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RESEARCH ARTICLE

Evaluation of powdery mildew resistant pyramid vegetable pea genotypes introgressed with *er1* and *er2* genes for yield and related traits in mid hills of Himachal Pradesh

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Abstract

Powdery mildew is among the most destructive disease of vegetable pea causing high yield losses and significant reduction in quality. To overcome this disease, vegetable pea lines developed through gene pyramiding were evaluated in randomized block design over two years to identify high-yielding powdery mildew-resistant line(s). The experiment was carried out during the *rabi* season of 2017-18 and 2018-19 at the experimental research farm of CSK HPKV, Palampur, using ten genotypes, including three checks. The analysis of data based on mean values of the studied traits revealed significant differences among all the genotypes. On the basis of the mean performance of two years, Line 1-2, P-227, P120-4 and P116-3 showed the best performance with respect to the number of primary branches per pod, number of pods per plant, number of seeds per pod, pod length, internodal distance and pod yield per plant and also exhibited resistance reaction against powdery mildew as these genotypes were introgressed with two recessive powdery mildew resistant genes i.e., *er1* and *er2*.

Keywords: Vegetable pea, powdery mildew, resistance, pod yield, gene introgression.

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Introduction

Vegetable pea (*Pisum sativum* L.) is an important crop grown throughout the world. In India, it is grown mainly as winter vegetable in the plains of North India and as summer vegetable in the hills. Garden pea is used as fresh vegetables, canned, processed or dehydrated and seeds are consumed as pulse. Green pods are highly nutritive, containing high percentage of digestible protein (7.2%), carbohydrates (19.8%) and minerals (0.8%). Lahaul-Spiti, Kinnaur, Shimla, Kullu, Sirmour and Mandi districts are the major vegetable pea producing areas and are the leading supplier of fresh market peas to northern plains in the summer season. Hilly grown peas fetch special place during the summer months in plains due to theirsweetness.The produce of hills is high-priced for its characteristics flavor, sweetness, tenderness and attractive pods. In Himachal Pradesh, Azad Pea-1 and Punjab-89 are being cultivated at commercial scale but of late, due to mono-cropping of garden pea the production potential of commercial varieties has declined due to plethora of diseases. Powdery mildew caused by *Erysiphe pisi* D.C. is one of the most devastating diseases which causes yield losses to the range of 25 to 50 per cent (Fondevilla and Rubiales, 2012)and significantly reduces the quality of marketable produce.Genetic resistance to powdery mildew has been identified in *Pisum sativum* and *Pisum fulvum* lines

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(Harland, 1948; Heringa et al., 1969; Marx, 1971; Kumar and Singh, 1981; Tiwari et al., 1999, Katoch et al., 2010, Fondevilla et al., 2007, 2008). Two recessive genes '*er1*' (Timmerman et al., 1994; Vaid and Tyagi, 1997; Janila and Sharma, 2004) and '*er2*' (Katoch et al., 2010) and a single dominant gene '*Er3*' (Fondevilla et al., 2007, 2010; Sharada and Makandar, 2023) have been reported to confer resistance to powdery mildew in peas, others reported duplicate recessive genes controlling resistance in several cultivars (Sokhi et al., 1979; Kumar and Singh, 1981). Moreover, Heringa et al. (1969) reported two independent powdery resistance genes, *er1* and *er2*, conferring different resistance phenotypes; while *er1* was reported to confer a high level of protection to all plant parts, the *er2* resistance was confined only to leaves, a phenomenon also observed by other workers (Marx, 1986; Tiwari et al., 1997). While investigating the histological basis of *er1* and *er2* mediated resistance, Fondevilla et al. (2006) reported that *er1* confers complete resistance to powdery mildew by limiting pathogen penetration, whereas the *er2* mediated resistance is mainly based on reduction in penetration success complemented by post-penetration cell death. Combining of resistance mechanisms mediated by *er1* and *er2* into a single genetic background is expected to broaden the spectrum and durability of resistance conditioned by each of these genes. However, incorporation of both genes into a single genetic background by conventional backcross breeding is difficult because the high level of penetration resistance mediated by *er1* will preclude the detection of *er2* in the breeding material (Fondevilla et al., 2006). The recessive nature of the powdery mildew resistance genes and difficulties associated to the handling of obligate pathogens like *E. pisi*, further complicate selection of resistant progenies in breeding programs.

