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Diversity of insects under the effect of Bt maize and insecticides

Diversidade de insetos sob a influência do milho Bt e inseticidas

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ABSTRACT: The genetically modified maize to control some caterpillars has been widely used in Brazil. The effect of Bt maize and insecticides was evaluated on the diversity of insects (species richness and abundance), based on the insect community, functional groups and species. This study was conducted in genetically modified maize MON810, which expresses the Cry1Ab protein from *Bacillus thuringiensis* Berliner, and conventional maize with and without insecticide sprays (lufenuron and lambda-cyhalothrin) under field conditions in Ponta Grossa (Paraná state, Brazil). Insect samplings were performed by using pitfall trap, water tray trap and yellow sticky card. A total of 253,454 insects were collected, distributed among nine orders, 82 families and 241 species. No differences were observed in the insect community based on the richness, diversity and evenness indices. Predators and pollinators were more abundant in genetically modified maize. Parasitoids, detritivores, sap-sucking herbivores and chewing herbivores were more abundant in conventional maize with insecticide sprays. Significant differences were found for the species *Colopterus* sp., *Colaspis occidentalis* (L.) and *Nusalala tessellata* (Gerstaecker) which were most abundant in Bt maize, and *Dalbulus maidis* and *Condylostylus* sp.2 in conventional maize.

KEYWORDS: Cry1Ab; biodiversity; pyrethroid; natural enemies.

RESUMO: O milho geneticamente modificado visando ao controle de lagartas tem sido amplamente utilizado no Brasil. Em estudo de campo realizado em Ponta Grossa (Paraná, Brasil), compararam-se, com base na diversidade (riqueza de espécies e abundância), os efeitos do milho Bt e do controle químico sobre a comunidade de insetos, grupos funcionais e espécies. A comunidade de insetos foi amostrada no milho geneticamente modificado MON810, que expressa a proteína Cry1Ab de *Bacillus thuringiensis* Berliner, e no milho convencional com e sem a aplicação de inseticidas (lufenuron e lambda-cialotrina). As amostragens foram realizadas por meio da coleta de insetos utilizando-se armadilha de queda, bandeja-d'água e cartão adesivo. Foram coletados 253.454 insetos, distribuídos em nove ordens, 82 famílias e 241 espécies. Não foram observadas diferenças na comunidade de insetos para os índices de riqueza, diversidade e equitabilidade nos tratamentos avaliados. Predadores e polinizadores foram mais abundantes no milho geneticamente modificado, e parasitoides, decompositores, sugadores e mastigadores, no milho convencional com inseticida. Diferenças significativas foram detectadas para as espécies *Colopterus* sp., *Colaspis occidentalis* (L.) e *Nusalala tessellata* (Gerstaecker), mais abundantes no milho Bt, e *Dalbulus maidis* e *Condylostylus* sp.2, mais abundantes no milho convencional.

PALAVRAS-CHAVE: Cry1Ab; biodiversidade; piretroide; inimigos naturais.

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INTRODUCTION

The global area of transgenic crops increased in recent years, reaching 181.1 million hectares in 2016, and Brazil is the second country in area planted with transgenic crops (49.1 million hectares) (ISAAA, 2016). The genetically modified maize MON810 expressing the Cry1Ab protein of *Bacillus thuringiensis* Berliner (Bt) was developed for the control of *Ostrinia nubilalis* (Hübner). In Brazil, the main target pest of Bt technology in maize is the fall armyworm *Spodoptera frugiperda* (J. E. Smith), the most important crop pest in the country. After the release of commercial planting of maize MON810 (CTNBIO, 2011), in 2007, the area planted with Bt crops has been progressively increasing. Currently, about 88.4% of the maize planted area in Brazil use transgenic hybrids (CELERES, 2017), and several events of transgenic maize are available for commercial planting, many containing two or more proteins.

