Significance of the family *Braconidae* in regulating moth population in agrobiocenosis

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Abstract. This article discusses the importance of representatives of the *Braconidae* family in regulating the number of harmful moths in various agrobiocenoses. In order to determine the species composition and biological features of the development of the entomophage in the Tashkent region, samples of eggs, larvae and butterflies occurring moth. Along with this, moth larvae affected by entomophages were collected and determined by which entomophage they were affected. As a result, in 2015-2016, 527 infected moth larvae were detected, of which 381 larvae were affected by species of the family *Braconidae*, the rest 146 by other entomophages. Of the braconids, 17 species were noted. The identified species include *Apanteles pallipes* Reinh, *Apanteles ruficrus* Hal., *Apanteles telengai* Tobias., *Apanteles kazak* Tel., *Apanteles vanessae* Reinh, *Meteorus rubens* Nees., *Microgaster mediator* Hal., *Microgaster sordipes* Nees, *Microgaster vidua* Ruthe., *Macrocentrus collaris* Spin., *Bracon hebetor* Say, *Bracon radialis* Tel., *Bracon telengai* Mul., *Rogas dimidiatus* Spin., *Rogas pallidator* Thunb., *Chelonus oculator* Panz., *Chelonus luzhetzkii*.
Keywords. Agrobiocenosis, agricultural crops, pests, moth, parasitic entomophages, biological efficiency.

1 Introduction

Representatives of the *Braconidae* family occupy a prominent place in the system of biological plant protection [1]. The parasite of caterpillars of harmful Lepidoptera Bracon (*Bracon hebetor* Say) is annually used in our republic against moth on an area of 1.8 million hectares and multiplies in more than 850 biological laboratories [2]. The quality of breeding technology and species composition affect its effectiveness in regulating abundance. Many world researchers paid attention to the development of bracon and its species composition [3-5].

According to Kopanevani [3], among the parasitic entomophages, the *Braconidae* family is the most richly represented in the species composition, since about 3000 species develop on the territory of the CIS [1-3, 6].

The Indian scientist Lal in the 40s of the last century pointed out that despite the absence of external differences between *Bracon hebetor* and *B. brevicornis*, the same pests feed on different species [7]. Also, Puttarudria and Chana Basavanna pointed out that the species *Bracon hebetor* and *B. brevicornis* do not differ in their genitalia and can interbreed, leaving

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fertile offspring, despite this they belong to different species [8]. Since 1956, it has been customary in India to classify existing Bracon species as *Bracon hebetor* [1, 2, 4].

Bogachev and Tobias [9], based on the work of many scientists, came to the conclusion that the species *Bracon brevicornis* Wesin; *Bracon vernalis* Sxepl.; *Bracon simonovi* Kok; *Bracon kitcheneri* D.Q.; *Bracon turcestanicus* Tel.; *Bracon juglandis* Ashm.; *Bracon plotnicovi* Bog.; and, *Bracon fkavus* Tel. are synonymous with *Bracon hebetor* Say. Tobias in his work gave a morphological description of this species [2, 10].

Kimsanbaev [1-4] carried out deep studies on the mass reproduction of bracons in the laboratory and obtained good results. He received 4 compositions of nutritious food for breeding bracon in the biolaboratory.

2 Materials and methods

The studies were carried out in horticultural, vegetable farms, on crops of corn and cotton in Kibrai, Bekabad, Buka and Akkurgan districts of the Tashkent region of Uzbekistan. In order to determine the species composition and biological features of the development of the entomophage, we collected samples of eggs, larvae and butterflies found moth. Along with this, moth larvae affected by entomophages were collected and determined by which entomophage they were affected. As a result, it was found that 95% of moth larval lesions were on *Bracon hebetor*.

The research was carried out in 2015-2016. The collected samples were placed separately in test tubes (50-HRP), delivered, and developed under favorable conditions of the biolaboratory [3, 5].

The systematic affiliation of the affected larvae and the entomophage that flew out of it was determined. The mean and maximum values of parasite species and their population density were calculated.