Identification of resistance sources and their incorporation into susceptible cultivars remains the most effective method of controlling the disease. Though chemical control is feasible but economically impractical and environmentally unsafe. Azad Pea-1 is one of the most popular variety of vegetablepea which is being commercially raised by garden pea growers of the state, but the variety is highly susceptible to powdery mildew hence horticulturally superior essentially derived pyramid lines of Azad Pea-1 bearing *er1*and *er2* gene have been developed through marker assisted backcross breeding.Keeping the above points in view, the present study was carried out to evaluate pea genotypes for yield and quality traits in garden pea as well as their reaction towards powdery mildew disease to identify resistant line(s).

Materials and Methods

The experiment was conducted at Department of Vegetable Science and Floriculture, College of Agriculture, CSKHPKV, Palampur during *rabi* 2017-18 and 2018-19. The experimental farm is situated at 32.12 °N latitude, 76.53 °E longitude at an elevation of 1,290.8 m above mean sea level. The experimental material consisted of ten lines of garden pea developed through marker assisted backcross breeding followed by pedigree selection (wherein two powdery mildew resistant genotypes, JI 1559 was utilized as a source of er1 gene and JI 2480 as a source of *er2* gene) along with three checks namely, Azad Pea-1, Palam Priya and Punjab-89 were evaluated in Randomized Block Design (RBD) with three replications. Each genotype was grown in six rows at spacing of 45 cm between rows and 10 cm between plant to plant. The observations were recorded on randomly taken ten plants of each genotype in each replication for quantitative traits *viz*., days to 50 per cent flowering, days to first picking, pod length (cm), number of seeds per pod, shelling percentage, number of primary branches per plant, number of pods per plant, internodal distance (cm), plant height (cm), pod weight (g), pod yield per plant (g) and qualitative traits *viz.,* total soluble solids (°Brix), ascorbic acid (mg per 100g fresh weight) and crude protein content (%). Powdery mildew reaction of vegetablepea lines was also evaluated by the detached leaf technique of Vaid and Tyagi (1997) using a single colony isolate of *Erysiphe pisi* collected from the naturally infected plants of garden pea. (%). Four detached leaflets from 25–30 day old F2 plants, F1s and parental genotypes were floated on 40 ppm solution of benzimedazole in 90 mm Petridishes. The leaflets were dusted with powdery mildew inoculum using a camel hairbrush and incubated at 25 ± 1C under 16 h photoperiod. After 10 days of inoculation, the disease reaction of the leaflets was assessed microscopically under a stereoscopic microscope (GSZ-66-77-1012, GENTER, India) using a 0–4 scale (Vaid and Tyagi, 1997): 0 = macroscopically or microscopically no mycelial growth is evident; 1 = microscopically sparse mycelial growth with rare conidiophores is seen; 2 = microscopically slight growth of mycelium with a little sporulation is seen and individual conidiophores on a colony can be easily counted; 3 = microscopically moderate development of mycelium with moderate to heavy sporulation is seen; 4 = microscopically abundant development of mycelium with heavy to very heavy sporulation is visible. The density of sporulation in reaction types 3 and 4 is such that individual conidiophores can neither be followed to the base nor their total number counted. The leaflets showing reaction type 0, 1 and 2 were rated as resistant, while those with reaction type 3 and 4 were considered susceptible. Analysis of variance was performed for individual season and error variance was tested for homogeneity (Gomez and Gomez, 1984). LSD test was utilized to determine the statistical significance of different genotypes using Microsoft excel.

Results and Discussion

The results presented in Table 1 and 2 indicated the presence of significant variation for all the growth and yield parameters among different genotypes of vegetable pea screened during *rabi* 2017-18 and 2018-19. It is evident from data in Table 1 that minimum days to 50 per cent flowering were exhibited by Punjab-89 (88.33 and 90.00 days) during both years. None of the genotypes were found significantly superior to best check Punjab-89 however, P138-2 (90.00 and 91.77 days) during both years and P116-2 (92.00 days), P116-3 (93.33 days), Azad Pea-1 (93.37 days) and P120-4 (93.40 days) during 2018-19 were statistically at par with Punjab-89. For days to first picking, Punjab-89 (126.33 and 125.03 days) was found to be the earliest with none of the genotypes being superior to it. Six genotypes *viz.,* P120-4 (126.67 and 126.33 days), P116-3 (126.67 and 127.73 days), P116-2 (126.67 and 127.87 days), Azad Pea-1 (126.67 and 127.87 days), P-227 (127.00 and 127.87 days) and P120-1 (127.33 and 128.83 days) were at par with the best check during both years, respectively. Days to 50 per cent flowering and days to first picking are a good indicative of earliness in vegetable pea which fetches good price in market. Genotypes exhibiting earliness with higher yield are considered superior over late maturing. Significant differences for days to 50% flowering and days to first picking were also observed by Afreen et al. (2017), Rahman et al. (2018) and Devi et al. (2018).

