



## Research Article

# Screening of pea germplasms against insect pests

J. V. Chauhan, Bindu K. Panickar, A. R. Prajapati, J. B. Delvadiya

### Abstract

A field experiment was conducted to screen fifteen germplasms of peas against different insect pests at Pulses Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat during *rabi* 2019-20 and 2020-21. The germplasm HFP 1502 recorded significantly minimum aphid (*Aphis craccivora* Koch) (3.78 aphids/10 cm shoot) whereas, the germplasm Pant P 476 recorded significantly lowest leafhopper (*Empoasca kerri* Pruthi) population (1.96 leafhoppers/3 leaves). Out of fifteen field pea germplasm significantly lowest whitefly (*Bemisia tabaci* Gennadius) population (0.94 whitefly/3 leaves) was noticed on the IPFD 10-12. The *Helicoverpa armigera* Hubner larval population indicated a significant minimum (0.39 larva/plant) on germplasm Pant P 418 and also recorded significantly lower (3.24%) pod damage. The significantly highest seed yield (937 kg/ha) was recorded on Pant P 476 followed by genotypes IPFD 10-12, Prakash, and IPF 18-14.

**Keywords** aphid, field pea, leafhopper, screening, whitefly

### Introduction

Global dietary habits have seen significant changes over the past ten years, primarily as a result of population expansion and prosperity [1]. A growing dietary pattern that can influence the global food system and our environment is the alternative of nourishment for a nutritious diet, such as replacing regular meals of meat with protein-rich plants [2]. Legumes are frequently regarded as inexpensive plant-based sources of protein for human consumption [3-4]. Due to their inherent capacity for symbiotic nitrogen fixing, which increases soil health and efficient use of water, growing legumes have major positive effects on agricultural systems and the ecosystem [5-7].

Despite the many dietary benefits of pulses, their area under cultivation comprised just 12.70 percent (93.18 Mha) as compared to cereal crops (736 Mha) area and 3.0 percent [89.82 Mt (million tons)] of the amount they produced in 2020 [8]. The data reveals how completely unaware governments and growers are regarding the development of pulses on a worldwide scale. Pulses have poor, highly fluctuating, and uncertain productivity in comparison to cereal since they are typically grown in rainfed ecosystems, on poor soils, and in adverse circumstances [9].

After soybeans, peas become the second essential grain legume [10-11]. The domestication of peas with wheat, barley, millet, and other crops dates back to the Stone Age, or more than 20,000 years earlier, making it considered to be one of the oldest crops to be domesticated [12]. The Mediterranean area of Europe and Western Asia in which peas originally emerged [13]. India is the main producer of pulses in worldwide [14]. The area occupied by pulses in India during 2021-22 is 28.80 million hectares with

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25.72 million tonnes of production and productivity to the tune of 892 kg/ha [15]. At a global level, field pea is cultivated over an area of 7.8 million hectares with a production of 13.53 million metric tonnes. In India, pea produces 3% of the total pulse production and 5% of the total pulse area [16]. India is the second largest producer of peas in worldwide [14]. Peas are grown on around 10 lakh hectares of farmland in India, combined with a total yield of 9.2 lakh metric tonnes [17].

Among the various insect pests listed above, leafhopper (*E. kerri*), whitefly (*B. tabaci*), aphid (*A. craccivora*), pod borer (*H. armigera*) and pea leaf miner (*Chromatomyia horticola*) are serious pests attacking plant parts like leaves, buds, flowers and pods of crop [18]. As a result of sucking the sap through the underside surface of leaves by aphids, whiteflies, and leafhoppers significantly reduce field pea yield [19]. During field circumstances, the production of field peas is reduced by 42% as a result of infestations of aphids [20]. Aphid sucks juice from growing tips then covers the whole plant [21]. Field pea crops are seriously harmed by the pod borer (*H. armigera*), a harmful pest that attacks on growing pods and seeds.

Relative susceptibility of different varieties of field pea is scanty in general and particularly in the North Gujarat Agro-climatic Zone. The overuse and unrestricted application of chemicals against infestations of pests causes the emergence of insecticidal resistance [22]. To know the mechanism of resistance against insect-pest complex is also essential for the development of a high-yielding tolerant variety of pea. The use of tolerant cultivars virtually does not involve any skill or costly investment in pest management. The primary goal of several investigators is to discover appropriate cultivars from current resources and release them for the benefit of the agricultural community. Today, testing of varieties for enhancement of production and resistance to particular diseases and pests is a continuous activity [23-25]. Keeping consideration of the losses due to insect pests, the following investigation was undertaken.

## Methodology

A field experiment was conducted to screen fifteen different field pea germplasm against different insect pests at Pulses Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat during *rabi* 2019-20 and 2020-21. The experiment was carried out using Randomized Block Design (RBD) with three replications. Seeds of these germplasms were obtained from the Fourteen different germplasms (Table 1) were obtained from the Pulses Research Station, SDAU, Sardarkrushinagar. The crop was raised by adopting standard agronomical practices and the whole experimental plot was kept free from the application of any pesticides.