Several studies have been carried out to evaluate the effect of genetically modified maize on pest insects (MENDES et al., 2011; VOJTECH et al., 2005) and on non-target organisms, both under laboratory (MEISSLE et al., 2005; MENDES et al., 2012) and under the field conditions (CANDOLFI et al., 2004; LOPEZ et al., 2005; FERNANDES et al., 2007). However, few studies have evaluated the effect of genetically modified maize on the insect community (CANDOLFI et al., 2004; ROSE; DIVELY, 2007).

Most field studies have revealed that the abundance and the activity of parasitoids and predators are similar in Bt and non-Bt crops (SISTERSON et al., 2004). In contrast, insecticide sprays have shown negative effects on biological control agents (MEISSLE; LANG, 2005; ROSE; DIVELY, 2007). Therefore, it is expected that the use of transgenic plants will reduce the application of insecticides, a fact that may contribute to biological control.

Under the hypothesis that different methods of pest control have different effects on the community of insects, functional groups and species, the objectives of this work were: to use the first event of genetically modified maize (MON810) released commercially in Brazil, as a model to evaluate the effect of Bt maize on insect diversity (abundance and species richness); and to compare, based on the insect community, functional groups and also, at the species level, the use of Bt maize and insecticides.

MATERIAL AND METHODS

The study was carried out in Ponta Grossa, PR, Brazil (25º05'42" S, 50º09'43" W and 969 m), during the first maize planting season from December 1999 to March 2000. Ponta Grossa is located in the Southern region of Brazil and represents an important area of maize production. The experiment was carried out according to the approval and recommendations of the biosafety regulations of the National Technical Biosafety Commission (CTNBio).

The event of the genetically modified maize used was MON810 (Monsanto do Brasil Ltda., São Paulo, Brazil), that expresses the Cry1Ab protein of *B. thuringiensis* aiming resistance to lepidopteran-pest species. The evaluated treatments were: genetically modified maize (MON) and conventional maize (hybrid DKB 806) with and without insecticide sprays (CCI and CSI, respectively). Each treatment was represented by an area of one hectare. The insecticides used in CCI treatment were lufenuron and lambda-cyhalothrin at a dose of 15 g (active ingredient) ha^{-1}. Two sprays of insecticides were carried out (5 and 18 January 2000) when reaching the threshold level for *S. frugiperda*. All cultural practices, except the insecticide sprays, were the same in all three treatments and followed the agronomic practices for the region. Planting was carried out on December 24, 1999.

The insect community was evaluated using a pitfall (plastic cylinder with 10 cm in diameter and 20 cm high, buried and maintained at ground level, containing water and detergent), water tray trap (yellow square container with 30 cm wide and 6 cm high, placed on the ground, containing water and detergent) and yellow sticky card (yellow rectangular plate of 24 × 10 cm with glue on both sides, that was affixed in wooden stake in three heights: 50; 100 and 150 cm). In each treatment 10 pitfalls and 10 water trays traps were installed, distributed uniformly (approximately 14 m between traps) on each of the diagonals of the area, and 12 yellow sticky cards at four sampling points. Insect collections were carried out weekly for pitfalls and water trays traps and biweekly for the yellow sticky cards throughout the crop cycle, starting three days after the maize emergence. The different types of traps aimed to capture insects of different habits to encompass the insect community present in the crop. The insects were sent to taxonomists and identified at the genus or species level. When it was not possible, the identification was made at the morphospecies level. The insects were separated into functional groups according to food habits: predators, parasitoids, pollinators, detritivores, sap-sucking herbivores and chewing herbivores, and selected species were highlighted for each group as to abundance and /or to be cited in the literature associated with the maize crop.