Pod length and number of seeds per pod directly influences the yield potential of a genotype and its market acceptance. Generally well filled, long and green pods are preferred. Among checks maximum pod length was observed in Punjab-89 (10.38 and 10.01 cm)during both years and none of the genotypes were found significantly superior to the best check (Table 1). Among all the genotypes, five genotypes *viz.,* P-227 (10.09 and 10.25 cm), Line 1-2 (9.30 and 9.42 cm), Azad Pea-1 (9.22 and 9.08 cm), P120-4 (9.12 and 9.79 cm) and P116-3 (9.02 and 9.46 cm) were statistically at par with the best check during both the years, respectively. Among the checks, maximum number of seeds per pod was recorded in Punjab-89 (9.05 and 9.72). Genotype P-227 (9.17 and 9.57) during both years and Line 1-2 (8.30), P120-4 (8.14) and P116-3 (8.10) during 2017-18 were found statistically at with the best check. Luitel et al. (2023) and Luitel and Bhandari (2023) also observed significant differences in pod length.

Shelling percentage among checkswas found maximum in Azad Pea -1 (54.19% and 53.49%) during both years (Table 1). All the genotypes were statistically at par with best check except P138-2 (51.24%) during 2017-18. P116-2 (55.76% and 54.76%) and P116-3 (54.10% and 55.57%) exhibited maximum shelling percentage during both years.Amongchecks, Palam Priya (1.73 and 2.00) and Punjab-89 (1.73) had maximum primary branches per plant during both years and 2017-18, respectively (Table 1). Line 1-2 (2.73) and P-227 (2.60)

Table 1: Mean Values for vegetables pea genotypes with respect to yield and morphological (2017-2018, 2018-19)

Genotype	*Days to 50% flowering*		*Days to first picking*		*Pod length*		*No. of seed/Pod*		*Shelling %age*		*Primary branches*		*No. of Pods/plant*	
	1st	*2nd*	*1st*	*2nd*	*1st*	*2nd*	*1st*	*2nd*	*1st*	*2nd*	*1st*	*2nd*	*1st*	*2nd*
Line 1-2	95.33	96.63	130.33	131.70	9.30	9.42	8.30	7.97	53.27	52.43	2.73	2.53	19.10	17.50
P116-2	91.33	92.00	126.67	127.87	8.19	8.67	7.30	7.13	55.76	54.76	1.60	1.73	13.78	12.73
P227	91.67	93.43	127.00	128.19	10.09	10.25	9.17	9.57	51.75	50.30	2.60	2.47	15.97	13.87
P120-4	91.33	93.40	126.67	126.33	9.12	9.79	8.14	8.53	51.83	53.10	1.67	1.73	15.79	14.67
P120-1	92.33	96.00	127.33	128.83	8.78	8.47	7.04	7.12	52.42	50.17	1.47	1.47	13.27	12.41
P116-3	91.67	93.33	126.67	127.73	9.02	9.46	8.10	8.33	54.10	55.57	1.33	1.40	14.82	13.68
P138-2	90.00	91.77	128.67	129.07	8.75	8.63	7.07	7.13	51.24	50.60	1.40	1.40	14.73	13.87
Azad P-1 (C)	91.33	93.37	126.67	127.87	9.22	9.08	7.30	7.23	54.19	53.49	1.37	1.33	12.83	11.75
Palam Priya (C)	95.67	96.73	133.33	134.30	7.92	7.99	7.18	7.37	51.75	50.56	1.73	2.00	15.42	14.07
Punjab-89 (C)	88.33	90.00	126.33	125.03	10.38	10.01	9.05	9.72	53.41	52.77	1.73	1.70	15.55	14.87
Mean	91.90	93.67	127.97	128.69	9.08	9.18	7.86	8.01	52.97	52.31	1.76	1.75	15.13	13.94
SE(m)	0.89	1.13	0.69	1.30	0.46	0.42	0.35	0.37	0.89	1.20	0.17	0.20	1.11	0.82
CD	2.66	3.40	2.08	3.90	1.38	1.26	1.05	1.12	2.65	3.60	0.52	0.60	3.33	2.45
CV	1.67	2.10	0.94	1.75	8.78	7.93	7.75	8.11	2.89	3.98	16.90	19.37	12.72	10.18