## Observations recorded

Fifteen germplasms were raised after following standard agronomical practices. Five plants from each of the treatments were chosen at random and labeled for recording data regarding the population of insect pests. From the second week after planting until the crop reached maturation, measurements were made every week in the early morning hours. A number of sucking pests *viz.*, Aphids were recorded from 10 cm shoots, leafhopper and whitefly were counted on 3 leaves of each tagged plant. Larva of *H. armigera* was recorded randomly from the same selected plants and percent pod damage was recorded at the harvesting stage of the crop. Insecticidal sprays were avoided in the experimental plot. Using the following calculation, the percentage of pod damage was determined:

$$\text{Pod damage (\%)} = \frac{\text{Number of damaged pods}}{\text{Total number of pods}} \times 100$$

The field pea yield was recorded from each plot at the harvesting stage and converted to kg/ha. The data thus obtained were analyzed using appropriate statistical techniques.



**Table 1. List of germplasms**

SN.	Germplasms
1	Pant P 418
2	Pant P 476
3	Pant P 415
4	HFP 1502
5	HFP 1545
6	HFP 1574
7	IPF 18-14
8	IPF 18-20
9	VL 68
10	RFP 2010-21
11	HFP 4
12	HFP 715
13	IPFD 10-12
14	Prakash
15	Adarsh

## Results and Discussion

### *Aphid, Aphis craccivora Koch*

#### *Year: 2019-20*

Significantly minimum aphid population was recorded on genotypes HFP 1502 and was at par with the Adarsh and HFP 1574. It was followed by genotypes HFP 4, IPFD 10-12, Pant P 476, and HFP 1545 with moderately less population of aphids. Whereas, the next group was IPF 18-14, HFP 715, IPF 18-20, Pant P 415, VL 68, and RFP 2010-21, with comparatively high aphids. Among the screened varieties/genotypes significantly maximum aphid population was recorded in Pant P 418 which was found at par with the variety Prakash.

#### *Year: 2020-21*

During the second year genotype HFP 1502 showed a significantly lowest aphid population and was at par with the Adarsh, HFP 1574, and HFP 4. It was followed by IPFD 10-12 with a relatively less population of aphids. While, genotypes Pant P 476, HFP 1545, IPF 18-14, HFP 715, IPF 18-20, Pant P 415, VL 68, and RFP 2010-21 held the third position. Significantly highest aphid population was found in Pant P 418 which was found at par with the variety Prakash.

#### *Pooled*

The pooled data of two successive years shown in Table 2 revealed that the aphid per ten cm shoot population of field pea varieties/genotypes was similar to both years. The ascending trend of varieties/genotypes was: HFP 1502 (3.78) < Adarsh (3.99) < HFP 1574 (5.74) < HFP 4 (7.02) < IPFD 10-12 (7.59) < Pant P 476 (8.45) < HFP 1545 (9.57) < IPF 18-14 (10.93) < HFP 715 (11.15) < IPF 18-20 (12.20) < Pant P 415 (12.37) < VL 68 (12.78) < RFP 2010-21 (15.21) < Prakash (17.59) < Pant P 418 (20.70). The pooled results ultimately indicated that genotype HFP 1502 recorded a significantly minimum aphid population and was at par with the Adarsh and HFP 1574. These were followed by HFP 4, IPFD 10-12, and Pant P 476 held a mediocre position. The next order in the effective group was HFP1545, IPF 18-14, HFP 715, IPF 18-20, Pant P 415, VL 68, and RFP 2010-21 which were at par with each other. However, genotype Pant P 418 was most susceptible as it exhibited significantly maximum infestation of aphids, but was at par with the variety Prakash, as far as susceptibility was concerned. Krishna et al., [26] performed a study in Uttar Pradesh and reported that the maximum aphid population was recorded in a variety Prakash.



Table 2. Screening of field pea varieties/genotypes against Aphid, *A. craccivora*

SN.	Varieties/genotypes	No. of aphid/10 cm shoot		
		2019-20	2020-21	Pooled
1	Pant P 418	4.73 <sup>h</sup> (21.85)	4.48 <sup>f</sup> (19.55)	4.60 <sup>h</sup> (20.70)
2	Pant P 476	3.09 <sup>bcde</sup> (9.07)	2.89 <sup>cd</sup> (7.84)	2.99 <sup>bcde</sup> (8.45)
3	Pant P 415	3.74 <sup>ef</sup> (13.46)	3.43 <sup>de</sup> (11.29)	3.58 <sup>efg</sup> (12.37)
4	HFP 1502	2.16 <sup>a</sup> (4.15)	1.98 <sup>a</sup> (3.42)	2.06 <sup>a</sup> (3.78)
5	HFP 1545	3.34 <sup>bcdef</sup> (10.65)	3.00 <sup>cde</sup> (8.49)	3.16 <sup>cdef</sup> (9.57)
6	HFP 1574	2.82 <sup>ab</sup> (7.44)	2.13 <sup>ab</sup> (4.04)	2.47 <sup>ab</sup> (5.74)
7	IPF 18-14	3.51 <sup>cdef</sup> (11.84)	3.25 <sup>de</sup> (10.03)	3.37 <sup>defg</sup> (10.93)
8	IPF 18-20	3.70 <sup>ef</sup> (13.16)	3.43 <sup>de</sup> (11.25)	3.56 <sup>efg</sup> (12.20)
9	VL 68	3.78 <sup>fg</sup> (13.82)	3.50 <sup>e</sup> (11.74)	3.64 <sup>efg</sup> (12.78)
10	RFP 2010-21	4.35 <sup>gh</sup> (18.43)	3.53 <sup>e</sup> (11.99)	3.94 <sup>gh</sup> (15.21)
11	HFP 4	2.89 <sup>bc</sup> (7.83)	2.59 <sup>abc</sup> (6.22)	2.74 <sup>bc</sup> (7.02)
12	HFP 715	3.55 <sup>def</sup> (12.11)	3.27 <sup>de</sup> (10.20)	3.41 <sup>defg</sup> (11.15)
13	IPFD 10-12	3.02 <sup>bcd</sup> (8.59)	2.66 <sup>bc</sup> (6.59)	2.84 <sup>bcd</sup> (7.59)
14	Prakash	4.41 <sup>h</sup> (18.99)	4.09 <sup>f</sup> (16.20)	4.25 <sup>hi</sup> (17.59)
15	Adarsh	2.20 <sup>a</sup> (4.34)	2.04 <sup>a</sup> (3.65)	2.11 <sup>a</sup> (3.99)
<b>S.Em.±T</b>		0.20	0.18	0.13
<b>Y</b>		-	-	0.04
<b>T × Y</b>				0.19
<b>C.D. at 5 % T</b>		0.58	0.53	0.38
<b>Y</b>		-	-	0.13
<b>T × Y</b>		-	-	0.53
<b>C.V. %</b>		10.15	10.33	10.25

