Vegetable Science (2024) 51(2): 236-241

doi: 10.61180/vegsci.2024.v51.i2.05

ISSN- 0970-6585 (Print), ISSN- 2455-7552 (Online)

www.isvsvegsci.in

RESEARCH ARTICLE

Evaluation of genetic resources and deciphering the inheritance of powdery mildew (*Erysiphe pisi*) resistance in pea (*Pisum sativum* L.) genotypes, EC865944 and EC865975

Jyoti Devi[1], Anmol S. Yadav[2], Rakesh K. Dubey[1], Vidya Sagar[1], K.K. Pandey[1] and Sudarshan Maurya[1]

Abstract

Pea, a major cool-season vegetable legume, suffer substantial yield and quality losses due to powdery mildew (PM), caused by the parasitic fungus species *Erysiphe*. This disease can lead to yield reductions of 25–70%, affecting the quality of the produce with notable economic impact. Resistance breeding is one of the most environmentally sustainable strategies to manage this devastating disease. Over a period of three years, a total of 172 diverse pea accessions were field-evaluated for powdery mildew resistance (PMR), among which 35 accessions displayed a disease score rating of 0-1, indicating a disease incidence of ≤1%. Notably, three accessions—IC296678, EC865944, and EC865975 demonstrated high resistance levels against *Erysiphe pisi*. Histopathological observations showed that no conidia germination occurred on the resistant lines IC296678, EC865975 and EC865944 at both 24 and 48 hours post-inoculation, indicating a pre-invasive type of immunity in these genotypes. To investigate the gene action and inheritance patterns of PM resistance in EC865944 and EC865975, we utilized five cross combinations *viz*., EC865975 × Kashi Udai, Kashi Ageti × EC865944, EC865944 × Kashi Nandini, EC865975 × Kashi Shakti and EC865944 × VRPM-903. Analysis of the F_2 population from these crosses revealed a segregation pattern of one resistant to three susceptible, indicating the presence of a single recessive gene in both genotypes. Horticultural characterization of these genotypes showed that both belonged to the late-maturing group of peas, characterized by a taller growth habit, an average pod weight ranging from 5.5 to 7.5 g, and an average yield of 75 to 100 g per plant. These newly identified PMR sources provide invaluable genetic resources, not only for Indian breeders but also for researchers globally, offering a significant step forward in sustainable pea improvement.

Keywords: Powdery mildew, *Erysiphe, Pisum*, Resistance and Inheritance and Yield.

[1]ICAR-Indian Institute of Vegetable Research, Post Box 1, Jakhini, Varanasi 221 305, India

[2]Department of Mycology and Plant Pathology, Instititute of Agricultural Sciences, Banaras Hindu University,Varanasi 221 005, India

***Corresponding author;** Email: jyoti.devi@icar.gov.in

Citation: Devi, J., Yadav, A.S., Dubey, R.K., Sagar, V., Pandey, K. K. & Maurya, S. (2024). Evaluation of genetic resources and deciphering the inheritance of powdery mildew *(Erysiphe pisi)* resistance in pea *(Pisum sativum L.)* genotypes, EC865944 and EC865975. Vegetable Science, 51(2), 236-241.

Source of support: Nil

Conflict of interest: None.

Received: 26/08/2024 **Revised:** 28/11/2024 **Accepted:** 10/12/2024

Introduction

Pea (*Pisum sativum* L.) is one of the most important cool-season leguminous crops worldwide, valued for its dual role as both a vegetable and a pulse. Besides their value as food and fodder, peas also play a significant role in ecosystem sustainability through biological nitrogen fixation and green manuring (Devi et al., 2023). This nutritional profile positions peas as a promising food source to meet the dietary needs of the more than 900 million undernourished people worldwide (Devi et al., 2019). The world cultivated area of green peas in 2022 was estimated to be 2.61 million hectares, with a total production of 20.94 million tonnes. With 11.5 mt and 6.18 million tonnes of production, respectively, China and India are the largest producers of fresh peas in the world (FAO, 2022). Despite a global increase in the cultivated area and production of peas, productivity gains have been modest over the past two decades (7.6 to 8.0 t/ha), highlighting the ongoing challenge of biotic

---

and abiotic stressors despite concerted efforts aimed at improving yields.

