

Resistant evaluation of chickpea genotypes against chickpea (*Cicer arietinum*) Pod Borer, *Helicoverpa armigera* in field

SH. AKBARI¹, Z. TAHMASEBI^{1✉} and H. KANOUNI²

1. Agricultural College, Ilam University, Ilam, Iran; 2. Research Associate, Agronomy and plant breeding department, Field and Horticultural Crops Research Unit, Agricultural and Natural Resources Research and Education Center of Kurdistan, Agricultural Research, Education and Extension Organization, Sanandaj, Iran

(Received: Dec. 2021; Accepted: June 2022)

Abstract

Chickpea pod borer (CPB), *Helicoverpa armigera* (Hubner) (Lepidoptera: Noctuidae), is the most important pest on chickpea (*Cicer arietinum*), which causes substantial yield losses. This study was carried out to screen resistance of 40 chickpea accessions against CPB in a field trial in a randomized complete block design (RCBD) with three replications in Eslamabad-e Gharb. Plant infestation with this pest was done at the podding stage. In this experiment several traits including pod borer's population, percentage of pod damage and grain yield were measured. The results indicated that genotypes responded differently to CPB. Also, the yield of all lines in infestation condition decreased, but there was a significant difference between the lines. FL IP99-48C demonstrated to be the most susceptible with the least yield. FL IP07-40C (that is Kabuli type) and Pirouz (that is a Desi genotype) recorded as the most resistant genotypes in terms of reducing the CPB population and the highest yield that can be used in breeding programs in the future.

Keywords: Breeding program, damage, grain yield

ارزیابی مقاومت ژنوتیپ‌های نخود *Cicer arietinum* در برابر کرم غلاف‌خوار *Helicoverpa armigera* در مزرعه

شکوفه اکبری^۱، زهرا طهماسبی^{۱✉}، همایون کانونی^۲

۱- گروه زراعت و اصلاح نباتات، دانشکده کشاورزی و منابع طبیعی، دانشگاه ایلام، ایلام، ایران؛ ۲- بخش تحقیقات گیاهان زراعی و باغی، مرکز تحقیقات کشاورزی و منابع طبیعی کردستان، سازمان تحقیقات، آموزش و ترویج کشاورزی، سنندج، ایران

چکیده

کرم غلاف‌خوار (*Helicoverpa armigera*) (Lepidoptera: Noctuidae) مهم‌ترین آفت مزارع نخود است که باعث کاهش عملکرد قابل توجهی در نخود می‌شود. این مطالعه برای غربالگری مقاومت ۴۰ لاین نخود در برابر کرم غلاف‌خوار در قالب طرح بلوک‌های کامل تصادفی در سه تکرار در مزرعه‌ای آزمایشی در شهرستان اسلام آباد غرب انجام شد. آلودگی در مرحله غلاف‌دهی انجام شد. در این آزمایش جمعیت کرم غلاف‌خوار، درصد خسارت غلاف و عملکرد دانه اندازه‌گیری شد. نتایج نشان داد که ژنوتیپ‌های نخود به آسیب ناشی از کرم غلاف‌خوار واکنش متفاوتی نشان دادند و میزان عملکرد همه لاین‌ها در شرایط آلودگی کاهش داشت ولی بین لاین‌ها تفاوت معنی‌داری وجود داشت. FL IP99-48C حساس‌ترین ژنوتیپ با کمترین عملکرد بود. ژنوتیپ‌های FL IP07-40C (از نوع کابلی) و پیروز (از نوع دسی) کمترین جمعیت کرم غلاف‌خوار و بالاترین عملکرد را داشتند و به‌عنوان مقاوم‌ترین ژنوتیپ‌ها انتخاب شدند. بنابراین از این ژنوتیپ‌ها می‌توان در برنامه‌های اصلاحی در آینده استفاده کرد.

واژه‌های کلیدی: برنامه‌های اصلاحی، خسارت، عملکرد دانه

Introduction

Chickpea, *Cicer arietinum* (L.), is the third most important grain legume in the world. It contains a great deal of protein as a highly nutritive food, insoluble and soluble fiber, and energy, which can be considered as the cheapest source available (Bhatt *et al.*, 2001).

Gram pod borer, *Helicoverpa armigera* (Hubner) (Lepidoptera: Noctuidae) is the most important pest limiting chickpea's yield potential that severely damages a great variety of crops (Karthik and Vastrad, 2018). This pest is a polyphagous insect and can be found on over 180 types of cultivated crops (Bouslama *et al.*, 2019). Such pests can cause significant losses in the semi-arid tropical regions, resulting in more than \$328 million in yield loss (ICRISAT, 1992). According to the available reports, In Iran, this species is found in most regions, including the provinces of Ilam, Hamedan, Kermanshah, Lorestan, East and West Azerbaijan, for example in the farms of Islamabad, Kermanshah, and has caused 14% damage (Noori, and Shahryari, 1985). The rate of contamination in Maragheh rainfed fields without spraying is 20.54% (Hashemi Aghajari, and Hasanpour Hosni, 1994).

