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YIELD POTENTIAL OF LOCAL AND EXOTIC GERMPLASM WITH SPECIAL REFERENCE TO POWDERY MILDEW DISEASE IN PEA (*PISUM SATIVUM* L.)

ZAHOOR AHMAD, ABDUL GHAFOOR, SH. MUHAMMAD IQBAL AND M. SAJJAD IQBAL*

Plant Genetic Resources Institute (PGRI), National Agricultural Research Centre (NARC), Islamabad, Pakistan.

Abstract

Pea germplasm consisting of 69 pure-lines from diverse origin was evaluated under screen-house and field conditions for 2 years for their resistance against powdery mildew and yield potential. The genotypes viz., 10607, 10645, 10646, 88 P050-6-9, 88 P090-5-15 and 88 P090-5-22 although susceptible to powdery mildew but exhibited yield potential of varying degrees. The genotypes, 10603, 10628, DMR 4, DMR 7 and DMR 20 were resistant to powdery mildew, 10603 and 10628 from Pakistan were high yielding. It is suggested to plant high yielding susceptible lines under disease free areas, whereas for development of high yielding resistant cultivars, hybridization between resistant and high yielding lines could be practiced.

Introduction

Powdery mildew disease caused by *Erysiphe pisi* DC sometime results in total failures of the pea crop. It is usually more prevalent in late planted or late maturing as compared to early planted or early maturing varieties of the crop (Iqbal *et al.*, 2000). The disease causes up to 50 percent yield losses coupled with poor pod quality (Singh, 1987). Gritton & Elbert, (1975) and Srivastava *et al.*, (1973) reported 21-30% decrease in pod number and 24-47% loss in pod weight due to this disease. Dixon (1987) found that the number of pickings were reduced from seven obtained from healthy crop to one due to the attack of powdery mildew, whereas Tariq *et al.*,(1983) recorded 10-18% yield losses. Importance of germplasm in crop improvement has been reported by many researchers (Anon., 1999; Ghafoor *et al.*, 1998). Experiments were conducted in the screen house as well as under field conditions to study the effect of powdery mildew on pea germplasm collected from different geographical zones of Pakistan and abroad. Further, yield potential was determined in a different set of experiment to investigate genetic variability for selecting desirable lines for future exploitation in breeding programs.

Materials and Methods

The experiment was conducted under screen-house as well as field conditions at the Plant Genetic Resources Institute (PGRI), National Agricultural Research Centre (NARC), Islamabad (33.40° N and 73.07° E) during winter 1997-98 (screen-house) and 1998-99 (field). The research material consisting of 69 pure-lines was obtained from PGRI and International Centre for Agricultural Research in Dry Areas (ICARDA), Syria. The germplasm screened consisted of 3 accessions (DMR 4, DMR 7 and DMR 20) from India, 2 (P75/87 and P157/87) from Romania, 13 (WA 933, 88P038-10-18, 88P050-6-9, 889090-5-21, 88P090-5-26, 88P106-2-5, Spring Pea 3, 88P001-4-9, 88P007-2-1, 88P101-10-2, 88P090-5-15, 88P090-5-16 and 88P090-5-21) from Australia, while others were locally collected. For recording yield data, each line was planted on 3 meter raised bed, with row to row and plant to plant distance of 75 and 8 cm, respectively, whereas single row of 3 meter length, with same planting geometry were sown on flat surface for disease screening.

*Department of Biological Sciences, Quaid-i-Azam University, Islamabad, Pakistan.

Table 1. Disease reaction of pea germplasm evaluated under green-house and field conditions.

Disease scale	Under screen-house conditions	Under field conditions	Selected
1	None	10610, 10628, DMR 4, DMR 7, DMR 20	All
2	10610, 10628, DMR 4, DMR 7,DMR 20	10603	10603
3	10603,	10599, 10629, 10634, 10639, 10642	10603
4	None	10599, 10629, 10634, 10639, 10642	None
5	10303,10506,10523,10566,10599,10413,10474,10475,10600,10601,10604,10605,10606,10607,10608,10609,10611,10612,10613,10614,10615,10616,10617,10618,10619,10620,10621,10622,10625,10626,10627,10629,10630,10631,10632,10633,10634,10635,10636,10637,10638,10639,10641,10642,10643,10644,10645,10646, WA933, 88P038-10-18, 88P050-6-9, 889090-5-21, 88P090-5-26, 88P106-2-5, Spring Pea 3, 808P001-4-9, 88P007-2-1,88P101-10-2, 88P090-5-15, 88P090-5-16, 88P090-5-21, P75/87, P157/87	10303, 10506, 10523, 10566, 10413, 10474, 10475, 10600, 10601, 10604, 10605, 10606, 10607, 10608, 10609, 10611, 10612, 10613, 10614, 10615, 10616, 10617, 10618, 10619, 10620, 10621, 10622, 10625, 10626, 10627, 10630, 10631, 10632, 10633, 10635, 10636, 10637, 10638, 10641, 10643, 10644, 10645, 10646, WA933, 88P038-10-18, 88P050-6-9, 889090-5-21, 88P090-5-26, 88P106-2-5,Spring Pea 3, 808P001-4-9,88P007-2-1, 88P101-10-2,,88P090-5-15, 88P090-5-16,88P090-5-21, P75/87, P157/87	10607,10645,10646, 88P050-6-9, 88P090-5-15, 88P090-5-22,

1= Highly Resistant, 2= Resistant, 3= Moderately resistant, 4= Susceptible, 5= Highly susceptible.

