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***Short communication***

# Identification of powdery mildew resistant genotypes of garden pea (*Pisum sativum* L.) following field and in-vitro screening

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## Abstract

**Powdery mildew caused by *Erysiphe pisi* is a major disease severely affect pea production in areas with warm and dry days, and cool nights. It is essential to identify/develop resistant genotypes for commercial use or to incorporate resistance in cultivars using different breeding approached supplemented with marker-assisted selection. Considering the high potential of pea production in India, a study was conducted to screen ten newly developed genotypes along with four recommended check varieties *viz*., Him Palam Matar-1, Azad P-1, Lincoln and Pb-89 under field and in-vitro conditions during the years 2020-21 to 2023-24. Three lines namely, DPPMR-09-1, DPP-MR-09-6 and DPP-SN-2 showed resistant reaction against powdery mildew while DPP-SP-6, DPP-SN-5 and DPP-SN-10 were identified with moderately resistant reaction. The identified resistant genotypes may be directly utilized or incorporated into high-yield, disease-susceptible genotypes through hybridization.**

**Keywords:** *Erysiphe pisi,* garden pea, resistance, screening, genetic improvement

Garden pea (*Pisum sativum* L.), is important leguminous crop worldwide and significantly contribute as an element of sustainable cropping systems. The use of green-shelled seeds in canned, frozen, or dehydrated products signifies its coveted position in processing industry (Sharma *et al*. 2022). It is a rich source of nutrients such as proteins, vitamins, minerals, and lysine (an essential amino acid lacking in cereals) and its consumption, therefore, help to maintain human health (Sharma *et al*. 2020). It is also a nitrogen-fixing legume crop that is suggested for crop rotation because of its abilities to improve soil quality, short growing seasons and higher yields. In garden pea, conventional breeding approaches are extensively employed to develop varieties with a range of targeted traits. The most important objective of pea breeding is to develop varieties with high and stable production, different maturity types and resistance against biotic and abiotic stresses (Rana *et al*. 2021). To overcome the further economic loss in the context of biotic and abiotic stresses, there is a dire need to breed resistant and high yielding varieties.

Garden pea is susceptible to various diseases and powdery mildew (*Erysiphe pisi Syd*.) stands out as the most critical disease impacting fresh pea production worldwide, with potential yield losses ranging from 25-50% globally (Fondevilla and Rubiales 2012). It is preferable to find alternative disease control methods other than fungicides which have social, health, and environmental impacts. Genetic resistance offers the most effective approach for sustainable crop breeding (Rana *et al*. 2023).Two single recessive genes (er1 and er2) and one dominant gene (Er3) have been identified for powdery mildew resistance in pea germplasms to date. The PM resistant pea varieties can be developed through hybridization by involving the available resistance sources in the germplasm, which broadly indicated monogenic recessive inheritance (Sharma 2003). Majority of pea powdery mildew breeding programs rely on the presence of the recessive gene er1 as it presents complete resistance from powdery mildew by constraining pathogen penetration. In India,

consumers prefer sweet, long and dark green pods of garden pea that put Azad P-1 as the most preferred choice among different varieties though it is highly susceptible to powdery mildew disease (Sharma *et al*. 2013). The efforts have been made to synthesize powdery mildew resistant lines from a series of cross combinations along with desirable horticultural traits. Precise screening of pea germplasm for disease resistance under natural conditions is challenging, particularly when pathogen development is influenced by weather factors like temperature, as seen with *E. pisi*. Thus, this study assessed resistance to powdery mildew in pea genotypes with varying levels of resistance utilizing both field and controlled conditions.

The present investigation was undertaken to screen 10 newly developed genotypes along with four recommended check varieties *viz*., Him Palam Matar-1, Azad P-1, Lincoln and Pb-89 under field and in-vitro conditions during 2020-21 to 2023-24 at Research Farm. Department of Vegetable Science and Floriculture, Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur. The individual plants were categorized into different classes of disease severity following (0-4) scale of Mains and Deitz (1930) *i.e*. 0 (no trace of infection), 1 (slight infection with approximately one in each four leaves), 2 (nearly 50 per cent leaves infected), 3 (Nearly 75 per cent of the foliage infected) and 4 (infection on all plant parts).The genotypes with score 0-1 were categorized as resistant while genotypes with score 2, 3 and 4 were categorized as Moderately susceptible, susceptible and highly susceptible, respectively. To avoid disease escape, conidial inoculums were brushed on the plants for even disease infection to enable effective screening under natural ventilated polyhouse conditions. In addition, detached leaf method was also employed to identify resistant genotypes under lab environment (Banyal and Tyagi 1998) by placing leaves from 3-4 weeks old plants over water solution in petri dishes followed by dusting of disease inoculum on the leaves.