Among the various biotic stresses, powdery mildew (PM) is the major fungal disease of peas, causing up to 25–70% yield losses. This disease is caused by the obligate fungus *Erysiphe,* with three distinct species, *Erysiphe pisi*, *E. trifolii*, and *E. baeumleri* reported to infect peas globally (Devi et al., 2022). The disease thrives under conditions of warm, dry days and cool nights and poses a greater risk, particularly when crops are grown for processing and seed production (Smith et al., 1996). Among various management strategies, breeding for resistance is considered the most effective approach. Furthermore, three resistance genes—*er1*, *er2*, and *Er3*—have been identified in distinct genomic locations on the pea genome, specifically on linkage groups VI, III, and IV, respectively (Katoch et al., 2010, Devi et al., 2023) and have shown promising resistance. Economic management of powdery mildew can be effectively achieved by incorporating these resistant genes into commercial cultivars. This approach is not only the most efficient but also environmentally sound and cost-effective. However, resistance variability, influenced by genetic differences, environmental conditions such as temperature and location, and species diversity, often leads to the breakdown of resistance (Devi et al. 2022). Thus, there is an urgent need to explore new sources of resistance and elucidate their mechanisms of resistance. Consequently, breeders have continuously made efforts to identify new sources of resistance in both cultivated and wild *Pisum* accessions.

ICAR-IIVR, Varanasi is the leading institute working on the genetic improvement of vegetable peas, with its major focus on developing cultivars that are resistant to powdery mildew. Accordingly, germplasm screening was conducted from *Rabi* season 2018-19 to 2022-23, where more than 172 germplasm lines, including both existing and newly augmented lines, as well as advanced breeding, were field screened for powdery mildew disease under natural epiphytic conditions and artificially. The present study unveils two newly identified resistant exotic germplasm lines, EC865975 and EC865944. Furthermore, in order to utilize these germplasm in improvement programs, understanding the inheritance of resistance sources is a fundamental prerequisite. Hence, the present experiment was undertaken to unravel the genetic basis of powdery mildew resistance in the newly identified resistant lines. Additionally, these lines were evaluated for key horticultural traits to generate basic information essential for their effective utilization in breeding programs.

Materials and Methods

Screening material and environments

A total of 172 diverse genotypes of peas, including the varieties, germplasm, exotic collections, and advanced breeding lines of peas, were screened at ICAR–Indian Institute of Vegetable Research, Varanasi, during the winter season (November–April) of 2018-19. These genetic resources are also part of our ongoing breeding program where plants were continuously evaluated for the development of high-yielding varieties in various maturity segments. We evaluated these lines year after year for various economic traits, including the screening for powdery mildew resistance (PMR) under natural epiphytic conditions. We initially identified a total of 72 lines showing a disease scale rating of 0-4 (during 2018-19) and again reevaluated the resistant lines in subsequent years during 2019-20 and 2020-21. The identified highly resistant lines were characterized for various horticultural traits during 2022-23 along with susceptible checks.

Artificial screening and disease scoring

Artificial screening was performed only for 35 accessions, showing the consistent resistance response along with the susceptible check Arkel. The artificial screening was performed by dusting the pathogen spore on the portrays under net house conditions to develop the disease. In order to prepare inoculum in the form of conidia for its use in the experiment, the completely infected leaves were selected, and the powdery growth of the pathogen was collected from the infected leaves with the help of a sterilized brush in aluminum foil. The collected powdery mass was dusted on the 28-day'-old tagged plant with the help of a sterile camel hair brush in the evening. The scoring was done twice, once after 7 to 10 days of inoculation and second at 15 days after inoculation. The disease score was then noted through the powdery mildew 0 to 9 scale (Warkentin et al., 1996). PM: 0 = no infection; 1 = <1%; 2 = 1–5%; 3 = 5–10%; 4 = 10–20%; 5 = 20–40%; 6 = 40–60%; 7 = 60–80%; 8 = 80–90%; 9 = >90%. Scores ranging between 0–4 were classified as resistant, while those falling within the range of 5 to 9 were classified as susceptible.