For the evaluation of the insect community, the treatments were analyzed by calculating the Margalef richness index (α), Shannon-Wiener diversity index (H') and Pielou evenness index (E). Through the faunistic analysis the predominant species were selected, those ones that stood out to obtain the highest levels of abundance, frequency, constancy and dominance. To compare the treatments, the principal component analysis (PCA) was used, by procedure PROC PRINCOMP (SAS INSTITUTE, 2001). PCA was performed on the covariance matrix computed between the predominant species of each treatment, using the collection periods as repetitions. With this procedure, the eigenvectors and their associated eigenvalues were extracted and projected on the first two orthogonal axes. The hypothesis of significant differences between the treatments was verified by the Kruskal-Wallis test of the principal components generated by the procedure PROC NPAR1WAY (SAS INSTITUTE, 2001). The variables abundance, number of species and richness (α) and diversity (H') indices were compared between the treatments using *t*-test at the 0.05 probability level (SAS INSTITUTE, 2001).

RESULTS AND DISCUSSION

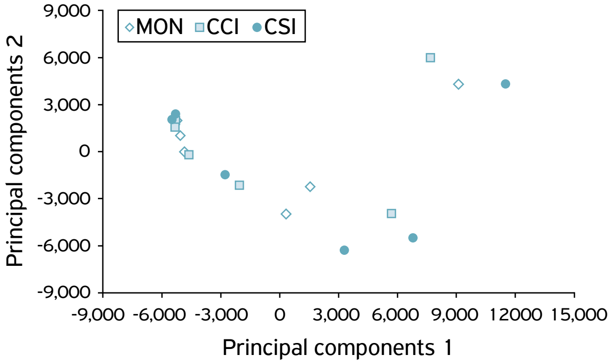
Effect on the insect community

A total of 253,454 specimens were collected, distributed in nine orders, 82 families and 241 species. The main orders were Diptera, with 73.9% of the total collected; Hemiptera (11.5%); Coleoptera (7.6%); Hymenoptera (5.5%) and others (1.5%) (sum of Orthoptera, Neuroptera, Dermaptera, Lepidoptera and Blattaria-Isoptera).

Of the total number of insects captured, the most abundant species were *Condylostylus* sp.1 (36.6%); *Rhinoleucophenga* sp. (20.1%); *Dalbulus maidis* (DeLong & Wolcott) (10.7%); *Euxesta* sp. (8.0%); Mycetophagidae sp. 83 (5.5%); *Astylus variegatus* Germar (2.3%); Formicidae sp. 28 (2.0%); *Neralsia splendens* (Borgmeier) (1.7%) and *Colaspis occidentalis* (L.) (1.3%).

For abundance, number of species and families and for values of richness (α), diversity (H') and evenness (E) indices, no significant differences were observed between treatments (Table 1). Generally, low rates of diversity are expected in agricultural environments. LOZZIA (1999), evaluating the effect of transgenic maize on the biodiversity of the Carabidae family, found diversity indexes lower than 0.99. MEN et al. (2003) found that the use of Bt cotton and the application of insecticides decreased species richness. However, as observed in this study, the index did not detect differences in the arthropod community. As for equitability (evenness), there was a low uniformity in the species distribution (about 0.40), showing that some species had a much higher number of individuals than the others.

In the PCA, 75 species (predominant species according to the faunistic analysis) and six observations (number of collections) were used. The first three axes explained 96.6% of the variation present in the covariance matrix. The first principal component explained 68.3% of the total variation; the second, 24.1%; and the third, 4.2%. The species *Condylostylus* sp.1 and *Rhinoleucophenga* sp. presented the highest values (0.750 and 0.627, respectively) in the first component. In the second component, the species were the same as the first component, however *Rhinoleucophenga* sp. presented higher absolute value than *Condylostylus* sp.1 (0.772 and 0.577, respectively). In the third component, the species *Euxesta* sp. and *D. maidis* presented the highest values (0.714 and 0.541, respectively). In the projection of treatments in the space of the first two principal components (Fig. 1), there was no separation of the



MON: genetically modified maize; CCI: conventional maize with insecticide sprays; CSI: conventional maize without insecticide sprays.