Although this pest is primarily managed chemically, several chemical insecticides have already been reported to have no effect; in other words, these pests became resistant to insecticides. (Ahmad *et al.* 2006; Xu *et al.* 2005). Using Host plant resistance (HPR) is vital in *H. armigera* management. The development of resistant crop cultivars against pod borer can be one of the most economical and ecological methods; especially under subsistence farming conditions in developing countries (Sharma *et al.*, 1999).

Similarly, several studies have investigated on the chickpea varieties screening to evaluate their resistance and tolerance ((Borikar *et al.*, 1982; Dias *et al.*, 1983; Nadeem *et al.*, 2011; Sarwar *et al.*, 2013; Bouslama, *et al.*, 2019; Jakhar *et al.*, 2018). The ICRISAT gene bank located at Patancheru, India protects a global repository with over 17,000 accessions of chickpea. In addition, more than 14,000 breeding lines and germplasm accessions were screened at ICRISAT, Patancheru and the All India Coordinated Pulses Improvement Project (AICPIP) centers that caused the introduction of numerous genotypes with resistance levels ranging from moderate to low against *H. armigera* and using

them in breeding programs. Under natural infestation conditions at test locations, some of these have been demonstrated to be resistant in various agro-climatic zones. Additionally, several chickpea wild relatives (such as *Cicer bijugum*, *C. judaicum*, and *C. pinnatifidum*) are known to have high levels of resistance to pod borer (Sharma *et al.*, 2003).

As the introduction of resistant plants against insect pests in IPM (integrated pest management) is of high importance, this study aimed to screen advanced Kabuli chickpea genotypes against pod borer in field circumstances.

Materials and Methods

Field trial and crop management

The experiment was performed at the experimental field area of Shian Agricultural Service Center, Eslamabad-e Gharb, Kermanshah, Iran. Forty advanced Kabuli chickpea genotypes (except for Pirouz that is Desi type) and a susceptible control FL IP99-48C (table 1) were sown in March 2019. All genotypes were of ICARDA¹ origin except Jam and Pirouz, which are of Iranian origin. The study was conducted in a randomized complete block design (RCBD) with three replications. The distance between plants and rows was 10 and 50 cm, respectively. There were four rows, each with 5 m length, in experimental plots. Two border-rows of linseed were cultivated to differentiate each experimental plot. All agronomic practices were performed under pesticide-free conditions during the entire growing season according to the crop requirements. The weeds were controlled manually and test materials were not fertilized or irrigated. In each replication, all of the cultural methods were carried out in the same way.

Pod borer infestation

The genotypes were closely examined at weekly interval from the germination but there isn't any natural infestation in the plots. Therefore, at the podding stage, plants of each plot were randomly infested with nearly ten chickpea pod borers collected from near fields, where naturally infested with this pest. The infestation was conducted by releasing larvae next to them to allow pests to enter.

¹ The International Center for Agricultural Research in the Dry Areas (ICARDA)

Table 1. The list of genotypes used in the present study.

No.	Genotype name	No.	
1	SEL99 TH150144	21	FLIP84-182C
2	FLIP97-85C	22	FLIP85-01C
3	FLIP00-39C	23	FLIP86-06C
4	FLIP97-230C	24	FLIP87-45C
5	FLIP99-26C	25	FLIP88-85C
6	FLIP02-84C	26	ILC72
7	FLIP02-512C	27	ILC484
8	FLIP00-84C	28	ILC482
9	FLIP01-9C	29	FLIP93-58C
10	FLIP01-18C	30	FLIP98-121C
11	FLIP98-15C	31	FLIP01-29C
12	FLIP99-45C	32	FLIP02-51C
13	FLIP98-108C	33	FLIP03-8C
14	FLIP97-26C	34	FLIP03-123C
15	FLIP99-48C	35	FLIP03-142C
16	FLIP93-255C	36	FLIP07-40C
17	FLIP97-211C	37	FLIP07-98C
18	Mansure (FLIP98-55C)	38	FLIP07-139C
19	Jam	39	FLIP07-297C
20	Pirouz	40	FLIP01-40C

Data collection

One week after infection. Larva count of pod borer were recorded per meter row per replication.