Histopathological studies

Naturally infected pea plants (susceptible cultivar—Arkel) showing typical symptoms of powdery mildew were collected, and the pathogen was confirmed by observing conidia exhibiting taxonomic key characteristics and identified as *Erysiphe pisi* using the concerned literature (Braun & Takamatsu, 2000; Braun et al., 2002; Singh, 2018). For histopathological studies, a clearing solution was prepared by mixing 1:1 absolute ethanol/glacial acetic acid (v/v). Ten ml of this mixture was taken in a petri plate. A filter paper (25 × 5 cm) with three longitudinal folds was placed in the mixture in such a way that only the lower part of the filter paper was dipped in the mixture and the upper part got the mixture through diffusion. Inoculated leaf segments (1 sq. cm) were placed on the upper part of the filter paper for 24 hrs to drain the entire chlorophyll. The leaf segments were transferred to filter paper moistened with tap water for 2 hours. After this, these segments were fixed in lacto glycerol (1:1:1 lactic acid/glycerol/water, v/v/v) for 2 hours. The determination of the pathogen development on resistant and susceptible genotypes, *viz*., conidial germination, appressorium formation, and mycelial elongation, was observed under a compound research microscope (Nikon Eclipse E 200) fitted with a camera (Nikon DS-Fi2).

Inheritance of resistance

In our repeated experiment for 3 years, we identified two exotic collections (EC865975 and EC865944) showing a highly resistant response. To know whether these materials carry recessive/dominant gene(s), we conducted the inheritance study of these lines (EC865975 and EC865944) by utilizing the five cross combinations, *viz*., EC865975 × Kashi Udai, Kashi Ageti × EC865944, EC865944 × Kashi Nandini, and EC865975 × Kashi Shakti and EC865944 × VRPM-903. The accessions EC865944 and EC865975, sourced from Banaras Hindu University, Varanasi, belong to the late maturity group. In contrast, the genotypes maintained at ICAR-IIVR, including Kashi Ageti, Kashi Udai, Arkel (check), and AP-3 are classified under the early maturity group, while Kashi Shakti and VRPM-903 fall into the mid-maturity group. The emasculation of female parents was done a day before the flower opening, and pollinations were performed with freshly dehisced anthers the following day. The crosses were attempted during the year 2019-20 (based on the first year of testing itself). The F_1s were raised during *Rabi*, 2020-21. A fraction of F_1 seeds were selfed to get F_2 seeds under pot culture conditions in a greenhouse during 2021-22. The number of plants of parental lines and F_1 progenies ranged from 25 to 30. All the parents, F_1s, and their F_2s population, along with the resistant and susceptible check, were grown in subsequent year into two sets; one set under open field conditions, while the other set was grown in plastic portrays for artificial screening under a protected structure at a temperature of 21-25°C. Each plant was tagged and numbered for disease scoring. Data on the inheritance of resistance were then tested for goodness of fit by chi-square test.

Results and Discussion

Initial screening of germplasm

The initial screening against the powdery mildew disease resistance started with a set of 172 accessions of peas under natural epiphytotic conditions. Figure 1 shows the screening of these germplasm at ICAR-IIVR under natural epiphytic conditions with the susceptible lines. Initial evaluation categorized the genotypes into 3 (disease scale; 0 = no infection), 32 (0-1), 35 (2-5), and 102 accessions as (5-9). In the second year (2019-20), a total of 71 accessions were selected and again reevaluated under field conditions.

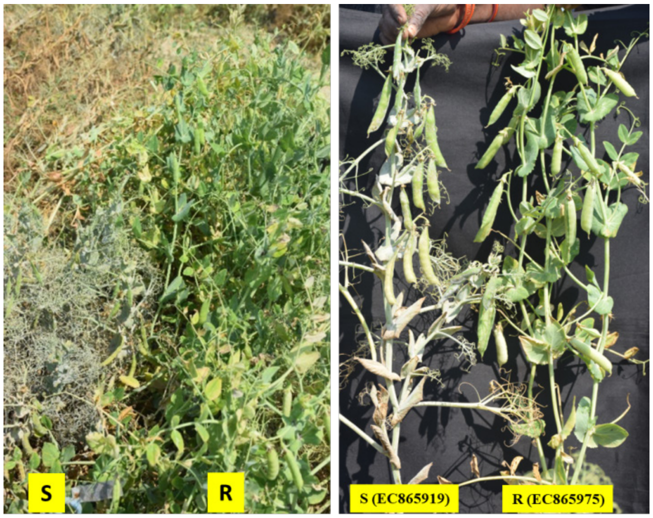

Figure 1: The representative field view of suceptible and resistant accession grown together under natural epiphytic conditions where EC865919 is suceptible genotype while EC865975 is showing resistant response (2018-19).