1st: 2017-18, 2nd: 2018-19, C:Check

Table 2: Mean Values for vegetable pea genotypes with respect to yield, morphological and quality traits (2017-2018, 2018-19)

Genotype	*Internodal distance*		*Plant height (cm)*		*Pod weight (g)*		*TSS*		*Ascorbic acid*		*Crude Protein*		*Pod yield/plant*	
	1st	*2nd*	*1st*	*2nd*	*1st*	*2nd*	*1st*	*2nd*	*1st*	*2nd*	*1st*	*2nd*	*1st*	*2nd*
Line 1-2	2.18	2.66	74.03	72.00	5.91	5.55	16.67	16.50	20.70	19.00	20.32	19.77	104.09	97.10
P116-2	3.24	3.76	72.60	72.57	7.47	7.24	15.00	14.00	22.90	21.33	14.58	13.23	85.99	80.40
P227	4.63	4.57	91.60	90.87	6.85	6.60	14.09	15.17	22.77	21.28	15.75	14.30	100.03	92.77
P120-4	4.10	3.91	80.73	81.23	6.75	6.49	13.50	13.83	20.37	21.33	16.33	15.77	98.13	90.63
P120-1	4.12	4.71	79.20	78.13	7.91	7.81	14.43	16.23	22.97	21.00	14.00	15.20	81.46	78.82
P116-3	3.67	3.33	75.53	76.17	7.64	7.54	15.72	15.99	21.23	20.33	14.00	13.73	93.82	88.60
P138-2	3.88	4.10	77.73	78.33	8.31	8.87	12.83	13.17	19.93	18.00	15.75	18.20	78.13	75.67
Azad P-1 (C)	4.40	4.14	78.13	77.53	8.13	7.01	13.83	14.33	21.64	20.30	17.26	16.37	89.74	85.80
Palam Priya (C)	3.66	3.81	70.83	71.47	6.67	6.70	15.00	14.23	21.92	22.00	15.17	14.03	86.99	83.00
Punjab-89 (C)	4.35	4.32	75.73	75.77	5.77	5.58	14.50	14.89	22.30	22.33	17.52	18.43	92.01	87.57
Mean	3.83	3.88	77.61	77.41	7.14	6.94	14.56	14.84	21.67	20.69	16.07	15.90	91.04	86.04
SE(m)	0.25	0.23	1.33	1.59	0.20	0.11	0.61	0.34	0.59	0.43	0.74	0.35	2.56	2.88
CD	0.75	0.70	3.97	4.75	0.60	0.31	1.84	1.02	1.77	1.27	2.23	1.05	7.66	8.64
CV	11.41	10.42	2.96	3.55	4.92	2.62	7.30	3.97	4.71	3.56	8.01	3.82	4.87	5.81

1st: 2017-18, 2nd: 2018-19, C:Check

exhibited significant superiority over best checks during 2017-18 while none of the genotypes were superior to best check in 2018-19. During 2017-18 remaining six genotypes were significantly at par with best checks while in 2018-19 except for Azad Pea-1 (1.33) all the genotypes were at par with the best check. Number of primary branches is a good index of plant vigour may contribute towards greater productivity. Different response to number of branches might be due to genetic characteristic of genotypes and adaptability to a prevailing environment as reported by Singh et al. (2018).

Number of pods per plant have a strong positive correlation with pod yield and other pod related traits making it pivotal for breeding programs aimed at improving yield efficiency in vegetable pea. For number of pods per plant, Line 1-2 (19.10 and 17.50) was found significantly superior to the best check Punjab-89 (15.55 and 14.87) during both years (Table 1). The remaining genotypes in 2017-18 were statistically at par with the best check while in 2018-19 except for P120-1 (12.41) and Azad Pea-1 (11.75) remaining six genotypes were statistically at par with the best check. Devi et al. (2018) and Rahman et al. 2018 also found significant differences among pea genotypes for same trait.