The disease reaction pattern of 10 selective genotypes and four check varieties were evaluated for field and in vitro conditions during 2020-21 to 2023-24 and are presented in Table 1. The genotypes expressed variable reaction to disease over the environments with DPPMR-09-1, DPPMR-09-6 and DPP-SN-2 witnessed resistant reaction under both the field and in-vitro conditions with score 0-1 (Figure 1). However, lack of durable resistance is a problem for airborne fungal pathogens such as powdery mildew (Sillero *et al*. 2006). Earlier, several sources of powdery mildew resistance have been identified following the screening of large collections of pea germplasm (Reddy *et al*. 2015; Singh *et al*. 2015; Leon *et al*. 2020; Bobkov and Selikhova 2021). Three genotypes *viz*., DPP-SP-6, DPP-SN-5 and DPP-SN-10 developed disease growth confined to lower leaves at economic threshold stage and therefore, were categorized as 'moderately resistant' based on their score under different conditions. Sharma *et al*. (2020) reported that the high-yielding genotypes 'DPP-SP-6', 'DPP-SP-7', 'DPP-SP-17' and 'DPP-SP-22' showed resistance to powdery mildew disease. On the other hand, DPP-SP-10, DPP-SP-12, DPP-SP-18, DPP-SP-24 expressed 'moderately susceptible' reaction in the field and in-vitro conditions. The performance of these genotypes for pod yield and related traits have been presented in Table 2 which clearly indicated that the resistant genotypes had comparatively low pod yield than DPP-SP-6, Him Palam Matar-1 and Pb-89. Therefore, after the rigorous evaluation of the newly developed genotypes under field and in vitro conditions resulted in identifying three powdery mildew resistant genotypes namely, DPPMR-09-1, DPP-MR-09-6 and DPP-SN-2, which can be further, utilized as a resistant source in pea breeding programmes. Rana *et al*. (2023) have also reported same disease reaction in the genotypes DPP-SP-6, DPP-SP-10, DPP-SP-24, DPP-SN-5, DPP-SN-2, HPM-1, Azad-P-1, Palam Sumool and Pb-89.

## Conclusion

The study led to the identification of resistance genotypes against the powdery mildew (*Erysiphe pisi*) based on field and in-vitro screening namely, DPPMR-09-1, DPP-MR-09-6 and DPP-SN-2 while DPP-SP-6, DPP-SN-5 and DPP-SN-10 showed moderately resistant reaction.

**Conflict of interest**: Authors declare no competing interest.

**Table 1. Screening of the newly developed pea genotypes for powdery mildew incidence under in vivo and in-vitro conditions**

| Genotypes | Field Conditions | | | | Polyhouse (2021-22, 2022-23 & 2023-24) | | Detached leaf assay (2021-22 & 2022-23) | | Overall disease reaction | |
|---|---|---|---|---|---|---|---|---|---|---|
| | 2020-21 | 2021-22 | 2022-23 | 2023-24 | Infection type | Disease reaction | Infection type | Disease reaction | Infection type | Disease reaction |
| DPPMR-09-1 | 0 | 0 | 0 | 0 | 1 | R | 1 | MR | 1 | R |
| DPPMR-09-6 | 0 | 0 | 0 | 1 | 1 | R | 1 | R | 1 | R |
| DPP-SP-6 | 2 | 1 | 2 | 2 | 2 | MR | 2 | MR | 2 | MR |
| DPP-SP-10 | 2 | 2 | 2 | 2 | 3 | MS | 3 | MS | 3 | MS |
| DPP-SP-12 | 2 | 2 | 2 | 2 | 3 | MS | 3 | MS | 3 | MS |
| DPP-SP-18 | 2 | 2 | 2 | 2 | 3 | MS | 3 | MS | 3 | MS |
| DPP-SP-24 | 2 | 2 | 2 | 2 | 3 | MS | 3 | MS | 3 | MS |
| DPP-SN-5 | 2 | 1 | 2 | 2 | 2 | MR | 2 | MR | 2 | MR |
| DPP-SN-2 | 0 | 0 | 0 | 0 | 1 | R | 1 | R | 1 | R |
| DPP-SN-10 | 2 | 1 | 2 | 2 | 2 | MR | 2 | MR | 2 | MR |
| Him Palam Matar-1 | 2 | 1 | 2 | 2 | 2 | MR | 2 | MR | 2 | MR |
| Azad-P1 | 3 | 2 | 3 | 3 | 4 | S | 4 | S | 4 | S |
| Palam Sumool | 1 | 0 | 1 | 1 | 1 | R | 1 | R | 1 | R |
| Pb-89 | 2 | 2 | 2 | 2 | 3 | MS | 3 | MS | 3 | MS |

