002 to form the reselected version of the Barmer Restorer Population.

The original Barmer Population, the restorer and reselected restorer versions of it were evaluated in replicated trials under dryland conditions at CAZRI, Jodhpur, and RAU, Nagaur from 2003 to 2005. Plots were of two 4 m rows spaced at 0.6 m; the trial was replicated 10 times. All panicles from the center 3 m of both rows were harvested, counted, dried, threshed and the grain weighed. Triplicate 100-grain samples of the threshed grain were counted and weighed and the data used to calculate grain number per panicle and per unit area.

One cycle of reselection for complete seed set resulted in a significant increase (11.5%) in grain number per unit area compared to the restorer population (Table 1). This increase appeared to result primarily from an increase in grain number per panicle (6.6%), although there was also a small increase (4.2%) in panicle number (Table 1). Neither the increase in grain number per panicle nor panicle number was significant, however. The increase in grain number in the reselected version

Table 1. Comparison of grain yield and its components in the original Barmer Population, its restorer and reselected restorer versions. Data are based on five field trials (48 replications)

Trait	Original Popln.	Restorer Popln.	Re-selected Popln.	SED	Effect of reselection
Grain number (m ⁻²)	12741.0	13301.0	14827.0	660	+11.5%
Panicle number (m ⁻²)	11.5	11.9	12.4	-	+4.2%
Grain number (panicle ⁻¹)	1113.0	1074.0	1145.0	-	+6.6%
100-grain mass (g)	0.531	0.552	0.536	0.0093	-2.9%
Grain yield (g m ⁻²)	71.3	79.4	86.3	3.71	+8.7%

SED = standard error of the difference between two values ($P < 0.05$) from the across-environment analysis of variance

was accompanied by a small and non-significant decrease (-2.9%) in grain size (100-grain mass). The overall result was a significant increase (8.7%) in grain yield (Table 1), which compares favorably with increases per cycle of recurrent selection for grain yield itself [7]. In view of the fact that incomplete seed set does not appear to be very severe in the Barmer material in these trials - both the original Barmer population and the restorer version produced >1000 grains per panicle (Table 1) this is probably a reasonable result. These data thus suggests (1) that incomplete seed set does not appear to have a major effect on grain yield in the Barmer population, but (2) that a useful yield gain can be achieved from incorporating selection for complete seed set into breeding programs using landrace materials.

Acknowledgements

This work was done as a part of the ICAR-ICRISAT Collaborative Research Project on pearl millet. The authors are grateful to the Director, Central Arid Zone Research Institute, Jodhpur, and to the Director of Research, Rajasthan Agricultural University, Bikaner, for the use of research facilities at CAZRI and RAU, Nagaur, respectively, and to Messrs D. Dharani, M. M. Sharma and Md. Basheer Ahmed for technical assistance in carrying out this research.

References

1. **Appa Rao S., Mengesha M. H., Vyas K. L. and Rajagopal Reddy C.** 1986. Evaluation of pearl millet germplasm from Rajasthan. *Indian J. Agric. Sci.*, **56**: 4-9.
2. **Jauhar P. P.** 1982. *Cytogenetics and Breeding of Pearl Millet and Related Species*. Alan R. Liss: New York. 310 pp.
3. **Devos K. M., Pittaway T. S., Reynolds A. and Gale M. D.** 2000. Comparative mapping reveals a complex relationship between the pearl millet genome and those of foxtail millet and rice. *Theor. Appl. Genet.*, **100**: 190-198.
4. **Craufurd P. Q. and Bidinger F. R.** 1989. Potential and realized yield in pearl millet (*Pennisetum americanum*) as influenced by plant population density and life-cycle duration. *Field Crops Res.*, **22**: 211-225.
5. **Bidinger F. R. and Raju D. S.** 2000. Response to selection for increased individual grain mass in pearl millet. *Crop Sci.*, **40**: 68-71.
6. **Yadav O. P. and Weltzien R. E.** 1998. New pearl millet populations for Rajasthan, India. Integrated Systems Project Report Series No 10. ICRISAT, Patancheru, India.
7. **Rattunde H. F. W. and Witcombe J. R.** 1993. Recurrent selection for increased grain yield and resistance to downy mildew in pearl millet. *Plant Breed.*, **110**: 673-72.