Disease was artificially created by spreading the infected debris of previous year's pea crop and was further supplemented by spraying spore suspension. Disease incidence was recorded at fortnightly intervals from mid February to mid of March. The severity of disease was recorded using an arbitrary scale 1-5 in terms of leaf coverage by the powdery mildew (Shrestha, 1985), where 1 means no disease and 5 indicated high susceptible response. Grain yield was recorded from 10 plants from each line sampled at random. The data were analyzed for simple statistics using computer software MS Excel 7.0 for windows 97.

Results and Discussion

Genetic based resistance against powdery mildew in peas could be the best possible solution to overcome these problems (Iqbal *et al.,* 2000). There were considerable differences among the genotypes for the level of resistance against the disease both under screen-house and field conditions (Table 1). The disease symptoms appeared in the last week of February on the lower leaves progressively spread to the terminal buds. Cousin (1974) also reported that the disease initiates from the lower and older leaves. The change

in response of genotypes for disease reaction under screen-house and field conditions was due to high intensity of disease under screen-house, therefore it was suggested to screen pea germplasm under screen-house conditions. Overall response of the genotypes was similar under screen-house and field conditions. Under screen-house conditions, the disease intensity was slightly higher that might be due to more conducive environments. Under screen-house conditions the genotypes 10610, 10628, DMR 4, DMR 7 and DMR 20 were highly resistant, and it was observed that 2 of these originated from Pakistan and others from India. Under field conditions one additional genotypes 10603 showed moderately resistant reaction. As this line was high yielding, therefore it should be tested under wide range of ecological zones and under disease free areas for its adaptation which will ultimately enhance the productivity. The resistant and high yielding genotypes (10610,10603, DMR 4, and DMR 20) should also be tested under a wide range of environments and better adapted genotypes could be used for general cultivation.

Out of a total 69 genotypes, 63 lines were susceptible to powdery mildew under screen houses and 58 were found susceptible under field conditions. Genotypes of Australia and Romania origin were found highly susceptible to powdery mildew in both the experiments, whereas the genotypes from South Asia (India & Pakistan) were resistant. The genotypes ranging from 1 to 5 scale varied in grain yield, and among resistant genotypes, 10610, DMR 4 and DMR 20 were observed high yielding (Fig. 1).

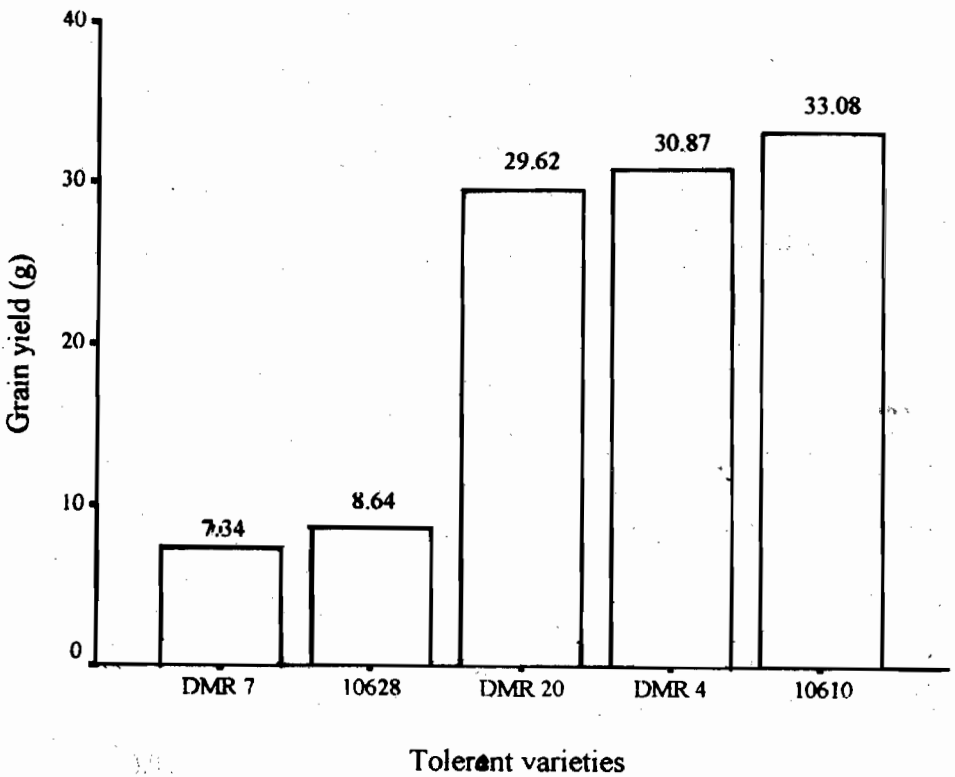

Fig. 1. Average grain yield of powdery mildew tolerant genotypes of pea (g/plant).