As presented in Table 2, for internodal distance Line 1-2 (2.18 and 2.66 cm) was significantly superior to best check Palam Priya (3.66 and 3.81 cm). In both years P116-2 (3.24 and 3.33 cm) had less internodal distance than the best check and was significantly at par with the best check Palam Priya along with six genotypes except for P-227 (4.63 cm) during 2017-18 and five genotypes except for P-227 (4.57 cm) and P120-1 (4.71 cm) during 2018-19.Less internodal distance is desirable in vegetable pea as less internodal distance leads to a greater number of nodes per plant which positively affects number of pods per plant. Significant differences among different vegetable pea genotypes had been observed by Kumar et al. (2019).

In vegetable pea, plants with dwarf stature are desirable. It is so because short plants do not require staking and causes a reduction in lodging thereby preventing wastage of resources such as time and money coupled with enhanced yield. For plant height, Palam Priya (70.83 and 71.47 cm) exhibited minimum height among checks (Table 2). None of the genotypes were superior for plant height in comparison to best check. P116-2 (72.60 and 72.57 cm) and Line1-2 (74.03 and 72.00 cm) were statistically at par with the best check in both years while P116-3 (76.17 cm) was statistically at par with the best check during 2018-19 only.This variation may be attributed to the varying genetic makeup of the plants studied as reported by Luitel and Bhandari (2023) and Sharma et al. (2020). For pod weight, among checks Azad Pea-1 (8.13 and 7.01 g) was superior and none of the genotypes exhibited superiority over best check during 2017-18 while in 2nd year, P138-2 (8.87 g), P120-1 (7.81 g) and P116-3 (7.54 g) were superior to the best check. In 1st and

Table 3: Powdery mildew resistant score of vegetable pea genotypes

Genotypes	*Scores*		*Reaction*
	2017-18	*2018-19*	
Line 1-2	1	1	Resistant
P116-2	1	1	Resistant
P227	1	1	Resistant
P120-4	1	1	Resistant
P120-1	1	1	Resistant
P116-3	1	1	Resistant
P138-2	1	1	Resistant
Azad P-1 (C)	4	4	Susceptible
Palam Priya (C)	4	4	Susceptible
Punjab-89 (C)	4	4	Susceptible

2nd year, three genotypes *viz.,*P138-2 (8.31 g), P120-1 (7.91 g) and P116-3 (7.64 g)and two genotypes *viz.,*P116-2 (7.24 g) and Palam Priya (6.70 g) were statistically at par with the best check, respectively.This might be due to that, a greater number of pods per plant and higher pod setting.

For TSS, during 2017-18 none of the genotypes were superior to the best check Palam Priya (15.00$^{\circ Brix}$). Except for P138-2 (12.83°Brix) all the genotypes were statistically at par with the best check. In 2018-19, three genotypes *viz.,*Line 1-2 (16.50°Brix), P120-1 (16.23°Brix) and P116-3 (15.99°Brix) were superior to the best check Punjab-89 (14.89°Brix) while four genotypes *viz.,*P-227 (15.17°Brix), Azad Pea -1 (14.33°Brix), Palam Priya (14.23$^{\circ Brix}$) and P116-2 (14.00°Brix) were statistically at par with the best check. Among checks, Punjab-89 (22.30 and 22.33 mg) exhibited maximum ascorbic acid content during both years and none of the genotypes were superior to the best check. In 2017-18, P120-1 (22.97 mg), Azad Pea-1 (21.64 mg), P116-3 (21.23 mg) and Line 1-2 (20.70 mg) while in 2018-19, P120-4 (21.33 mg) were at par with the best check.Genotypes P116-2 (22.90 and 21.33 mg), P-227 (22.77 and 21.28 mg) and Palam Priya (21.92 and 22.00 mg) were statistically at par with the best check.In terms of crude protein, Line 1-2 (20.32% and 19.77%) was found superior to the best check Punjab-89 (17.52% and 18.43%) during both years.Azad Pea-1 (17.26%), P120-4 (16.33%), P-227 (15.75%) during 2017-18 and P138-2 (15.75% and 18.20%) during both were found statistically at par with the best check. This variability in the quality traits may be due to the inherent potential of the genotypes and due to the climatic factors. Earlier workers *viz.,* Khichi et al. (2016), Rahman et al. (2018) also reported such variation of quality traits in their respective material.