figures in parentheses are retransformed values of  $\sqrt{X} + 0.5$  transformation, Treatment means with the letter(s) in common are not significant by DNMR at 5 percent level of significance

As per the results of Omar et al., [27] among pea germplasm maximum population of aphid were recorded in germplasm KPF 1024 and Pant P 223 (22.80 Aphids/2.5cm long shoots/5 plants) and the minimum in germplasm Vikas, HFP 12, HFP 9907, VL 59, Pant 243, RAU 37, RFP 2009-3, HUDP 15 and Pant P 195 (00 Aphids/2.5cm long shoots/plants). Among the above reference genotypes IPFD 10-12, HFP 4, and HFP 715 strongly support the present finding.

### Leafhopper, *Empoasca kerri Pruthi*

Year: 2019-20

As far as leafhopper population per three leaves was concerned, (Table 3) the chronological order observed was: Pant P 476 (2.45) < IPFD 10-12 (2.58) < HFP 4 (2.66) < IPF 18-20 (2.70) < Pant P 418 (3.62) < IPF 18-14 (3.94) < HFP 1574 (4.23) < Adarsh (4.29) < HFP 1545 (5.13) < Prakash (5.37) < Pant P 415 (5.39) < VL 68 (6.51) < RFP 2010-21(7.03) < HFP 1502 (7.27) < HFP 715 (7.77).



Amongst the fifteen varieties/genotypes screened against the leafhopper population during 2019-20, a significant minimum population was recorded on genotype Pant P 476 and was at par with the IPFD 10-12, HFP 4, IPF 18-20, Pant P 418, IPF 18-14. The second at par series was HFP 1574 and Adarsh. These were followed by HFP 1545, Prakash, Pant P 415, VL68, RFP 2010-21, and HFP 1502. Whereas, a significantly maximum leafhopper population was found on HFP 715.

#### **Year: 2020-21**

The chronological trend of varieties/genotypes based on leafhopper per three leaves population during 2020-21 was (Table 3): Pant P 476 (1.48) < IPFD 10-12 (1.77) < HFP 4 (1.95) < IPF 18-20 (2.07) < Pant P 418 (2.61) < IPF 18-14 (3.09) < HFP 1574 (3.51) < Adarsh (3.53) < HFP 1545 (4.33) < Prakash (4.46) < Pant P 415 (4.58) < VL 68 (5.65) < RFP 2010-21 (6.10) < HFP 1502 (6.35) < HFP 715 (6.99). During *rabi* 2020-21, the significantly lowest leafhopper population was recorded on genotype Pant P 476 and was at par with the IPFD 10-12, HFP 4, IPF 18-20, and Pant P 418. These were followed by IPF 18-14 and the rest of the varieties/genotypes which held a middle position except HFP 715 with the highest leafhopper population.

#### **Pooled**

Two years pooled data of leafhopper revealed (Table 3) the ascending trend of varieties/genotypes based on leafhopper per three leaves as: Pant P 476 (1.96) < IPFD 10-12 (2.17) < HFP 4 (2.30) < IPF 18-20 (2.38) < Pant P 418 (3.11) < IPF 18-14 (3.51) < HFP 1574 (3.87) < Adarsh (3.91) < HFP 1545 (4.73) < Prakash (4.91) < Pant P 415 (4.98) < VL 68 (6.08) < RFP 2010-21 (6.56) < HFP 1502(6.81) < HFP 715 (7.38). The pooled result indicated that Pant P 476 recorded the significantly lowest leafhopper population and was in turn at par with genotypes IPFD 10-12, HFP 4, IPF 18-20, Pant P 418, IPF 18-14 which held a mediocre position. It was followed by HFP 1574 and Adarsh. Whereas, HFP 1545, Prakash, Pant P 415, VL 68, and RFP 2010-21 were at par and held the next position. Among the evaluated varieties/genotypes maximum leafhopper population was found on HFP 715 which was at par with genotype HFP 1502. Biswal and Patel [29] screened out fifteen genotypes, genotype Pant P167, IPFD 10-12, and IPFD 10-13 recorded the minimum population of leafhoppers. Among the above reference genotypes IPFD 10-12 is more or less in line with the present finding.