To obtain moth eggs, the butterflies were placed in 3 liter jars inside which black rags of matter were introduced and oviposition was noted within 24 hours. Along with this, to determine the biological features of development and species, moth larvae were individually placed in test tubes (50-HP), fed with a softened mass of mung bean seeds, the time of transition to the pupal phase and the emergence of butterflies was noted.

3 Results and discussion

As a result of research on cotton, mung beans, beans, corn, vegetable crops and in gardens, 17 moth species were identified. Samples of juices belonging to the following species were selected: *Agrotis segetum* Schiff., *Agrotis obesa.* B, *Agrotis exclamationis.* L, *A.ipsilon* Hufn., *Agrotis xanthgrapha* F., *Autographa gamma*. L, *Helicoverpa armigera.*Hbn, *Heliothis virihlaca* Hufn, *Noctua arbona* Hnfn, *Spodoptera exigua* Hb, *Mamestra suase* Schiff, *Syngrapha circumflexa* L, *Xestia c-ni Turn*. L, *Leucania loreyi* Dup., *Euxoa agricola* B.

The most common in agrocenoses were: cotton moth, winter moth, gamma moth, and wild moth. Depending on the crop, cotton moth, winter moth, wild moth, alfalfa moth, and gamma moth have been frequently observed on cotton. On tomato crops: cotton moth, gamma moth, black moth, garden or excellent moth, arbon moth, tobacco moth, winter moth, and circuflex moth. On corn: cotton moth, moth leokani, winter moth, moth-gamma, exclamation moth. Mung beans and beans are damaged by winter moth, cotton moth, caradryna, moth-gamma, wild moth, tobacco moth, and excellent moth. Moth composition data are shown in Tables 1 and 2.

Table 1. Species of moth and their parasites - representatives of this family (Tashkent region, 2018).

#	**Order Lepidoptera: Family *Noctuidae***	**Parasite moth-species of the family *Braconidae***	**Identified moth hosts**	**Parasite:host ratio**
1	*Heliothis virihlaca Hufn.*	*Microgaster sordipes Nees,*	*Syngrapha circumflexa L*	1:18
2	*Noctua arbona Hnfn.*	*Microgaster vidua Ruthe.*	*Autographa gamma. L*	1:21
3	*Leucania loreyi Duponchel.*	*Macrocentrus collaris Spin.*	*Agrotis segetum Schiff*	1:16
4	*Laphigma exigua Hb.*	*Bracon hebetor Say*	*Helicoverpa armigera.Hbn Heliothis virihlaca Hufn*	1:8

According to our observations, moth larvae are most severely affected by parasites during the year in July, August, September and October. In other periods, the defeat of larvae is less noticeable, mainly infected larvae of young ages were noted. Mainly older larvae of *Helicoverpa armigera.* Hbn, *Heliothis virihlaca* Hufn, *Noctua arbona* Hnfn, *Leucania loreyi* Dup., *Agrotis segetum* Den. species were affected.

Table 2. Moth species and their parasites are representatives of the family *Braconidae* found in agrobiocenoses (Tashkent region, 2020).

#	**Order *Lepidoptera*: Family *Noctuidae***	**Parasite moth-species of the family *Braconidae***	**Identified moth hosts**	**Parasite: host ratio**
1	*Agrotis segetum Den.et Schiff.*	*Apanteles pallipes Reinh*	*Autographa gamma. L*	1:14
2	*Agrotis obesa B.*	*Apanteles ruficrus Hal.*	*Helicoverpa armigera.Hbn*	1:11
3	*Agrotis exclamationis L.*	*Apanteles telengai Tobias.*	*Agrotis segetum Schiff Autographa gamma. L*	1:12
4	*Agrotis ipsilon Hufn.*	*Apanteles kazak Tel.*	*Helicoverpa armigera.Hbn Leucania loreyi Dup.*	1:18
5	*Agrotis xanthgrapha F.*	*Apanteles vanessae Reinh*	*Autographa gamma. L*	1:22
6	*Autographa gamma L.*	*Meteorus rubens Nees.*	*Autographa gamma. L Agrotis ipsilon Hufn. Agrotis segetum Schiff*	1:28
7	*Helicoverpa armigera Hbn.*	*Microgaster mediator Hal.*	*Autographa gamma. L Noctua arbona Hnfn Spodoptera exigua Hb Mamestra suase Schiff*	1:43

