

Diversity of arthropods communities in transgenic cotton varieties in Santa Fe province, Argentina.

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Genetically modified (GM) crops have been widely expanded within the agricultural systems in Argentina, being BT/ RR cotton well adopted since its commercial approval in 2009. However no has been study and compared the arthropods diversity in cotton crops Bt and non Bt with one and two stacks trait events and its possible impacts on the environment. The aim of this study was to compare single-trait event cotton (non Bt) to stacked trait event cotton (Bt) evaluating abundance, richness and diversity of arthropod for the environmental conditions of the northern region of Santa Fe and to obtain information useful for Integrated Pest Management (IPM) Programs. Experiments were conducted during three growing seasons (Y1: 2009/10, Y2: 2010/11 and Y3: 2011/12) at the Agricultural Experimental Station of INTA Reconquista, Santa Fe (Argentina). A randomized complete block design with five replications was used with two Treatments: 1) No Bt: (RR) G2000, herbicide resistant and 2) Bt Crop: (BR) NuOpal, Lepidoptera and herbicide-resistant, using two sampling methods (pitfall traps and G-Vac). The abundance and species richness showed no differences between the Bt and non Bt cotton and years analyzed, except for the diversity index did show differences between Y1 and Y2. A high proportion of beneficial arthropods were recorded for both treatments throughout the entire sampling period. According to the results obtained in three cotton seasons, the diversity of arthropods present in both events cotton crops were not affected and may be considered as a control strategy in a IPM for maintaining this fauna and sustainability in this crops.

Key words: genetically modified crops, *Gossypium hirsutum*, arthropods, Integrated Pest Management, species richness

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Los cultivos genéticamente modificados (GM) se han extendido ampliamente dentro de los sistemas agrícolas en Argentina, tal es el caso del algodón BT/RR aprobado comercialmente desde el 2009. Sin embargo no ha sido estudiado y comparado la diversidad de artrópodos en cultivos de algodón Bt y no Bt con uno y dos eventos apilados y su posible impacto sobre el medioambiente. El objetivo de este estudio fue comparar el cultivo de algodón con un solo evento (no Bt) y con dos eventos apilados (Bt) evaluando abundancia, riqueza y diversidad de artrópodos bajo las condiciones ambientales del norte de Santa Fe y obtener información que podrá ser utilizada dentro de programas de Manejo Integrado de Plagas (MIP). Los muestreos se llevaron a cabo durante tres temporadas de algodón (Y1: 2009/10, Y2: 2010/11 y Y3: 2011/12) en la Estación Experimental Agropecuaria del INTA Reconquista, Santa Fe (Argentina). Se utilizó un diseño de bloques completos al azar con cinco repeticiones y dos tratamientos: 1) Cultivo no Bt: (RR) G2000, resistente a herbicida y 2) Cultivo Bt: (BR) NuOpal, resistente a lepidópteros y herbicida, usando dos métodos de muestreo (trampas de caída y G-Vac). La abundancia y riqueza de especies no mostraron diferencias entre el algodón Bt y no Bt y años analizados, excepto para el índice de diversidad que mostro diferencias entre Y1 y Y2. Una alta proporción de artrópodos benéficos fueron registrados para ambos tratamientos durante todo el ciclo de muestreo. Según los resultados obtenidos en las tres campañas de algodón, la diversidad de artrópodos presentes en ambos eventos no fueron afectados y podría ser considerado como una estrategia de control dentro de un MIP para mantener la fauna y sustentabilidad del cultivo.

Palabras clave: Cultivos genéticamente modificados, *Gossypium hirsutum*, artrópodos, Manejo Integrado de Plagas, riqueza de especies

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INTRODUCTION

Genetically modified crops (GM) have been widely expanded within the agricultural systems in Argentina in the last few years presenting a planted area of more than 24 million hectares in 2012 (ArgenBio, 2014). The process of adoption of GM technologies began in 1996 with the introduction of glyphosate herbicide-tolerant soybeans, followed by corn and Bt cotton in 1998; In 2001, single-trait events RR cotton (MON1445), glyphosate herbicide-tolerant was introduced and since 2009, Argentina approved the commercial production of cotton stacked trait events, BR/RR (MON 531 x MON 1445), Bt resistant to Lepidoptera and glyphosate herbicide-tolerant (ArgenBio, 2014). The adoption of cotton BR/RR marks a turning point in the commercial production of cotton in Argentina, superficies increasing planting (Trigo, 2011).