Figure 1. Ordering of the treatments genetically modified maize and conventional maize with and without insecticide sprays in the first two principal components generated in the principal component analysis.

Table 1. Total insects collected, number of species and families, richness, diversity and evenness indices and significance of the *t*-test (p = 0.05) for the treatments genetically modified maize and conventional maize with and without insecticide sprays in Ponta Grossa, PR, Brazil.

	Treatments			*t*-test
	MON	CCI	CSI	
Insects (total)	70,904.00	78,046.00	104,504.00	NS
Number of species	193.00	194.00	211.00	NS
Number of families	70.00	72.00	76.00	NS
Margalef richness index (α)	17.19	17.13	18.17	NS
Shannon-Wiener diversity index (H')	2.24	2.33	2.25	NS
Pielou evenness index (E)	0.43	0.44	0.42	NS

NS: not significant at the 0.05 probability level; MON: genetically modified maize; CCI: conventional maize with insecticide sprays; CSI: conventional maize without insecticide sprays.

treatments in different groups. Thus, based on the species selected, there were no differences among the insect communities collected as a function of the treatment analyzed, which was also confirmed by the Kruskal-Wallis test, in which there was no statistical difference between treatments (K = 0.152; gL = 2; p = 0.927).

Effect on functional groups and species

CSI treatment had the highest number of specimens and species in the six functional groups (Table 2). Comparing genetically modified maize with conventional corn, it was observed that predators and pollinators were more frequently collected in transgenic maize, and parasitoids, detritivores, sap-sucking herbivores and chewing herbivores in conventional maize with insecticide application (Table 2).

The mechanisms by which transgenic plants can affect natural enemies are very complex and depend on a wide range of factors such as the level of plant resistance; the specificity of the expressed protein, in which plant tissues and for how long this protein will be expressed; and crop management, involving the application of insecticides and weed control (FRIZZAS; OLIVEIRA, 2006). In general, *B. thuringiensis* proteins are expressed in high doses in plant tissues and, depending on the promoter used, can also be expressed on pollen, seeds and roots. Thus, predators can be affected by feeding on the pollen, on prey that fed on the sap or directly from the prey that the transgenic plant aims to control, both by the direct effect of the protein on the natural enemy and by the reduction in the nutritional quality of the prey (FRIZZAS; OLIVEIRA, 2006). Parasitoids may be affected by reduction in host quality and quantity, by feeding on flowers, sap, nectar and pollen of transgenic plants, by changes in emission of volatile compounds by the plant or by changes in host behavior (SCHULER et al., 2000).

Our results suggest that, due to the great mobility and greater range of prey, predators are generally less affected by the reduction in the abundance of a particular prey species, such as *S. frugiperda* caterpillars in Bt maize. However, the parasitoids may be more affected by the severe decrease in the supply of hosts, especially those ones that exclusively feed on the pest that the transgenic plant has specificity to control and so were less collected in the Bt maize. The greater presence of predators in Bt maize may also be responsible for the reduction in the population of sap-sucking herbivores, detritivores and chewing herbivores. Regarding pollinators (*Apis mellifera* L.), the highest abundance in Bt maize may have occurred due to a higher sensitivity to the insecticides used in conventional maize.

For some 80% of the evaluated species, regardless of the functional group, it was observed that, either there was no statistical difference between the treatments, or the genetically modified maize and the conventional maize with insecticide differed from conventional maize without application of insecticides, they did not differed from each other (Table 3).

Predators

A total of 100,798 insects, six orders, 17 families and 55 species were collected. The main families were Dolichopodidae, Coccinellidae, Carabidae and Forficulidae. The species *Condylostylus* sp.1 was the most abundant (92.8%), although it was not mentioned in the literature as representative of the fauna of the maize crop. Among the neuropterans species, *Chrysoperla externa* (Hagen) was one of the least abundant predators. LOZZIA (1999) also found few larvae and adults of this species in Bt maize compared to other predators. However, the *Nusalala tessellata* (Gerstaecker) hemerobiid was more abundant in Bt maize, differing statistically between treatments (Table 3).