The genotypes, *viz*., EC865944, IC296678 and EC865975 were identified as highly resistant with a disease score rating of 0. The phenotypic appearances of these three genotypes are given in Figure 2. While, EC865929, EC865925, EC865943, EC865982, EC866032, EC71944, EC6621, IC208366, IC208378, VRP-147, VRP-186, VRP-322, VRP-351, VRP-345, VRP-314, VRP-343, VRP-310, VRP-304, VRP-370, VRP-358, VRP-306, VRP-311, NDVP-12, VRP-90, VRP-27, VRPD-3, VRPD-2, VRPSel-17, Kashi Samridhi, Arka Sampoorna, Arka Karthik, and Kashi Samrath were classified as resistant with a disease score rating of 0-1. Further, the lines, *viz*., EC865951, EC86603, EC865994, IC395609, HUDP-15, VRPSel-17, Arka Ajeet, EC1199, VRPMR-10, CHP-2, VRP-166, VRP-321, VRP-305, VRP-339, VRP-703, VRP-354, VRP-701, VRP-378, No-6, EC-97280, VRP-152, VRP-150, VRPR-1, VRPD-2, VRPD-3, VRP-308, VRP-171, VRP-32, VRP-83, VRP-77, VRP-39, VRP-215, PC-531, VRP-61, VRP-168, and VRP-96 were recorded with disease rating of 2-4 under natural field screening. Finally, we narrowed down the material to around 35 lines (0-1; < 1%) and reconfirmed the resistance response through artificial screening. We want to share that these genotypes belonged to a diverse group, including five varieties, eight exotic and three indigenous collections, two multiple disease-resistant genotypes, and 17 other genotypes. Surprisingly, all these materials were from mid- and late-season groups. We would further like to share that the line IC296678 was augmented from NBPGR, New Delhi, and is already being registered for powdery mildew resistance. Our present findings further validated the resistance in IC296678 under ICAR-IIVR, Varanasi conditions.

In a screening of a large set of germplasm in pea against the powdery mildew, Rana et al. (2013) identified 64 accessions resistant in field screening for two years. However, only fourteen accessions showed resistance under

Figure 2: Plant morphology of identified resistant lines *viz.*, IC296678, EC865944 and EC865975

artificial screening. These studies suggest that there is a low frequency of resistance against the PM disease in the natural population of peas. Thus, the identified sources of resistance against PM may serve as useful genetic material for plant breeders for breeding for resistance against PM in peas.

Histopathological studies

Histopathological studies were also conducted for IC296678, EC865944, and EC865975 along with the susceptible check EC865962. There was no conidial germination on the resistant entries IC296678, EC865975, and EC865944 after 24 and 48 hours after inoculation. The conidia on the moderately resistant entry EC865925 showed less germination in comparison to the susceptible entry EC865962. The appressorium formation was also observed in the susceptible entries (Figure 3). The result of the experiment suggests that there was no spore germination on IC296678, EC865975, and EC865944 and represents a type of pre-invasive immunity against the PM. Artificial screening on the detached leaf of pea is a widely used method for the identification of susceptible and resistant lines in pea and for confirmation of pathogenicity (Tiwari et al. 1997; Thomas and Kenyon 2004; Rana et al. 2012; Rana et al. 2023).