#### **Whitefly, *Bemisia tabaci* Gennadius**

##### **Year: 2019-20**

Amongst the different 15 varieties/genotypes, the significantly lowest population was observed on the IPFD 10-12 and was at par with the variety/genotype RFP 2010-21 and Prakash. The second at-par series was Pant P 476 and IPF 18-14. These were followed by IPF 18-20, Pant P 418, HFP 4, HFP 1574, VL 68, Adarsh, Pant P 415, HFP 1545 and HFP 715. Whereas, the significantly highest whitefly population was recorded on HFP 1502.

##### **Year: 2020-21**

During the second year also genotype IPFD 10-12 recorded the least whitefly population and was at par with the RFP 2010-21 and Prakash. The second effective group is Pant P 476 and IPF 18-14 with a relatively less population of whiteflies. Whereas moderate whitefly population was recorded in IPF 18-20, Pant P 418, HFP 4, HFP 1574, VL 68, Adarsh, Pant P 415 and HFP 1545 held a mediocre position. Significantly highest whitefly population was found on HFP 1502 which was found at par with genotype HFP 715.

#### **Pooled**

Two years pooled data of whitefly per three leaves revealed the ascending trend of varieties/genotypes as (Table 4): IPFD 10-12 (0.94) < RFP 2010- 21 (1.81) < Prakash (1.88) < Pant P 476 (3.21) < IPF 18-14 (3.23) < IPF 18-20 (3.39) < Pant P 418 (3.99) < HFP 4 (4.87) < HFP 1574 (4.99) < VL 68 (5.10) < Adarsh (5.51) < Pant P 415 (6.57) < HFP 1545 (6.67) < HFP715 (7.28) < HFP 1502 (7.93).

**Table 3. Screening of field pea varieties/genotypes against leafhopper, *E. kerri***

SN.	Varieties/genotypes	No. of leaf hopper/3 leaves		
		2019-20	2020-21	Pooled
1	Pant P 418	2.03 <sup>abc</sup> (3.62)	1.76 <sup>abc</sup> (2.61)	1.90 <sup>abc</sup> (3.11)
2	Pant P 476	1.72 <sup>a</sup> (2.45)	1.41 <sup>a</sup> (1.48)	1.56 <sup>a</sup> (1.96)
3	Pant P 415	2.43 <sup>cd</sup> (5.39)	2.25 <sup>de</sup> (4.58)	2.34 <sup>def</sup> (4.98)
4	HFP 1502	2.79 <sup>de</sup> (7.27)	2.62 <sup>ef</sup> (6.35)	2.70 <sup>f</sup> (6.81)
5	HFP 1545	2.37 <sup>cd</sup> (5.13)	2.20 <sup>de</sup> (4.33)	2.28 <sup>cde</sup> (4.73)
6	HFP 1574	2.18 <sup>bc</sup> (4.23)	2.00 <sup>cd</sup> (3.51)	2.09 <sup>bcd</sup> (3.87)
7	IPF 18-14	2.11 <sup>abc</sup> (3.94)	1.90 <sup>bcd</sup> (3.09)	2.00 <sup>abcd</sup> (3.51)
8	IPF 18-20	1.79 <sup>ab</sup> (2.70)	1.60 <sup>abc</sup> (2.07)	1.70 <sup>ab</sup> (2.38)
9	VL 68	2.65 <sup>de</sup> (6.51)	2.48 <sup>ef</sup> (5.65)	2.57 <sup>efg</sup> (6.08)
10	RFP 2010-21	2.74 <sup>de</sup> (7.03)	2.57 <sup>ef</sup> (6.10)	2.66 <sup>efg</sup> (6.56)
11	HFP 4	1.78 <sup>ab</sup> (2.66)	1.56 <sup>ab</sup> (1.95)	1.67 <sup>a</sup> (2.30)
12	HFP 715	2.88 <sup>e</sup> (7.77)	2.74 <sup>f</sup> (6.99)	2.81 <sup>f</sup> (7.38)
13	IPFD 10-12	1.75 <sup>a</sup> (2.58)	1.51 <sup>ab</sup> (1.77)	1.63 <sup>a</sup> (2.17)
14	Prakash	2.42 <sup>cd</sup> (5.37)	2.23 <sup>de</sup> (4.46)	2.33 <sup>def</sup> (4.91)
15	Adarsh	2.19 <sup>bc</sup> (4.29)	2.01 <sup>cd</sup> (3.53)	2.10 <sup>bcd</sup> (3.91)
<b>S.Em.± T</b>		0.13	0.13	0.09
<b>Y</b>		-	-	0.03
<b>T × Y</b>		-	-	0.13
<b>C.D. at 5 % T</b>		0.37	0.38	0.26
<b>Y</b>		-	-	0.09
<b>T × Y</b>		-	-	0.36
<b>C.V. %</b>		10.06	11.20	10.60

figures in parentheses are retransformed values of  $\sqrt{X} + 0.5$  transformation, Treatment means with the letter(s) in common are not significant by DNMR at 5 per cent level of significance

The results ultimately indicated that genotype IPFD 10-12 had significantly the lowest whitefly population and was at par with IPFD 2010-21 and Prakash followed by genotype Pant P 476. Whereas, IPF 18-14, IPF18-20, Pant P 418, HFP 4, HFP 1574, VL 68, Adarsh, Pant P 415, HFP 1545 held a mediocre position. Among the evaluated genotypes, significantly the highest population was found on HFP 1502 which was at par with genotype HFP 715. Biswal and Patel [29] revealed that the genotypes IPFD 10-12, Pant P 167, and IPFD 10-13 had significant minimum population whereas, RFP 2009-4, HFP-4, HUDP 954, KPMF 400, HFP 715, IPFD-1, LEP 477, Pant P101, HFP 716, DF-1 and IPF 99-25 which exhibited maximum population. Among the above reference genotypes IPFD 10-12, HFP 4, and HFP 715 conformed with the present finding.