Table 2. Abundance and species richness by functional group for the treatments genetically modified maize and conventional maize with and without insecticide sprays in Ponta Grossa, PR, Brazil.

Functional group	Treatments					
	Abundance			Species richness		
	MON	CCI	CSI	MON	CCI	CSI
Predator	28,640 (40.4%)$^{(1)}$	27,590 (35.4%)	44,568 (42.6%)	49	44	52
Parasitoid	2,088 (2.9%)	3,088 (4.0%)	5,416 (5.2%)	15	17	19
Pollinator	102 (0.2%)	71 (0.1%)	113 (0.1%)	7	6	8
Detritivore	648 (0.9%)	705 (0.9%)	803 (0.8%)	11	10	11
Sap-sucking herbivore	7,998 (11.3%)	10,012 (12.8%)	10,814 (10.4%)	34	32	35
Chewing herbivore	8,664 (12.2%)	10,561 (13.5%)	15,903 (15.2%)	45	48	52
Others	22,764 (32.1%)	26,019 (33.3%)	26,887 (25.7%)	32	37	34
Total	70,904 (100.0%)	78,046 (100.0%)	104,504 (100.0%)	193	194	211

(1): Number in parentheses represents the relative percentage of each functional group in relation to the treatments (MON: genetically modified maize; CCI: conventional maize with insecticide sprays; CSI: conventional maize without insecticide sprays).

There was no negative effect of MON810 maize on the main evaluated predators. Similar results with genetically modified plants have been observed to lacewings, hemerobiids, coccinellid (LOZZIA, 1999; WOLD et al., 2001) syrphids, antocorids (MENDES et al., 2012) and spiders (MEISSLE; LANG, 2005). Only for the species *Condylostylus* sp.2 there was statistical difference showing a smaller number of individuals in the MON treatment (Table 3). Many of the evaluated predators feed on various prey, especially aphids. Our results suggest that Bt maize is providing sufficient prey for these species and acting as a refuge for predators.

Table 3. Total number of specimens of the selected species in each functional group captured in water tray trap, pitfall trap and yellow sticky card in the treatments genetically modified maize and conventional maize with and without insecticide sprays in Ponta Grossa, PR, Brazil.