Inheritance study

To understand the nature of gene action in the newly identified PMR accessions EC865975 and EC865944, we undertook a genetic study for devising further breeding program strategies to use them as donor parents. The inheritance of powdery mildew was worked out by utilizing the five cross combinations, *viz.*, EC865975 × Kashi Udai; Kashi Ageti × EC865944; EC865944 × Kashi Nandini (early maturity group); and EC865975 × Kashi Shakti and EC865944 × VRPM-903 (mid-maturity group) on a total F_2 plant population of 908 plants. The parental lines Kashi Udai, Kashi Shakti, Kashi Ageti, VRPM-903, and Arkel are highly susceptible to the powdery mildew. The segregation pattern of the F_2 population of these five crosses revealed a ratio of 1 resistant to 3 susceptible, thereby indicating the presence of a single recessive gene in the donor parents (Table 1). Further, the plants of EC865975 were showing complete resistance with a zero disease score over the years. Previous researchers have investigated the inheritance of powdery mildew resistance and reported different types of inheritance in the pea accessions, including single recessive (León et al. 2020; Harland 1948), single dominant (Fondevilla et al. 2007; Bobkov and Selikhova 2021), and duplicate recessive gene actions (Kumar and Singh 1981). Further, to date, three resistance genes (*er1*, *er2*, and *Er3*) have been known to impart resistance to plants with varying degrees. Of these three genes, two are recessive and one is dominant and widely used in the breeding program. Gene *er1* provides complete to moderate levels of resistance to all plant parts compared to providesed resistance that is confined only to leaves, which is location-specific and reported to be influenced by temperature and leaf age so that complete resistance is expressed only at a temperature of 25°C (Fondevilla et al. 2006). In addition, the resistance gene *er2* is found to be harbored by a few resistant pea accessions only (Devi et al., 2022). The *Er3* gene research is still in the blooming phase, with limited information available.

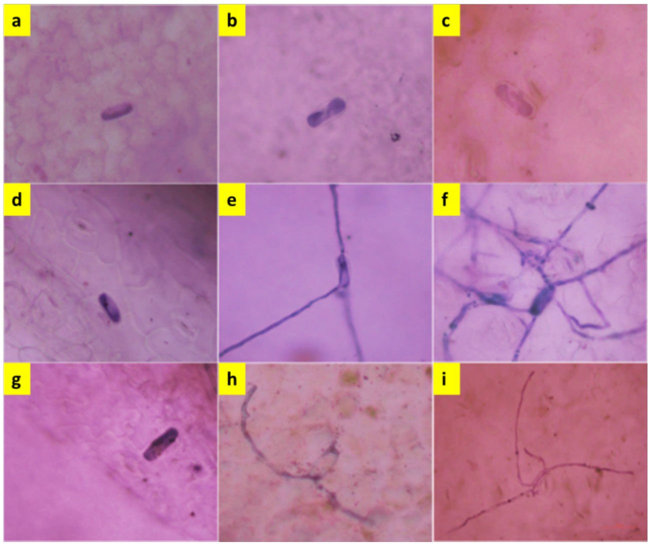

Figure 3: Depicting the conidia germination of powdery mildew on the different test entries where (a): No observed germination of conidia on the leaf of resistant genotype EC865975 after 24 h; (b): No observed germination of conidia on the leaf of resistant genotype EC865975 after 48h; (c): No observed germination of conidia on the leaf of entry resistant genotype EC865944; (d): No observed germinated conidia (just after inoculation) on the susceptible genotype EC865962; (e): Germinated conidia after 24 h on the susceptible test genotype EC865962; (f): Germinated conidia after 48 h on the genotype EC865962; (g): No observed germinated conidia (just after inoculation) on moderately resistant entry EC865925; (h): Germinated conidia on MR genotype EC865925 after 24h after inoculation; (i): Germinated conidia on MR genotype EC865925 after 48h after inoculation.

Horticultural characterization of identified lines along with parents and checks

Since higher yield is always a top priority for the breeders, it is important to characterize these lines for various economic traits. The 10 genotypes evaluated in this study showed

Table 1: Evaluation of F_2 population to study the inheritance of resistance against powdery mildew of pea caused by Erysiphe pisi

Cross	*F_1 Reaction*	*Observed Plants in F_2*	*F_2 segregations*		*Fitness ratio (S:R)*	*χ^2 Cal*	*χ2 Tab (p = 0.05)*
			Susceptible	*Resistant*			
EC865975 × Kashi Udai	S (6)	147	118	29	3:1	2.17	
Kashi Ageti × EC865944	S (6)	192	140	52	3:1	0.44	
EC865944 × Kashi Nandini	S (6)	245	175	70	3:1	1.66	3.841
EC865975 × Kashi Shakti	S (7)	130	104	26	3:1	1.73	
EC865944 × VRPM-903	S (7)	194	150	44	3:1	0.55	