Table 4. Screening of field pea varieties/genotypes against whitefly, *B. tabaci*

SN.	Varieties/genotypes	No. of whitefly/3 leaves		
		2019-20	2020-21	Pooled
1	Pant P 418	2.25 <sup>cd</sup> (4.55)	1.99 <sup>cd</sup> (3.44)	2.11 <sup>def</sup> (3.99)
2	Pant P 476	2.08 <sup>bc</sup> (3.80)	1.77 <sup>bc</sup> (2.62)	1.92 <sup>bcd</sup> (3.21)
3	Pant P 415	2.93 <sup>ef</sup> (8.03)	2.37 <sup>elg</sup> (5.12)	2.64 <sup>ghi</sup> (6.57)
4	HFP 1502	3.08 <sup>f</sup> (8.93)	2.73 <sup>g</sup> (6.93)	2.89 <sup>hi</sup> (7.93)
5	HFP 1545	2.93 <sup>ef</sup> (8.07)	2.41 <sup>elg</sup> (5.28)	2.66 <sup>ghi</sup> (6.67)
6	HFP 1574	2.47 <sup>cde</sup> (5.58)	2.22 <sup>de</sup> (4.40)	2.34 <sup>efg</sup> (4.99)
7	IPF 18-14	2.08 <sup>bc</sup> (3.80)	1.78 <sup>bc</sup> (2.66)	1.92 <sup>cd</sup> (3.23)
8	IPF 18-20	2.12 <sup>cd</sup> (3.97)	1.83 <sup>c</sup> (2.82)	1.97 <sup>de</sup> (3.39)
9	VL 68	2.52 <sup>cde</sup> (5.80)	2.22 <sup>de</sup> (4.40)	2.37 <sup>efg</sup> (5.10)
10	RFP 2010-21	1.59 <sup>a</sup> (2.02)	1.46 <sup>ab</sup> (1.61)	1.51 <sup>a</sup> (1.81)
11	HFP 4	2.43 <sup>cd</sup> (5.37)	2.21 <sup>de</sup> (4.38)	2.32 <sup>defg</sup> (4.87)
12	HFP 715	2.95 <sup>ef</sup> (8.20)	2.62 <sup>g</sup> (6.36)	2.78 <sup>hi</sup> (7.28)
13	IPFD 10-12	1.22 <sup>a</sup> (0.98)	1.19 <sup>a</sup> (0.91)	1.20 <sup>a</sup> (0.94)
14	Prakash	1.64 <sup>ab</sup> (2.16)	1.46 <sup>ab</sup> (1.61)	1.54 <sup>a</sup> (1.88)
15	Adarsh	2.60 <sup>def</sup> (6.23)	2.31 <sup>def</sup> (4.79)	2.44 <sup>fgh</sup> (5.51)
<b>S.Em.± T</b>		0.15	0.11	0.09
<b>Y</b>		-	-	0.03
<b>T × Y</b>		-	-	0.13
<b>C.D. at 5 % T</b>		0.44	0.34	0.27
<b>Y</b>		-	-	0.09
<b>T × Y</b>		-	-	0.38
<b>C.V. %</b>		11.45	10.05	10.89

figures in parentheses are retransformed values of  $\sqrt{X} + 0.5$  transformation, Treatment means with the letter(s) in common are not significant by DNMR at 5 per cent level of significance

### Pod borer, *Helicoverpa armigera* Hubner

#### Year: 2019-20

As far as varieties/genotypes based on larval population (larvae/plant) was concerned, (Table 5) the ascending order was: Pant P 418 (0.49) < IPF 18-20 (0.55) < IPFD 10-12 (0.69) < Prakash (0.80) < Pant P 476 (0.99) < HFP 1545 (1.00) < RFP 2010-21 (1.17) < VL 68 (1.20) < HFP 715 (1.33) < IPF 18-14 (1.39) < HFP 1502 (1.40) < Pant P 415 (1.55) < Adarsh (1.60) < HFP 1574 (1.69) < HFP 4 (1.84). Genotype Pant P 418 showed significantly lowest larval population and was at par with IPF 18-20, IPFD 10-12, Prakash, Pant P 476, and HFP 1545. The next effective group was RFP 2010-21, VL68, and HFP 715 with a relatively less population of *H. armigera*. These were followed by IPF 18-14, HFP 1502, Pant P 415, Adarsh, and HFP 1574 which were at par with each other. Genotype HFP 4 showed the significantly highest larval population.