8	*Heliothis virihlaca Hufn.*	*Microgaster sordipes Nees,*	*Euxoa agricola B. Syngrapha circumflexa L*	1:23
9	*Noctua arbona Hnfn.*	*Microgaster vidua Ruthe.*	*Autographa gamma. L*	1:34
10	*Leucania loreyi Duponchel.*	*Macrocentrus collaris Spin.*	*Agrotis segetum Schiff Agrotis ipsilon Hufn.*	1:26
11	*Laphigma exigua Hb.*	*Bracon hebetor Say*	*Helicoverpa armigera.Hbn Heliothis virihlaca Hufn Leucania loreyi Dup. Agrotis ipsilon Hufn. Agrotis segetum Schiff*	1:9
12	*Mamestra suase Schiff.*	*Bracon radialis Tel.*	*Syngrapha circumflexa. L*	1:36
13	*Ochopleura flammarta Den.et. Schiff.*	*Bracon telengai Mul.*	*Agrotis obesa. B Agrotis segetum Den.et Schiff.*	1:32
14	*Plusia chrysitis L.*	*Rogas dimidiatus Spin.*	*Agrotis exclamationis.L*	1:44
15	*Syngrapha circumflexa L.*	*Rogas pallidator Thunb.*	*Helicoverpa armigera.Hbn Spodoptera exigua Hb Leucania loreyi Dup.*	1:38
16	*Xestia c-ni Turn L.*	*Chelonus oculator Panz.*	*Spodoptera exigua Hb*	1:27
17	*Euxoa agricola B.*	*Chelonus luzhetzkii Tobias.*	*Helicoverpa armigera.Hbn Agrotis exclamationis.L*	1:19

According to the collected samples, 527 infected moth larvae were found, of which 381 larvae were affected by species of the fam. *Braconidae*, the rest 146 by other entomophages. Of the braconids, 17 species were noted. The identified species include *Apanteles pallipes* Reinh, *Apanteles ruficrus* Hal., *Apanteles telengai* Tobias*., Apanteles kazak* Tel., *Apanteles vanessae* Reinh, *Meteorus rubens* Nees., *Microgaster mediator* Hal*., Microgaster sordipes* Nees, *Microgaster vidua* Ruthe., *Macrocentrus collaris* Spin., *Bracon hebetor* Say, *Bracon radialis* Tel., *Bracon telengai* Mul., *Rogas dimidiatus* Spin., *Rogas pallidator* Thunb., *Chelonus oculator* Panz., *Chelonus luzhetzkii.*

4 Conclusions

It follows from our study that representatives of the *Braconidae* family, parasites of harmful moth, are of great importance for obtaining environmentally friendly products in agrobiocenoses. In the regulation of their numbers, a large place is given to the prevalence of parasites, the volume of their population, and species composition.

We have identified more than 30 species of parasitic entomophages of the main phytophages of cotton agrobiocenosis. Of the most frequently encountered species were braconid species. Of the total number of entomophages, braconids accounted for 29.2%. The dominant species were *Apanteles talengai, A.vanessae, A.spectabilis, Bracon hebetor, Rogas dimidiatus, R.pallidator, R.rossicus.* On horticultural crops, representatives of the *Braconidae* family accounted for 42.6%. These include *Apanteles talengai, Bracon hebetor, Rogas dimidiatus, R.pallidator, R.rossicus, Microgaster mediator Hal., M. sordipes*. *Apanteles talengai, Bracon hebetor, Rogas pallidator, R.rossicus* (38,6%) were noted on vegetables, and on cereals, *Apanteles talengai, A.vanessae, A.spectabilis, Bracon hebetor, Rogas dimidiatus, R.pallidator, R.rossicus* were detected, which accounted for 22.3% of the total number of entomophages.

Therefore, braconids play an important and effective role in regulating the abundance of harmful moth. Mass reproduction of bracon in laboratory conditions creates a resource-saving and effective technology for the control of lepidoptera pests, as well as a reduction in the harmful effects of moth in agrobiocenoses.

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