^{a}Reaction rating of F_1 plants is given in parentheses

Table 2: Horticultural characteristics of resistant lines and checks

Traits / *Genotypes*	*DTF*	*PL*	*PW*	*PH*	*PPP*	*10-PW*	*100-SW*	*SPP*	*YPP*
AP3	41.0^d	8.3^{ab}	1.4^a	79.7^c	9.7^d	70.7^a	57.3^a	8.8^a	62.7^{de}
Arkel	34.0^e	7.6^d	1.4^a	34.0^e	5.3^f	62.0^b	50.0^{bc}	7.1^c	29.0^g
EC865975	78.3^a	5.5^f	1.3^a	200.3^a	17.3^b	55.0^c	15.7^f	7.0^{cd}	75.0^{cd}
IC296678	80.7^a	6.1^e	1.0^b	94.3^b	8.7^{de}	43.7^d	37.3^e	6.1^e	31.0^g
EC865944	80.0^a	7.5^d	1.3^a	88.0^b	22.8^a	48.3^{cd}	42.0^d	6.5^{de}	100.7^a
Kashi Ageti	40.0^d	8.5^a	1.4^a	38.0^e	13.0^c	74.3^a	52.0^b	8.3^{ab}	81.7^{bc}
Kashi Nandini	32.0^e	8.2^{abc}	1.4^a	33.7^e	7.2^{ef}	72.3^a	56.0^a	7.4^c	41.7^{fg}
Kashi Shakti	62.7^b	7.9^{bcd}	1.3^a	58.0^d	8.3^{de}	72.0^a	48.3^c	8.2^b	49.3^{ef}
Kashi Udai	33.3^e	7.8^{cd}	1.3^a	36.0^e	6.5^{ef}	74.3^a	52.0^b	7.3^c	41.7^{fg}
VRPM-903	56.3^c	8.2^{abc}	1.4^a	60.7^d	13.6^c	75.3^a	50.0^{bc}	8.5^{ab}	96.7^{ab}

Where mean followed by the same superscripts are not significantly different ($p < 0.05$); DTF: Days To Flower; PL:Pod Length (cm);PW: Pod Width (cm);PPP: Pods/Plant (No.); 10-PW: 10 Pod Weight (g); 100-SW;100-seed weght (g); SPP: Seeds/Pod (no.) and YPP: Yield/Plant (g)

significant variation for various horticultural traits Table 2. Genotypes exhibited significant variation in flowering time, with Kashi Nandini (32.0 days) and Arkel (34.0 days) being the earliest in flowering. In contrast, EC865975 (78.3 days) and EC296678 (80.7 days) showed delayed flowering. Pod length and width were found to be small in EC865975, while it was identified as the tallest among all genotypes. The genotypes, although they have a low 10-pod weight, are statistically at par with AP-3. The genotype EC865944 was also identified among the late-flowering group, with a medium-tall growing habit and a high pod yield/plant contributed mainly by a high pod number. Thus, both these genotypes have equal opportunity for PMR gene introgression with high resistance and pod yield.

Conclusion

We identified three resistant lines, including one previously registered resistant material reconfirmed from the germplasm augmented by NBPGR, New Delhi. Additionally, two exotic lines, EC865944 and EC865975, were also identified as novel sources of powdery mildew resistance governed by a single recessive gene.

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Acknowledgments

The authors express their sincere gratitude to Dr. Ramesh Chand, Former Director, Institute of Agricultural Sciences, BHU, Varanasi, for generously providing the exotic collection for testing at ICAR-IIVR, Varanasi.

References

Bobkov, S.V., Selikhova, T. N. (2021) Introgession of powdery mildew resistance into cultural pea from wild accession of *P. fulvum*. IOP Conference Series Earth and Environmental Science 650, 012091. https://doi.org/10.1088/1755-1315/650/1/012091

Braun, U., & Takamatsu, S. (2000). Phylogeny of *Erysiphe*, *Microsphaera*, Uncinula (Erysipheae) and Cystotheca, Podosphaera, Sphaerotheca (Cystotheceae) inferred from rDNA ITS sequences–some taxonomic consequences. Schlechtendalia, 4, 1-33.