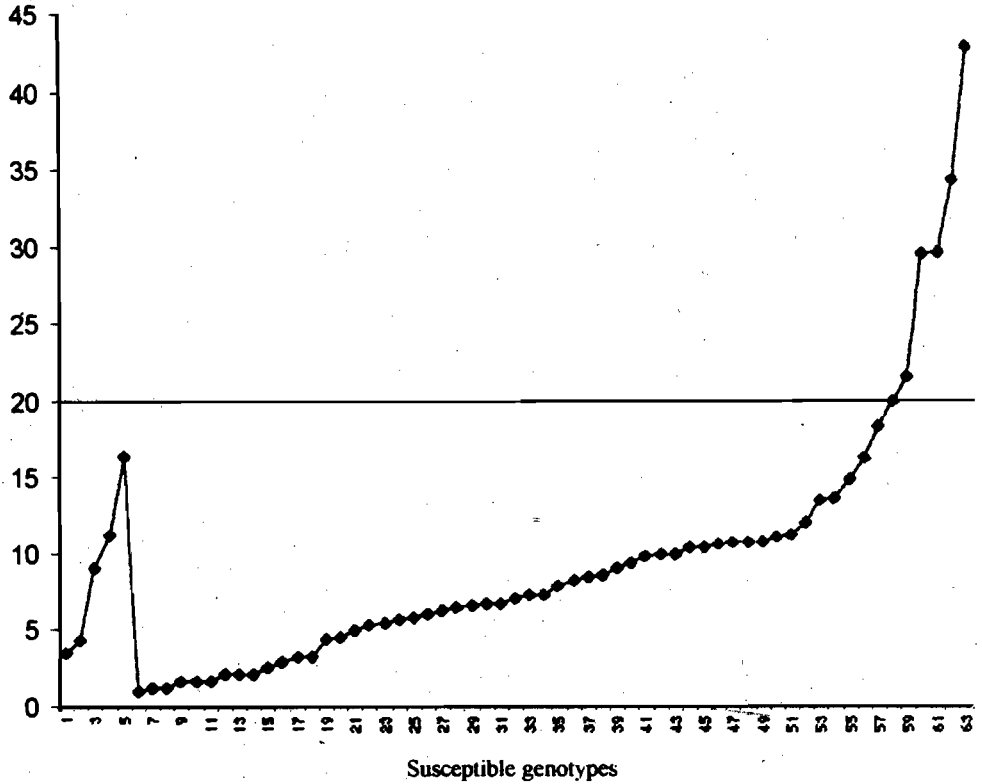

Fig. 2. Average grain yield of powdery mildew susceptible genotypes of pea (g/plant).

Table 2. Performance of pea genotypes selected on the basis of powdery mildew tolerance and yield potential.

Variety	Origin	Days to flowering	Pods per plant	100-Seed weight (g)	Grain yield per plant (g)	Harvest index (%)	Disease reaction	
							A	B
10603	Pakistan	71	41.4	20.32	20.96	17.85	3	2
10607	Pakistan	105	51.0	14.69	21.60	30.26	5	5
10610	Pakistan	70	40.0	19.12	33.08	34.09	2	1
10628	Pakistan	100	22.0	16.97	8.64	11.67	2	1
10645	Pakistan	92	82.0	16.76	42.78	40.25	5	5
10646	Pakistan	104	53.0	12.40	34.28	53.75	5	5
DMR 4	India	100	44.0	16.26	30.87	25.06	2	1
DMR 7	India	78	30.8	11.45	7.34	7.94	2	1
DMR 20	India	100	78.6	17.58	29.62	24.53	2	1
88P050-6-9	Australia	101	33.0	10.55	19.92	21.60	5	5
88P090-5-15	Australia	113	56.4	14.11	29.62	20.60	5	5
88P090-5-22	Australia	100	98.6	12.26	29.53	17.27	5	5

A- Disease under screen-house, B- disease under field conditions.

Some of the susceptible genotypes were high yielding, whereas resistant ones mostly were low yielding (Fig. 2). As disease and yield data were recorded under different sets of experiment, hence low yielding cultivars could not prove their worth and some elite lines were selected on the basis of yield and disease reaction (Table 2). On the basis of these findings it can be proposed that genotypes 10610, 10628, DMR4, DMR7, DMR20 and 10603 identified as resistant should be used in breeding programs for the development of powdery mildew resistant and better yielding varieties of pea.

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