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Effectiveness of Within-progeny Selection for Downy Mildew Resistance in Pearl Millet

KN Rai*, VN Kulkarni, RP Thakur, AK Singh and **VP Rao** (ICRISAT, Patancheru 502 324, Andhra Pradesh, India)

*Corresponding author: k.rai@cgiar.org

Introduction

Development of trait-specific breeding lines with high grain yield and resistance to downy mildew (DM) (*Sclerospora graminicola*) is a major research and development objective of the pearl millet improvement program at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India. While selecting for grain yield and agronomic traits during the course of inbreeding and generation advance, it is not uncommon to find progenies that have good combinations of these traits, but have unacceptable levels of DM susceptibility. The question, therefore, arises as to whether or not such progenies should be discarded from further selection, or can within-progeny selection be used to improve resistance to acceptable levels. A high-tillering and early-maturing Mandor Restorer Composite (MRC) has recently been jointly developed by ICRISAT and the All India Coordinated Pearl Millet Improvement Project (AICPMIP) Unit at Mandor, Rajasthan from diallel crosses among 10 diverse restorer lines selected for high tillering, early maturity and adaptation to dry environments of northwestern India. During the course of S_2 progeny selection in this composite, it was observed that several progenies with outstanding performance for grain yield potential, high tillering ability, and other agronomic traits were highly susceptible to DM assessed in unreplicated single pots (30–40 seedlings) under high disease pressure in the greenhouse. The objective of this study was to determine whether single-pot DM screening of a limited number of seedlings would be effective enough for mass evaluation of a large number of progenies in a breeding program, and whether within-progeny selection would be effective to improve the DM resistance to acceptable levels.

Materials and Methods

Based on the visual assessment of agronomic performance of 1200 S_2 progenies in an unreplicated observation nursery during summer 2002 at Patancheru and DM incidence against Durgapura pathotype (Sg 212) in a greenhouse seedling screening (Singh and Gopinath 1985) done in unreplicated single pots consisting of 30–40 seedlings (hereafter referred to as screen 1), a large proportion of the progenies in the test were selected for further selection and R-line development. Using remnant seed, 51 progenies with high agronomic scores were re-screened in unreplicated two pots with a total of 50–60 seedlings (hereafter referred to as screen 2). Eighteen of these progenies tracing to as many different S_1 progenies and with varying DM incidence levels were selected for conducting the DM resistance selection efficiency trial. The DM incidence in the inoculated seedlings was recorded and the DM-free seedlings of each progeny were transplanted. Selfed seeds from 8 to 10 plants from each progeny were bulked to generate selected S_3 progeny bulks. Using the remnant seed, these 18 S_2 progenies were also grown in the field under disease-free condition, and seeds of 8–10 selfed plants were bulked to produce unselected S_3 progeny bulks. These 36 progenies along with two susceptible checks (7042S and 843B) were evaluated in the greenhouse under high disease pressure (>90% DM incidence in 843B and 7042S) in a split-plot design with four replications. Progenies were treated as main plots, and selected and unselected bulks as sub-plots. A plot consisted of two pots, each with 30 seedlings. The experiment was repeated twice and the two experiments were analyzed as two environments. Since the genotype × environment interaction was not significant, pooled residual from combined analysis of the data from both experiments was used for statistical test of significance.

Results and Discussion

The disease pressure in all three tests was very high with >90% DM incidence in both the susceptible checks 7042S and 843B (Table 1). The DM incidence among the

Table 1. Downy mildew (DM) incidence in S_2 and S_3 progenies derived from Mandor Restorer Composite against Durgapura pathotype (Sg 212) under greenhouse conditions at ICRISAT, Patancheru, India.

	DM incidence (%) in S_3 progeny[1]		DM incidence (%) in S_2 progeny[2]	
Progeny	Unselected	Selected	Screen 1	Screen 2
MRC HS-82-2-1	9	15	10	29
MRC HS-84-2-2	48	24*	35	68
MRC HS-86-1-2	51	49	51	47
MRC HS-98-3-1	33	23	29	11
MRC HS-130-6-5	35	14*	36	54
MRC HS-139-4-2	22	17	41	45
MRC HS-142-3-6	28	22	46	34
MRC HS-161-3-2	29	38	19	30
MRC HS-167-4-2	36	29	26	21
MRC HS-176-5-1	31	20	24	19
MRC HS-178-1-3	48	29*	20	22
MRC HS-179-1-2	48	33*	57	64
MRC HS-183-2-2	13	20	14	13
MRC HS-192-2-1	6	2	15	7
MRC HS-198-1-1	8	4	17	0
MRC S1-1-1	69	61	53	68
MRC S1-122-1	48	19*	41	66
MRC S1-467-2	72	46*	30	78
Control (susceptible)				
7042S		96	93	100
843B		90	93	100
LSD (0.05)		13	–	–

1. Mean of 4 replications; * = Significant at 5% level.
2. Unreplicated data.

S_2 progenies varied from 10 to 57% in screen 1 and from 0 to 68% in screen 2, with a highly significant positive correlation (r = 0.75; $P<0.01$) between the DM incidence in the progenies in the two screens. This suggests that for mass screening of the breeding lines where rejection rather than selection at high intensity is the primary objective, single-pot DM screening is adequate to economize resources. There was only a marginal increase in the correlation for DM incidence in S_2 progenies in screen 2 and the unselected set of the S_3 progenies (r = 0.78; $P<0.01$). These strong relationships could be attributed to the high heritability of DM resistance under high disease pressure and uniform inoculum distribution under the controlled greenhouse screening.