Braun, U., Cook, R. T. A., Inman, A. J., & Shin, H. D. (2001). The taxonomy of the powdery mildew fungi. *The Powdery Mildews:* A Comprehensive Treatis, 13-55.

Devi, J, Mishra, G,P., Sagar, V., Kaswan, V., Dubey, R.K., Singh, P.M., Sharma, S.K., Behera, T.K (2022) Gene-based resistance to *Erysiphe* species causing powdery mildew disease in peas (*Pisum sativum* L.). Genes, 8, 13(2):316. doi: 10.3390/genes13020316.

Devi, J., Dubey, R. K., Sagar, V., Verma, R. K., Singh, P. M., & Behera, T. K. (2023). Vegetable peas (*Pisum sativum* L.) diversity: An analysis of available elite germplasm resources with relevance to crop improvement. Spanish Journal of Agricultural Research, 21(2), e0701. doi.org/10.5424/sjar/2023212-19457.

Devi, J., Sanwal, S. K., Koley, T. K., Mishra, G. P., Karmakar, P., Singh, P. M., & Singh, B. (2019). Variations in the total phenolics and antioxidant activities among garden pea (*Pisum sativum* L.) genotypes differing for maturity duration, seed and flower traits and their association with the yield. Scientia Horticulturae, 244, 141-150.

FAOSTAT (2022) Food and agriculture data. Available at: http://www.fao.org/faostat/en/#home (Accessed 8 May, 2024).

Fondevilla, S., Carver, T.L.W., Moreno, M.T. & Rubiales, D. (2006) Macroscopic and histological characterization of genes *er1* and *er2* for powdery mildew resistance in pea. Eur. J. Plant Pathology, 115, 309–321. doi: 10.1007/s10658-006-9015-6.

Fondevilla, S., Torres, A.M., Moreno, M.T., Rubiales, D. (2007) Identification of a New Gene for Resistance to Powdery Mildew in *Pisum fulvum*, a Wild Relative of Pea. Breeding Science 57, 181–184. https://doi.org/10.1270/jsbbs.57.181

Harland, S. C. (1948). Inheritance of immunity to mildew in peruvian forms of *Pisum sativum*. Heredity 2, 263–269. https://doi.org/10.1038/hdy.1948.15

Katoch, V., Sharma, S., Pathania, S., Banayal, D.K., Sharma, S.K., Rathour, R. (2010) Molecular mapping of pea powdery mildew resistance gene *er2* to pea linkage group III. Mol. Breed. 25, 229–237. doi: 10.1007/s11032-009-9322-7.

Kumar, H., Singh, R. B. (1981) Genetic analysis of adult plant resistance to powdery mildew in pea (*Pisum sativum* L.). Euphytica 30, 147–151. https://doi.org/10.1007/bf00033671

León, D. P., Checa, Ó. E., Obando, P. A. (2020) Inheritance of resistance of two pea lines to powdery mildew. Agronomy Journal 112, 2466–2471. https://doi.org/10.1002/agj2.20253

Rana, C., Sharma, A., Rathour, R., Bansuli, N., Banyal, D. K., Rana, R. S., Sharma, P. (2023) In vivo and in vitro validation of powdery mildew resistance in garden pea genotypes. Scientific Reports 13. https://doi.org/10.1038/s41598-023-28184-0

Rana, J. C., Banyal, D. K., Sharma, K. D., Sharma, M. K., Gupta, S. K., Yadav, S. K. (2012) Screening of pea germplasm for resistance to powdery mildew. Euphytica 189, 271–282. https://doi.org/10.1007/s10681-012-0798-6

Singh, R. S. (2018). *Plant diseases*. Oxford and IBH Publishing. New Delhi, India.

Smith, P.H., Foster, E.M., Boyd, L.A.& Brown, J.K.M. (1996) The early development of *Erysiphe pisi* on *Pisum sativum* L. Plant Pathol. 45:302–309.