Functional group/Specie	Order/Family	Treatments(1)		
		MON	CCI	CSI
Predators				
Allograpta sp.	Diptera/Syrphidae	164 a	139 a	125 a
Chrysoperla externa (Hagen)	Neuroptera/Chrysopidae	5 b	7 ab	14 a
Doru luteipes (Scudder)	Dermaptera/Forficulidae	215 a	152 a	245 a
Eriopis connexa (Germar)	Coleoptera/Coccinellidae	36 b	50 ab	56 a
Hyperaspis sp.	Coleoptera/Coccinellidae	96 b	138 b	273 a
Lebia concinna (Germar)	Coleoptera/Carabidae	173 ab	138 b	215 a
Megacephala brasiliensis Kirby	Coleoptera/Cicindelidae	71 a	34 b	63 a
Nusalala tessellata (Gerstaecker)	Neuroptera/Hemerobiidae	291 a	213 b	131 c
Scymnus sp.	Coleoptera/Coccinellidae	414 a	558 a	534 a
Hippodamia sp.	Coleoptera/Coccinellidae	2 b	6 b	27 a
Cycloneda sanguinea (L.)	Coleoptera/Coccinellidae	9 a	22 a	10 a
Condylostylus sp.1	Diptera/Dolichopodidae	26,107 b	25,270 b	42,203 a
Condylostylus sp.2	Diptera/Dolichopodidae	175 b	343 a	324 a
Parasitoids				
Archytas sp.	Diptera/Tachinidae	421 b	454 b	944 a
Tachinidae sp.31	Diptera/Tachinidae	806 b	1,011 b	1,650 a
Pollinators				
Apis mellifera L.	Hymenoptera/Apidae	82 a	39 b	86 a
Detritivores				
Canthon conformis Harold	Coleoptera/Scarabaeidae	262 a	242 a	293 a
Colopterus sp.	Coleoptera/Nitidulidae	205 a	123 b	87 b
Sap-sucking herbivores				
Dalbulus maidis (DeLong & Wolcott)	Hemiptera/Cicadellidae	7,509 b	9,423 a	10,300 a
Peregrinus maidis (Ashm.)	Hemiptera/Delphacidae	28 a	39 a	33 a
Chewing herbivores				
Astylus variegatus (Germar)	Coleoptera/Melyridae	310 b	2,202 ab	3,408 a
Diabrotica speciosa (Germar)	Coleoptera/Chrysomelidae	397 b	410 b	599 a
Euxesta sp.	Diptera/Ulidiidae	5,424 b	5,882 b	9,045 a
Gryllus assimilis Fabr.	Orthoptera/Gryllidae	552 ab	438 b	643 a
Colaspis occidentalis (L.)	Coleoptera/Chrysomelidae	1,346 a	821 c	1,028 b
Orphulella sp.	Orthoptera/Acrididae	95 ab	71 b	133 a
Elasmopalpus lignosellus (Zeller)	Lepidoptera/Pyralidae	40 b	36 b	70 a
Spodoptera frugiperda (JE Smith)	Lepidoptera/Noctuidae	20 a	26 a	31 a

(1): Numbers followed by the same letter in the rows do not differ from each other by the *t*-test at 0.05 probability level. MON: genetically modified maize; CCI: conventional maize with insecticide sprays; CSI: conventional maize without insecticide sprays.

Parasitoids

A total of 10,592 specimens were collected, belonging to two orders, six families and 21 species. The main family was Tachinidae and the main species were *Tachinidae* sp.31 (32.7%) and *Archytas* sp. (17.2%). The genus *Archytas* includes parasitoids of pupae and small caterpillars of *S. frugiperda*. Small caterpillars are found in genetically modified maize, since the caterpillar needs to feed on the foliar tissue to ingest the Bt protein. *Archytas* species show a preference for the pupa stage, which may explain the higher amount of this species in the conventional maize without insecticide. In CSI treatment, the parasitoids had higher chances of finding hosts in various stages of development. No statistical differences were found for this genus between the MON and CCI treatments (Table 3).

Pollinators

A total of 286 pollinators belonging to the order Hymenoptera were collected, including four families and eight species. The main family was Apidae, and the main species was *A. mellifera*, which represented 72.4% of the total collected. No negative effects of transgenic maize were observed on the number of bees collected. Depending on the promoter used, Bt proteins are also expressed in pollen, which could affect pollinators, especially bees. However, there is a large variation in the amount of protein present in pollen in the different maize events. For example, the event 810 presents about 40 times less protein than the event 176 (WRAIGHT et al., 2000). Therefore, the fact that MON810 maize had no effect on bees could have occurred both by the specificity of the Cry1Ab protein for lepidopterans and by the smaller amount of the protein in the pollen.

Detritivores

A total of 2,156 specimens were distributed in two orders, three families and 12 species. The main family was Scarabaeidae, and the main species were *Canthon conformis* Harold (37.0%) and *Colopterus* sp. (19.2%), the latter being significantly more abundant in Bt maize.

Sap-sucking herbivores

A total of 28,824 specimens were collected, represented by the order Hemiptera, 11 families and 45 species. The main family was Cicadellidae, and the main *D. maidis* species with 94.5% of the total collected. Sap-sucking herbivores can acquire the protein expressed in the sap of transgenic plants when they feed. However, studies have shown that Cry1Ab protein was not detected in the honeydew of sap-sucking herbivores such as *Rhopalosiphum padi* (L.) (RAPS et al., 2001).