Table 5. Screening of field pea varieties/genotypes against pod borer, *H. armigera*

SN.	Varieties/genotypes	No. of pod borer larvae/plant		
		2019-20	2020-21	Pooled
1	Pant P 418	1.00 <sup>a</sup> (0.49)	0.90 <sup>a</sup> (0.30)	0.94 <sup>a</sup> (0.39)
2	Pant P 476	1.23 <sup>abcd</sup> (0.99)	1.12 <sup>abcd</sup> (0.75)	1.16 <sup>abcd</sup> (0.87)
3	Pant P 415	1.44 <sup>d</sup> <sup>e</sup> (1.55)	1.40 <sup>ef</sup> (1.46)	1.41 <sup>ef</sup> (1.50)
4	HFP 1502	1.39 <sup>cde</sup> (1.40)	1.34 <sup>def</sup> (1.27)	1.35 <sup>def</sup> (1.33)
5	HFP 1545	1.23 <sup>abcd</sup> (1.00)	1.19 <sup>bcde</sup> (0.92)	1.20 <sup>bcde</sup> (0.96)
6	HFP 1574	1.49 <sup>de</sup> (1.69)	1.48 <sup>f</sup> (1.66)	1.47 <sup>f</sup> (1.67)
7	IPF 18-14	1.38 <sup>cde</sup> (1.39)	1.33 <sup>def</sup> (1.26)	1.35 <sup>def</sup> (1.32)
8	IPF 18-20	1.03 <sup>a</sup> (0.55)	0.98 <sup>ab</sup> (0.45)	0.99 <sup>ab</sup> (0.50)
9	VL 68	1.31 <sup>bcde</sup> (1.20)	1.23 <sup>bcdef</sup> (1.00)	1.26 <sup>cdef</sup> (1.10)
10	RFP 2010-21	1.30 <sup>bcde</sup> (1.17)	1.22 <sup>bcdef</sup> (0.97)	1.25 <sup>cdef</sup> (1.07)
11	HFP 4	1.53 <sup>e</sup> (1.84)	1.47 <sup>f</sup> (1.66)	1.49 <sup>f</sup> (1.75)
12	HFP 715	1.36 <sup>bcde</sup> (1.33)	1.27 <sup>cdef</sup> (1.10)	1.31 <sup>def</sup> (1.21)
13	IPFD 10-12	1.09 <sup>ab</sup> (0.69)	1.02 <sup>abc</sup> (0.53)	1.05 <sup>abc</sup> (0.61)
14	Prakash	1.14 <sup>abc</sup> (0.80)	1.12 <sup>abcd</sup> (0.74)	1.12 <sup>abcd</sup> (0.77)
15	Adarsh	1.45 <sup>de</sup> (1.6)	1.40 <sup>ef</sup> (1.46)	1.42 <sup>ef</sup> (1.53)
<b>S.Em.± T</b>		0.07	0.07	0.05
<b>Y</b>		-	-	0.01
<b>T × Y</b>		-	-	0.07
<b>C.D. at 5 % T</b>		0.22	0.21	0.14
<b>Y</b>		-	-	0.05
<b>T × Y</b>		-	-	0.21
<b>C.V. %</b>		10.37	10.43	10.40

figures in parentheses are retransformed values of  $\sqrt{X} + 0.5$  transformation, Treatment means with the letter(s) in common are not significant by DNMR T at 5 per cent level of significance

#### Year: 2020-21

In the second year, the significantly lowest larval population was recorded on Pant P 418 and was turned at par with the IPF 18-20, IPFD 10-12, Prakash and Pant P 476. The mediocre series were HFP 1545, RFP 2010-21, and VL 68. These were followed by HFP 715, IPF 18-14, HFP1502, Pant P 415 and Adarsh. Among the evaluated genotypes, the significantly highest population of *H. armigera* was found on HFP 4 which in turn at par with genotype HFP 1574.

#### Pooled

Two years pooled data (Table 5) indicated the ascending order of susceptibility of field pea genotypes to *H. armigera* larval population: Pant P 418 (0.39) < IPF 18-20 (0.50) < IPFD 10-12 (0.61) < Prakash (0.77) < Pant P 476 (0.87) < HFP 1545 (0.96) < RFP 2010-21 (1.07) < VL 68 (1.10) < HFP 715 (1.21) < IPF 18-14 (1.32) < HFP 1502 (1.33) < Pant P 415 (1.50) < Adarsh (1.53) < HFP 1574 (1.67) < HFP 4 (1.75).





The results ultimately indicated that the significantly lowest larval population was observed on genotype Pant P 418 and was at par with the IPF 18-20, IPFD 10-12, Prakash, and Pant P 476. The next effective genotype was HFP 1545. Whereas, a moderate larval population was recorded in RFP 2010-21, VL68, HFP 715, IPFD 18-14, HFP 1502, Pant P 415 and Adarsh. While the significantly highest larval population was found on HFP 4 which was a turn at par with HFP1574. Krishna et al., [28] at Ayodhya, Uttar Pradesh reported that out of the 50 germplasms, none of the germplasm evaluated could find places under resistant, susceptible, and highly susceptible categories. In which germplasm Prakash, HFP 4, and Adarsh were placed in moderately resistant categories which more or less supported the present findings. As per the findings of Omar et al., [30], maximum pod borer population was recorded in field pea germplasm VL 201 (4.47 pod borer per plant) and minimum in germplasm IPFD 12-2, Pant P 222, RAU 37, HUDP 1302, Pant 243, IPF 13-13, HFP 5, IPF 13-14, HFP 8909 and Pant P 195 (00 pod borer per plant).