Thomas, J., Kenyon, D. (2004) Evaluating resistance to downy mildew (*Peronosporaviciae*) in field peas (*Pisum sativum* L.) and field beans (*Vicia fabae* L.). In: AEP (ed) Proceedings of 5th European conference on grain legumes, Dijon, pp 81–82

Tiwari, K. R., Penner, G. A., Warkentin, T. D., Rashid, K. Y. (1997) Pathogenic variation in *Erysiphepisi*, the casual organism of powdery mildew of pea. Can. J. Plant Pathol. 19, 267–271.

Warkentin, T.D., Rashid, K.Y., Zimmer, R.C. (1995) Effectiveness of a detached leaf assay for determination of the reaction of pea plants to powdery mildew. Can. J. Plant Pathol. 17, 87–89. doi: 10.1080/07060669509500724.

सारांश

मटर, जो ठंडे मौसम की प्रमुख सब्जी वाली दलहनी फसल है, पाउडरी मिल्ड्यू रोग के कारण उत्पादन और गुणवत्ता में भारी नुकसान होता है। यह रोग परजीवी कवक प्रजाति एरिसिफे द्वारा होता है, जिससे उपज में 25-70% तक की कमी हो सकती है, जिससे उत्पाद की गुणवत्ता पर प्रभाव पड़ता है और आर्थिक नुकसान होता है। इस विनाशकारी रोग को प्रबंधित करने के लिए प्रतिरोधी प्रजनन; पर्यावरणीय रूप से स्थायी रणनीतियों में से एक है। तीन वर्षों की अवधि में, पाउडरी मिल्ड्यू प्रतिरोध (PMR) के लिए कुल 172 विभिन्न मटर के प्रभेदो का मूल्यांकन किया गया, जिनमें से 35 प्रभेदो में रोग स्कोर रेटिंग 0-1 पाई गई, जो ≤1% रोग प्रकोप का संकेत देती है। तीन प्रभेद—आई सी 296678, इ सी 865944 और इ सी 865975 में एरिसिफे पिसी के खिलाफ उच्च प्रतिरोधी क्षमता पायी गयी। हिस्टोपैथोलॉजिकल अवलोकनों से पता चला कि प्रतिरोधी लाइनें आई सी 296678, इ सी 865975 और इ सी 865944 पर रोगाणु संक्रमण के 24 और 48 घंटे बाद कोई कवक बीजाणु अंकुरण नहीं हुआ, जो इन जीनोटाइप्स में संक्रमण-पूर्व प्रकार की रोग प्रतिरोधकता को दर्शाता है। इ सी 865944 और इ सी 865975 में पाउडरी मिल्ड्यू प्रतिरोध के जीन क्रिया और वंशागति पैटर्न की जांच के लिए, पाँच क्रॉस संयोजनों का उपयोग किया गया, जैसे इ सी 865975 × काशी उदय, इ सी 865944 × वीआरपीम-903, काशी अगैती × इ सी 865944, इ सी 865944 × काशी नंदिनी, और इ सी 865975 × काशी शक्ति। इन क्रॉस से प्राप्त F2 संख्या के विश्लेषण में 1 प्रतिरोधी और 3 संवेदनशील के पृथक्करण पैटर्न का पाया गया, जो दोनों जीनोटाइप्स में एक एकल अप्रभावी जीन की उपस्थिति का संकेत देता है। इन जीनोटाइप्स का उद्यानिकी लक्षणकरण दर्शाता है कि दोनों, मटर की देर से पकने वाली समूह से संबंधित हैं, जिनकी बढ़वार अधिक होती है, प्रति फली का औसत वजन 5.5 से 7.5 ग्राम के बीच पाया गया और प्रति पौधा औसत उपज 75-100 ग्राम पाया गया। वर्तमान शोध से पहचाने गए पाउडरी मिल्ड्यू प्रतिरोध (PMR) स्रोत न केवल भारतीय प्रजनकों के लिए बल्कि वैश्विक शोधकर्ताओं के लिए भी अमूल्य आनुवंशिक संसाधन प्रदान करेगा, जो टिकाऊ मटर सुधार कार्यक्रम में एक महत्वपूर्ण कदम है।