*Scale: 0-4; Where, R-Resistant (1); MR-Moderately resistant (2); MS-Moderately susceptible (3); S-Susceptible (4)*

**Table 2: Mean performance of pea genotypes for yield and its component traits during 2021-22 & 2022-23**

| Genotype | Days to 50% flowering | Days to first picking | Pod length (cm) | Pod width (cm) | Seeds per pod | Shelling (%) | Average pod weight (g) | Primary branches per plant | Nodes per plant | Plant height (cm) | Pods per plant | Pod yield per plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DPPMR-09-1 | 99.00 | 136.00 | 9.00 | 1.66 | 5.80 | 45.00 | 4.28 | 1.60 | 23.00 | 85.40 | 13.24 | 56.67 |
| DPPMR-09-6 | 95.00 | 128.00 | 9.36 | 2.12 | 6.90 | 49.80 | 4.71 | 2.30 | 26.60 | 72.20 | 21.19 | 99.80 |
| DPP-SP-6 | 85.00 | 135.00 | 11.65 | 1.86 | 8.90 | 49.90 | 5.47 | 2.10 | 26.20 | 77.40 | 22.08 | 120.75 |
| DPP-SP-10 | 85.00 | 128.00 | 10.18 | 1.72 | 7.40 | 47.50 | 5.34 | 2.20 | 28.40 | 82.20 | 16.38 | 87.50 |
| DPP-SP-12 | 84.00 | 128.00 | 9.84 | 1.64 | 8.20 | 47.70 | 4.74 | 2.70 | 30.20 | 80.80 | 21.57 | 102.14 |
| DPP-SP-18 | 82.00 | 128.00 | 11.14 | 1.72 | 8.30 | 44.90 | 5.51 | 2.10 | 26.80 | 87.00 | 17.56 | 96.67 |
| DPP-SP-24 | 84.00 | 134.00 | 10.80 | 1.70 | 8.00 | 49.40 | 5.25 | 2.70 | 29.40 | 74.00 | 15.13 | 79.38 |
| DPP-SN-5 | 91.00 | 136.00 | 11.20 | 1.66 | 8.40 | 45.30 | 5.75 | 1.80 | 23.10 | 82.60 | 15.00 | 86.25 |
| DPP-SN-2 | 83.00 | 128.00 | 10.50 | 1.80 | 7.20 | 47.40 | 5.17 | 1.20 | 19.80 | 77.40 | 18.10 | 92.58 |
| DPP-SN-10 | 91.00 | 130.00 | 11.10 | 1.86 | 7.20 | 47.00 | 5.44 | 1.50 | 22.80 | 75.60 | 15.80 | 86.00 |
| Him Palam Matar-1 | 83.00 | 123.00 | 10.10 | 1.62 | 8.40 | 49.10 | 5.28 | 2.10 | 25.80 | 81.50 | 20.78 | 109.66 |
| Azad P-1 | 92.00 | 138.00 | 9.40 | 1.84 | 6.40 | 49.40 | 5.42 | 1.90 | 27.40 | 77.40 | 13.64 | 73.89 |
| Palam Sumool | 90.00 | 141.00 | 13.02 | 2.26 | 6.50 | 42.20 | 6.60 | 2.00 | 28.40 | 84.20 | 11.44 | 75.56 |
| Pb-89 | 88.00 | 119.00 | 10.50 | 1.76 | 8.70 | 48.40 | 6.27 | 1.50 | 22.30 | 76.00 | 15.92 | 99.81 |
| CD at $P \leq 0.05$ | 2.76 | 3.15 | 0.70 | 0.11 | 0.84 | 3.76 | 0.40 | 0.17 | 3.12 | 5.36 | 1.52 | 6.35 |


**Fig. 1 Comparative disease reaction of DPP-09-6 and Azad P-1 at Kukumseri**

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