### ***Pod damage***

#### ***Year: 2019-20***

Significantly minimum per cent pod damage was found in genotype Pant P 418 and was turned at par with IPF 18-20, IPFD 10-12, Prakash, Pant P 476, HFP 1545, and RFP 2010-21. The next effective genotypes were VL 68 and HFP 715 with relatively less per cent pod damage which was at par with IPF 18-14, HFP 1502, Pant P 415, Adarsh, and HFP 1574. Significantly maximum per cent pod damage was recorded on genotype HFP 4.

#### ***Year: 2020-21***

Genotype Pant P 418 recorded significantly lowest percent pod damage and was turned at par with IPF 18-20, IPFD 10-12, Prakash, Pant P 476, HFP 1545, RFP 2010-21, VL 68, HFP 715, and IPF 18-14. The medium effective genotype was HFP 1502. While, Pant P 415, Adarsh, and HFP 1574 were at par with genotype HFP 4 which recorded significantly higher pod damage (%).

### ***Pooled***

The pod damage (%) pooled results presented in (Table 6) in ascending order was: Pant P 418 (3.24) < IPF 18-20 (3.37) < IPFD 10-12 (3.83) < Prakash (4.13) < Pant P 476 (4.30) < HFP 1545 (4.45) < RFP 2010-21 (4.75) < VL 68 (5.19) < HFP 715 (5.27) < IPF 18-14 (5.53) < HFP 1502 (5.74) < Pant P 415 (6.73) < Adarsh (7.12) < HFP 1574 (7.31) < HFP 4 (7.60). The results ultimately indicated that genotype Pant P 418 recorded the lowest percent pod damage and was in turn at par with IPF 18-20, IPFD10-12, Prakash, Pant P 476, HFP 1545, RFP 2010-21, VL 68, and HFP 715. These were followed by IPF 18-14 and HFP 1502 which had relatively high pod damage. Whereas, Pant P 415 and Adarsh held mediocre positions. Significantly maximum per cent pod damage was found on HFP 4 which was turn at par with HFP 1574. According to Mittal and Ujagir [31] screened 165 germplasm of pea at Pantnagar and revealed that the minimum percent pod borer damage was found in germplasm P 4107 (0.33 %) and maximum in P 4039 (4.33%). Whereas, germplasm HFP 4 recorded medium (1.67) per cent pod damage, these results are in support of present findings.

### ***Seed yield***

#### ***Year: 2019-20***

The yield data of field pea seeds in different fifteen varieties/genotypes at harvest are presented in Table 7. There was a significant difference among the varieties/genotypes for seeds yield. The chronological order of varieties/genotypes based on seed yield (kg/ha) was: Pant P 476 (922) < IPFD 10-12 (802) < Prakash (791) < IPF 18-14 (710) < RFP 2010-21 (673) < IPF 418 (660) < HFP 4 (613) < IPF 18-20 (544) < Adarsh (503) < VL 68 (428) < HFP 1574 (353) < Pant P 415 (328) < HFP 1502 (288) < HFP 1545 (270) < HFP 715 (257). Genotype Pant P 476 produced significantly maximum field pea seeds. The second effective group was IPFD 10-12, Prakash, and IPF 18-14.



Table 6. Pod damage of *H. armigera* in different varieties/genotypes of field pea

SN.	Varieties/genotypes	Pod damage (%) at harvest		
		2019-20	2020-21	Pooled
1	Pant P 418	10.40 <sup>a</sup> (3.30)	10.21 <sup>a</sup> (3.18)	10.31 <sup>a</sup> (3.24)
2	Pant P 476	11.92 <sup>abc</sup> (4.30)	11.76 <sup>abc</sup> (4.30)	11.84 <sup>ab</sup> (4.30)
3	Pant P 415	15.10 <sup>def</sup> (6.81)	14.89 <sup>cde</sup> (6.66)	15.00 <sup>cd</sup> (6.73)
4	HFP 1502	13.85 <sup>cdef</sup> (5.75)	13.79 <sup>bcde</sup> (5.73)	13.82 <sup>bcd</sup> (5.74)
5	HFP 1545	12.21 <sup>abc</sup> (4.50)	12.04 <sup>abc</sup> (4.40)	12.13 <sup>ab</sup> (4.45)
6	HFP 1574	15.65 <sup>ef</sup> (7.37)	15.49 <sup>de</sup> (7.26)	15.57 <sup>d</sup> (7.31)
7	IPF 18-14	13.63 <sup>cdef</sup> (5.59)	13.49 <sup>abcde</sup> (5.47)	13.56 <sup>bcd</sup> (5.53)
8	IPF 18-20	10.74 <sup>ab</sup> (3.50)	10.31 <sup>a</sup> (3.24)	10.53 <sup>a</sup> (3.37)
9	VL 68	13.25 <sup>bcde</sup> (5.28)	13.02 <sup>abcde</sup> (5.11)	13.14 <sup>abcd</sup> (5.19)
10	RFP 2010-21	12.63 <sup>abcd</sup> (4.80)	12.52 <sup>abcd</sup> (4.71)	12.58 <sup>abc</sup> (4.75)
11	HFP 4	16.07 <sup>f</sup> (7.72)	15.81 <sup>e</sup> (7.48)	15.95 <sup>d</sup> (7.60)
12	HFP 715	13.39 <sup>bcde</sup> (5.39)	13.07 <sup>abcde</sup> (5.16)	13.23 <sup>abcd</sup> (5.27)
13	IPFD 10-12	11.49 <sup>abc</sup> (4.00)	11.04 <sup>ab</sup> (3.67)	11.27 <sup>ab</sup> (3.83)
14	Prakash	11.80 <sup>abc</sup> (4.20)	11.61 <sup>ab</sup> (4.06)	11.71 <sup>ab</sup> (4.13)
15	Adarsh	15.38 <sup>ef</sup> (7.12)	15.31 <sup>de</sup> (7.13)	15.35 <sup>cd</sup> (7.12)
<b>S.Em.± T</b>		0.80	0.96	0.62
<b>Y</b>		-	-	0.22
<b>T × Y</b>		-	-	0.88
<b>C.D. at 5 % T</b>		2.32	2.78	1.75
<b>Y</b>		-	-	0.63
<b>T × Y</b>		-	-	2.47
<b>C.V. %</b>		10.52	12.85	11.73