Yield is the goal of all crop improvement programmes. To develop a variety with high yield and its related traits surpassing commercially adopted cultivars is the primary objective of a breeder. It is evident from the data presented in Table 2 that pod yield per plant was significantly influenced by the genotypes. Line 1-2 (104.09 and 97.10 g) and P-227 (100.03 g) were significantly superior to the best check Punjab-89 (92.01 and 87.57 g) during both years and 2017-18, respectively. Five genotypes *viz.,* P120-4 (98.13 and 92.77 g), P116-3 (93.82 and 88.60 g), Azad Pea-1 (89.74 and 85.80 g), Palam Priya (86.99 and 83.00 g) and P116-2 (85.99 and 80.40 g) were statistically at par with the best check during both years while P-227 (92.77 g) was at par with Punjab-89 during 2018-19 only. Devi et al. (2018) and Rahman et al. (2018) also observed similar results with significant differences among genotypes for pod yield.

The severity of powdery mildew disease was observed in the range of resistant (1) to susceptible (4) in ten genotypes (Table 3). Their screening for powdery mildew indicated that the three standard checks *viz.,* Azad Pea-1, Palam Priya and Punjab-89 were susceptible to powdery mildew disease, while Line 1-2, P116-2, P227, P120-4, P120-1, P116-3 and P138-2 exhibited resistant reaction. These genotypes showed resistant reaction as these lines harbour two recessive genes *er1* and *er2*. The resistance response of gene was characterized by sparse mycelia growth and reduced sporulation of pathogen and frequent occurrence of hypersensitive cell death of the invaded tissue. In contrast, an abundant mycelia growth and profuse sporulation of the pathogen without any visible necrosis of the tissue was observed on the leaves of susceptible check *viz.,*Azad Pea-1, Palam Priya and Punjab-89.Earlier report of many researchers *viz.,*Ullah et al. (2013), Sun et al. (2016) and Rahman et al. (2018) has found different varieties resistant to powdery mildew.

Conclusion

Hence from the present study, it can be concluded that genotypes *viz.,* Line 1-2, P-227, P120-4 and P116-3 had higher yield and performed better for majority of horticultural traits in comparison to standard checks. These genotypes also exhibited resistance to powdery mildew disease as they have been introgressed with two single recessive genes namely, *er1* and *er2* which confer resistance to powdery mildew. Based on the results these lines show promise for cultivation in mid hill conditions of Himachal Pradeshand can be released as varieties after multi location testing across the state or can be further utilized in breeding programs.

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सारांश

चूर्णसिता फफूंदी सब्जी मटर की सबसे विनाशकारी बीमारियों में से एक है, जिससे उपज में भारी नुकसान होता है और गुणवत्ता में उल्लेखनीय कमी आती है।इस बीमारी पर काबू पाने के लिए, उच्च उपज देने वाली चूर्णसिता फफूंद प्रतिरोधी लाइन (लाइनों) की पहचान करने के लिए जीन पिरामिडिंग के माध्यम से विकसित सब्जी मटर लाइनों का दो वर्षों में रेंडमाइज्ड ब्लॉक डिज़ाइन में मूल्यांकन किया गया था। यह प्रयोग 2017-18 और 2018-19 के रबी सीज़न के दौरान सी.एस. के.एच.पी.के.वी, पालमपुर के प्रायोगिक अनुसंधान फार्म में तीन चेक सहित दस जीनोटाइप का उपयोग कर के किया गया था। अध्ययन किए गए लक्षणों के औसत मूल्यों के आधार पर डेटा के विश्लेषण से सभी जीनोटाइप के बीच महत्वपूर्ण अंतर पाया गया। दो वर्षों के औसत प्रदर्शन के आधार पर, लाइन 1-2, पी-227, पी120-4 और पी116-3 ने प्रति फली प्राथमिक शाखाओं की संख्या, प्रति पौधाफली की संख्या, प्रति बीज की संख्या के संबंध में सर्वश्रेष्ठ प्रदर्शन दिखाया। फली, फली की लंबाई, इंटरनोडल दूरी और प्रति पौधे फली की उपज और चूर्णसिता फफूंद के खिलाफ प्रतिरोध प्रतिक्रिया भी प्रदर्शित की गई क्योंकि ये जीनोटाइप दो अप्रभावी चूर्णसिता फफूंद प्रतिरोधी जीनों यानी er_1 और er_2 के साथ अंतःस्थापित थे।