The corn leafhopper the *D. maidis* is a very common species in maize, typically found in high populations of plants in the cartridge (OLIVEIRA et al., 2004). In general, there is a negative correlation between the population dynamics of *S. frugiperda* and *D. maidis* (PERFECTO, 1990), as these pests compete for the same feeding site in the plant. Thus, it could be expected an increase in the corn leafhopper population in transgenic maize due to the reduction in the *S. frugiperda* population, a fact that was not verified in the present study, since the MON treatment presented the least quantity of *D. maidis* (Table 3).

Chewing herbivores

A total of 35,128 of specimens were distributed in five orders, 27 families and 63 species. The main families were Ulidiidae, Chrysomelidae and Melyridae, and the main species, *Euxesta* sp. (57.9%), *A. variegatus* (16.8%) and *C. occidentalis* (9.1%). The genus *Euxesta* includes species considered pest of maize ear. In general, its occurrence is associated with the presence of the corn earworm [*Helicoverpa zea* (Boddie)]. The lower abundance of this species in Bt maize (Table 3) is probably due to the control of the *S. frugiperda* e *H. zea* provided by this treatment.

It was observed in this study that differences between genetically modified maize and conventional maize are only detected when analyzing the species (Table 3) and not the insect community (Table 1). In addition, studies with insect communities turn out to be less attractive options due to several difficulties such as: the need for an efficient and trained team, the availability of time for screening the collected material, and the lack of specialists in the taxonomy of most groups. It is important to highlight that the insect community varies between crops, regions and localities (FRIZZAS et al., 2003), so generalizations or even the choice of indicator species should be made respecting these particularities.

Transgenic and chemical control

The insecticides used (lufenuron and lambda-cyhalothrin) appear to negatively affect the species *Megacephala brasiliensis* Kirby and *N. tessellata* (predators), *A. mellifera* (pollinator), *Colopterus* sp. and *C. occidentalis* (chewing herbivore) in comparison with transgenic maize (Table 3). Transgenic maize significantly decreased the number of insects collected from the species *Condylostylus* sp. 2 (predator) and *D. maidis* (sap-sucking herbivore) (Table 3).

Field studies have shown little or no effect on the abundance and activity of non-target organisms in Bt crops and have shown that Bt technology is less toxic to predators and parasitoids than lambda-cyhalothrin pyrethroid (MUSSER; SHELTON, 2003; ROSE; DIVELY, 2007). On the other hand, applications of insecticides such as pyrethroids have shown negative effects on biological control agents (MEN et al., 2004; MEISSLE; LANG, 2005). However, in this study, there was no significant effect of Bt maize and insecticides on the abundance of syrphids, earwigs, coccinellids and spiders (Table 3).

When comparing the effects of transgenic plants with the application of insecticides on the insect community, the use of broad spectrum insecticides has generally reduced the diversity of arthropods more than genetically modified plants (ROSE; DIVELY, 2007). In this study, the use of the two technologies together (Bt and insecticides) seems to be the best strategy, since the pest probably will not be able to complete its development under these conditions (JACKSON et al., 2004). Thus, the use of transgenic maize is an alternative for integrated pest management, since it could reduce the need for insecticides, in relation to the target pests of the technology, probably due to less negative impact on natural enemies.

CONCLUSIONS

Significant differences in the abundance and/or species richness between genetically modified maize and conventional maize are only detected when analyzing species and not the insect community. Among the predominant species, there are significant differences for the species *Colopterus* sp., *Colaspis occidentalis* (L.) and *Nusalala tessellata* (Gerstaecker), which were most abundant in Bt maize, and *Dalbulus maidis* (DeLong & Wolcott) and *Condylostylus* sp.2 in conventional maize (with or without insecticide sprays).

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