figures in parentheses are retransformed values of arc sine transformation, Treatment means with the letter(s) in common are not significant by DNMR at 5 per cent level of significance

Whereas, a significantly minimum yield was observed on genotype HFP 715 which was found at par with HFP 1502 and HFP 1545.

#### Year: 2020-21

Field pea seed yield is concerned (Table 7), there was a significant difference among the varieties/genotypes for yield. The chronological order of varieties/genotypes based on seeds yield (kg/ha) was: Pant P 476 (952) < IPFD 10-12 (828) < Prakash (800) < IPF 18-14 (739) < RFP 2010-21 (700) < Pant P 418 (685) < HFP 4 (641) < IPF 18-20 (565) < Adarsh (530) < VL 68 (442) < HFP 1574 (370) < Pant P 415 (359) < HFP 1502 (311) < HFP 1545(297) < HFP 715 (271). Genotype Pant P 476 produced a significantly highest (952 kg/ha) field of pea seeds. The next effective groups were IPFD 10-12, Prakash, and IPF 18-14. Whereas, significantly lowest yield was observed on genotype HFP 715 which was at par with HFP 1502 and HFP 1545.



Table 7. Seed yield of field pea varieties/genotypes

SN.	Varieties/genotypes	Yield (kg/ha)		
		2019-20	2020-21	Pooled
1	Pant P 418	660 <sup>c</sup>	685 <sup>d</sup>	673 <sup>c</sup>
2	Pant P 476	922 <sup>a</sup>	952 <sup>a</sup>	937 <sup>a</sup>
3	Pant P 415	328 <sup>fg</sup>	359 <sup>gh</sup>	344 <sup>fg</sup>
4	HFP 1502	288 <sup>g</sup>	311 <sup>h</sup>	300 <sup>g</sup>
5	HFP 1545	270 <sup>g</sup>	297 <sup>h</sup>	284 <sup>g</sup>
6	HFP 1574	353 <sup>fg</sup>	370 <sup>gh</sup>	362 <sup>fg</sup>
7	IPF 18-14	710 <sup>bc</sup>	739 <sup>bcd</sup>	725 <sup>bc</sup>
8	IPF 18-20	544 <sup>de</sup>	565 <sup>ef</sup>	555 <sup>de</sup>
9	VL 68	428 <sup>f</sup>	442 <sup>gh</sup>	435 <sup>ef</sup>
10	RFP 2010-21	673 <sup>c</sup>	700 <sup>cd</sup>	687 <sup>c</sup>
11	HFP 4	613 <sup>cd</sup>	641 <sup>de</sup>	627 <sup>cd</sup>
12	HFP 715	257 <sup>g</sup>	271 <sup>h</sup>	264 <sup>g</sup>
13	IPFD 10-12	802 <sup>b</sup>	828 <sup>b</sup>	815 <sup>b</sup>
14	Prakash	791 <sup>b</sup>	800 <sup>bc</sup>	796 <sup>b</sup>
15	Adarsh	503 <sup>ef</sup>	530 <sup>fg</sup>	517 <sup>ef</sup>
<b>S.Em.± T</b>		35.62	32.99	24.27
<b>Y</b>		-	-	8.86
<b>T × Y</b>		-	-	34.33
<b>C.D. at 5 % T</b>		103.27	95.64	67.97
<b>Y</b>		-	-	24.82
<b>T × Y</b>		-	-	96.13
<b>C.V. %</b>		11.33	10.07	10.70

Treatment means with the letter(s) in common are not significant by DNMRT at 5 percent level of significance

### Pooled

The two years pooled data (Table 7), showed significant differences among the varieties/genotypes for yield. The sequential order of varieties/genotypes based on seeds yield (kg/ha) was: Pant P 476 (937) < IPFD 10-12 (815) < Prakash (796) < IPF 18-14 (725) < RFP 2010-21(687) < Pant P 418 (673) < HFP 4 (627) < IPF 18-20 (555) < Adarsh (517) < VL 68 (435) < HFP 1574 (362) < Pant P 415 (344) < HFP 1502 (300) < HFP 1545 (284) < HFP 715 (264). Whereas, genotype Pant P 476 produced significantly highest yield of field peas. These were followed by IPFD 10-12, Prakash, and IPF 18-14. Whereas, significantly lowest yield was observed on genotype HFP 715 which was at par with HFP 1502 and HFP 1545. Mittal and Ujagir [28] reported that germplasm HFP 4 recorded comparatively less (344.91 kg/ha) grain yield.

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