At the harvest time, considering the border effects in five plants of each row per replicate were randomly selected. The pod damage was determined by counting the total number of pods and damaged ones by dividing the number of damaged pods by the total number of pods and multiplying 100, the percentage (%) of damaged pod was calculated. Furthermore, the number of healthy and damaged seeds and the number of larvae were counted. The seed yield was determined. In addition, the percentage of damage and yield of genotypes compared to check genotype (FL IP99-48C) was calculated as a percentage (Nadeem *et al.*, 2011).

Data analysis

Data analysis was performed using SAS software (SAS Institute Inc., 2013). ANOVA analysis was performed with a randomized complete block design, and LSD (Least Significant Difference) was used for mean comparisons at the 5% significance level.

Studied genotypes differed significantly in the survival of *H. armigera* larvae ($F_{df=39, dfe=78}=5.63, P=0.01$), explaining how parents were selected for the study.

FL IP98-121C has achieved the highest (5) average larval population (number) on plants per meter row length. FL IP99-48C had the lowest larval population mean (1.94) (table 2).

Results**Pod damage**

In terms of resistance to pod borer, there were significant differences among genotypes ($F_{df=39, dfe=78}=12.64, P=0.01$). According to Table 2, damaged pods of CPB were reported at the lowest level (1.37 and 1.93 %, respectively) during the maturity of Pirouz and FL IP07-40C genotypes with 75.59 and 65.48 %, respectively decrease in pod damage over the check; however, the highest pod damage (5.6%) was observed in check genotype FL IP99-48C.

Grain yield

The results revealed that the studied genotypes differ significantly in terms of grain yield ($F_{df=39, dfe=78}=21.25, P=0.01$). Pirouz and FLIP 07-40C recorded the highest average of grain yield (838.77 and 716.07 kg ha⁻¹, respectively) compared to others with 77.8% and 46.49 % increase over the check, respectively. This genotype proved to be highly resistant against *H. armigera*; which finally, led to excellent yield that can be used by farmers for general agriculture. The lowest yield (617.07 kg ha⁻¹) was observed in check genotype FL IP99-48C caused by its susceptibility (table 2).

Table 2. Mean larval population, pod damage of CPB and grain yield and their difference (%) over check in chickpea genotypes
(Means sharing similar letters are statistically non-significant at $P = 0.05$).

Genotypes	Larval population	Pod damage (%)	Pod damage difference over check (%)	Grain yield (kg/ha)	Grain yield difference over check (%)
Pirouz	2.63g-j	1.37p	-75.59	838.77a	71.59
FLIP 07-40C	2.67g-j	1.93op	-65.48	716.07a	46.49
FLIP 87-45C	3.97a-f	2.17no	-62.5	625.93n	28.05
FLIP 07-98C	2.6g-j	2.1no	-61.31	617.07n	26.24
FLIP 07-297C	3.93a-f	2.23m-o	-60.71	655.47g-l	34.09
FLIP 01-40C	4.13a-e	2.23m-o	-60.71	650.57h-m	33.09
FLIP 02-51C	2.33ij	2.27l-o	-60.71	812.1a	66.14
Jam	2.57h-j	2.2m-o	-60.12	660.27g-k	35.07
FLIP 07-139C	2.97f-j	2.2m-o	-60.12	668.47f-j	36.75
ILC 482	3.67c-g	2.2m-o	-59.52	682.23c-h	39.57
FLIP 00-39C	3.77b-f	2.33k-o	-58.93	670.3e-j	37.13
FLIP 84-182C	3f-j	2.33k-o	-58.93	638.43j-n	30.61
FLIP 97-85C	3.6e-h	2.37k-o	-58.33	624.3n	27.72
SEL 99 TH150454	4.37a-e	2.3k-o	-58.33	681.43c-h	39.40
FLIP 97-26C	4.67a-d	2.3k-o	-57.74	676.73d-i	38.44
FLIP 86-06C	3.4e-i	2.43k-o	-57.14	647.97i-n	32.56
FLIP 85-01C	3f-j	2.4k-o	-56.55	642.4j-n	31.42
FLIP 97-230C	3f-j	2.57i-n	-54.17	687.73	40.69
FLIP 88-85C	3.67c-g	2.7h-n	-51.79	712.97b-e	45.86
ILC 484	4.17a-e	2.87f-l	-50	630.93k-n	29.078
Mansour	2.47j	2.8g-m	-50	658.97g-k	34.81
ILC 72	3.67c-g	2.8g-m	-48.81	638.43j-n	30.61
FLIP 97-211C	2.3j	2.9f-k	-48.21	630.93k-n	29.07
FLIP 98-108C	4.5a-d	2.9f-k	-48.21	656.57g-l	34.32
FLIP 99-45C	3.67c-g	3.03e-j	-45.83	642.6j-n	31.46
FLIP 99-26C	4.73a-c	3.13d-i	-44.05	687.43b-g	40.63
FLIP 02-512C	3.83b-f	3.23c-h	-42.86	662.1g-k	35.45
FLIP 93-58C	3.67c-g	3.27c-h	-42.86	621.8mn	27.20
FLIP 93-255C	2.3j	3.2d-h	-42.26	701.43b-e	43.50
FLIP 01-9C	3.67c-g	3.2d-h	-41.67	621.8mn	27.20
FLIP 98-121C	1.93j	3.37c-g	-41.07	708.77b-d	45.00
FLIP 01-29C	2.2j	3.37c-g	-39.88	656.57g-l	34.32
FLIP 00-84C	4.83ab	3.3c-h	-39.88	658.97g-k	34.81
FLIP 02-84C	2.6g-j	3.43c-f	-38.69	700.77b-f	43.36
FLIP 03-123C	2.5ij	3.67b-d	-35.71	642.6j-n	31.46
FLIP 03-8C	2.33ij	3.6b-e	-34.52	686.1b-g	40.36
FLIP 03-142C	2.6g-j	3.83bc	-31.55	715.17b	46.31
FLIP 98-15C	4a-f	4.17b	-26.79	666.1g-j	36.27
FLIP 01-18C	4a-f	4.1b	-25.59	682.23c-h	39.57