There were significant differences ($P<0.05$) between the selected and unselected versions in the six S_3 progenies with the DM incidence levels in the selected versions reduced from half to one-third of those in the unselected versions (Table 1). The lack of response in other progenies could be because some of them were initially resistant (<8% DM incidence in two progenies), while the other susceptible ones could have less genetic variability for resistance, leading to poor phenotypic selection response. Also, the DM incidence in the six selected progenies varied from 14 to 46%, indicating that one-stage selection during the inbreeding process, even under very high disease pressure, was not effective in improving the resistance to acceptable levels, generally considered to be <10%. Two alternative options that might improve the DM resistance levels of these responsive progenies within the acceptable range are: (1) Further multi-stage phenotypic selection during the inbreeding process; and (2) Progeny-based selection. Exploitation of residual variability to select for DM resistance in the otherwise susceptible inbred lines using pedigree breeding has been shown to be effective (Singh et al. 1988, 1992). The most successful example of this selection approach is the development of resistance in ICMA 841 and ICMB 841 from their otherwise susceptible versions 5141A and 5141B (Singh et al. 1990), which are the seed parents of a most widely cultivated hybrid Pusa 23 in India. Progeny selection for DM resistance under high disease pressure in the greenhouse has been found to be effective in developing highly DM resistant versions of

two commercially released maintainer lines and a restorer line (CT Hash, ICRISAT, Patancheru, India, personal communication). Thus, if a population progeny has been found to possess excellent combination of high yield potential and agronomic traits, but is moderately susceptible to DM, within-progeny selection for DM resistance may be pursued. However, the likelihood of its effectiveness in improving the resistance to an acceptable level will depend on the genetic variability for DM resistance in the progeny.

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Evaluation of New Grain Pearl Millet Hybrids in Australia

CA Douglas* and **PK Lawrence** (Queensland Department of Primary Industries and Fisheries, Locked Bag 1, Biloela, Queensland 4715, Australia)

*Corresponding author: col.douglas@dpi.qld.gov.au

Introduction

Sorghum (*Sorghum bicolor*) is the predominant dryland summer crop in northern Australia, grown as a feed grain for intensive livestock industries such as poultry, cattle and pigs. However, the dryland cropping environments of central and southwestern Queensland are highly variable and characterized by unpredictable rainfall and summer temperatures (>40°C). Increasingly the feed grain industry is looking for alternative crops to spread production risks and stabilize grain supply.

Pearl millet (*Pennisetum glaucum*) is a potential new crop for the Australian grains industry; it has a short crop duration and is grown widely across the semi-arid tropics of Africa and the Indian subcontinent in environments similar to those of northern Australia. As a high-protein coarse grain, pearl millet will find its key market as an alternative feed grain to sorghum in the intensive production of monogastric animals such as poultry and pigs (Singh and Perez-Maldonado 2003). High-yielding grain pearl millets developed in India and the United States retain the grain quality and early maturity of traditional pearl millets but are of dwarf stature and well suited to mechanized farming systems. Since these new pearl millets have been successfully produced and marketed in the United States (Andrews et al. 1995), the challenge now is to develop a grain pearl millet industry in Australia.

Materials and Methods

Hybrid seed production. Eighty-six F_1 hybrids of grain pearl millet were produced in February 2002 (32 hybrids) and September 2002 (54 hybrids) in hand-pollinated nurseries at the Queensland Department of Primary Industries and Fisheries (QDPI&F) Biloela Research Station in central Queensland (24°22' S, 150°31' E). Nine male sterile lines in the A_4 cytoplasmic male sterility system (CMS) were crossed in all combinations with nine R_4 restorer lines. Four hybrids were produced from line 59135A4 and a single hybrid (293A5 × NM-7R1R5) was available in the A5 CMS.

Evaluation of hybrids. Pearl millet hybrids were evaluated against four check lines; open-pollinated pearl millet breeding lines, NPM-1 (Andrews and Rajewski 1995a) and NPM-3 (Andrews and Rajewski 1995b), and two early-maturing commercial sorghum hybrids (referred to as sorghum #1 and sorghum #2). Trials were planted in September 2002 (spring) and February 2003 (autumn) at Biloela Research Station under high fertility levels (69 kg N ha^{-1} in spring, 92 kg N ha^{-1} in autumn) and with supplementary irrigation. In both trials hybrids were planted in twin-row plots of 7 m length with 1 m row spacing. Trial design was a randomized complete block design with four replications. Established plants were hand-thinned to an effective plant population of 10 plants m^{-2}. Phenology observations were recorded every second day from flag leaf emergence; anthesis was recorded as the day on which stigmas emerged on 50% of the main tiller panicles within each plot. Trial plots were cut to 5 m length and harvested with a small plot mechanical header. Grain mass was measured as the mass of one thousand seeds from a single sample taken from each replication in the autumn trial. No replicated data on grain size was available from the spring trial.