Discussion

Results on chickpea genotypes screening illustrated that all genotypes responded differently to gram pod borer, *H. armigera*, under field situation. Similarly, Nadeem *et al.*, 2011 and Sarwar, 2013 reported *Helicoverpa* moths were more attracted to some chickpea genotypes than others. Many morphological characteristics, which contribute to antixenosis, have been used to breed pod borer-resistant varieties. Morphological traits such as pod trichome length and density, pod wall thickness, pod length, breadth and area, and the number of pods per plant showed influence on pod borer resistance in chickpea (Hossain *et al.* 2008). Our results showed that some chickpea genotypes were more attractive to *Helicoverpa* moths than the others. The preference or non-preference for oviposition on chickpea by female moth may be due to its varying behavioral response possibly due to different canopy structure of the plants. One possible explanation for these variations may be the variability in oviposition response of adult females due to chickpea foliar secretions containing high concentrations of malic acid (Rembold, 1981).

The mean pod damage among the test entries ranged from 1.36 to 5.6%. Similarly, Shabbir *et al.* (2014) reported CPB damage up to 7.16% on chickpea genotypes. But these results were highly significant with those of other researches, the range of damage recorded by others varied greatly that is, 19.53 to 40.83% (Parvez *et al.*, 1996); 12.63 to 33.05% (Sarwar *et al.*, 2009); 11.55 to 48.11% (Khan *et al.*, 2009); 13.24 to 38.0% (Sarwar *et al.*, 2011); and 12.18 to 23.12%

(Sarwar, 2013). These deviations in pod damage may be conceivably owing to variations in local climatic conditions and the type of genotypes tested.

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Pirouz and FLIP 07-40C had the greatest grain yield (838.77 and 716.07 kg ha⁻¹, respectively). These lines also had the least *H. armigera* damage. These results are in agreement with Shankar *et al.*, (2014) and Jakhar *et al.*, (2018) who revealed that grain yield was significantly greater in resistance lines than in susceptible check and significantly maximum pod damage among the selected genotypes.

The results demonstrated the potentials of host plant resistance in the management of *H. armigera*. As compared to other genotypes FL IP07-40C and Pirouz genotypes exhibited least pod damage. Different nutritive values of host plants may also influence the rate of development of *H. armigera* larvae, thus affecting the population dynamics of this pest (Hemati *et al.*, 2012). These genotypes can be used in a plant breeding program in the future. High resistance in our study represents a valuable insect tolerance source that could be exploited by their direct release as a variety or by development of resistant germplasms by using them in hybridization. Inheritance of resistance to pod borer and grain yield were different in some chickpea types under unprotected conditions. An understanding of inheritance of resistance is essential for a systematic and efficient approach for genetic enhancement of pod borer resistance in chickpea. Such pest management tools like host plant resistance, if extensively deployed may have positive impact on the environment by reducing the amount of chemical pesticide uses in chickpea crop.

Acknowledgments

Chickpea accessions were obtained from Agricultural and Natural Resources Research and Education Center of Kurdistan, Sanandaj, Iran. Also This study was supported financially by Ilam University

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