Bt cotton provides resistance to bollworms (*Heliothis* complex Boisduval), leafworm (Noctuidae: *Alabama argillacea* Hübner), and the pink bollworm (Gelechiidae: *Pectinophora gossypiella* Saunder). Farmers use about 50 % less insecticide in Bt fields compared with conventional ones (Qaim et al., 2003).

In all agroecosystem, over 90% of all species may be arthropods (Erwin, 1982); they comprise the most diverse taxa in most ecosystems and may play important functional roles in ecosystem processes such as their trophic interactions and functions of ecosystem. Beneficial arthropods, including native bees, predators, and parasitoids, provide valuable ecosystem services including decomposition, pollination, and biological control of crop pests (Losey & Vaughan, 2006; Gardiner et al., 2009), which helps to maintain agricultural productivity and reduce the need for pesticide inputs (Isaacs et al., 2009).

Potentially harmful effects of these crops on non-target organisms (NTOs) is a major concern as many of those provide important ecological functions such as pest regulation. The bulk of evidence to date suggest that Bt crops are highly selective and that negative effects, if any, are minor which be associated with any meaningful changes in the function of the natural enemy community (Naranjo et al., 2008; Marvier et al., 2007; Romeis et al., 2012). One of the benefits of GM crops is a decrease of broad-spectrum insecticides use, which allows an increase of natural enemies and control of other pests. Therefore, the Integrating Insect-Resistant GM crop is one optimal control technique to be used within IPM (Integrated Pest Management) Programs (Naranjo et al., 2008).

Many studies related to arthropod biodiversity for Bt and non-Bt crops has been developed under different conditions in Brazil, United States and Australia, mainly for aspects of natural enemies preservation, contributing to the integration of pest management systems, with sustainable production and preservation of the environment (Thomazoni et al., 2010; Xingyuan et al., 2003; Whitehouse et al., 2005) but there is no information in regards to diversity of species for different field conditions in Argentina and its effect on the sustainability of crop.

Therefore, the present studies were undertaken to obtain information comparing two varieties of cotton with single-trait events (non Bt) and stacked trait events (Bt)

in Argentina during three years study, comparing abundance, richness and diversity of arthropod for the environmental conditions in northern region of Santa Fe, Argentina. This information would be useful to compare relative effects of GM crops in the ecosystem and be part of IPM Programs for sustainable crop production.

MATERIALS AND METHODS

This research work was carried out during three cotton season (Y1: 2009/10, Y2: 2010/11 and Y3: 2011/12) at the Research Station of INTA Reconquista, (29° 11 'S and 59° 52'W), Santa Fe (Argentina). The region was characterized by annual average temperatures, above 20°C and rainfall exceeding the 1100-1200 mm annual (Pereyra, 2003).

A randomized complete block design was used with two GM varieties with five replications. The plot included 12 rows spaced 0.52 m by 15 m long. Treatments used were: 1) Non Bt Crop, single-trait events (RR) G2000 herbicide resistant and 2) Bt Crop, stacked trait events (BR) NuOpal Lepidoptera and herbicide-resistant. Delinted seed to acid was used, treated with systemic insecticide and fungicide. Sowing was done in late December under conventional tillage (Y1-Y2) and no tillage (Y3). No pesticide application was made after planting because the pest insects number was under the recommended thresholds during monitoring; only growth regulator and defoliant was applied.

Sampling of arthropods was conducted from season summer, at 30, 60 and 90 days after crop emergence. For the survey of soil stratum, two pitfall traps with saline solution (NaCl: water in solution 1:8): were placed per plot, separated by 6 m, during 7 days. For the aerial plant survey, two samples of G-Vac (garden-vaccum) using a STIHL blower were taking by plot. Each sample by suction during one minute represents one square meter. About 120 samples for both GM varieties were taken per year including those for each sampling techniques, each event and each sampling date.

The collected material was preserved in individual containers with 70% ethyl alcohol, properly labeled and taken to the laboratory for further identification.

The samples were identified at least to family and often to species for most insects and to order for most other invertebrates. Identifications were conducted using a reference collection the insects Agricultural Experimental Station of INTA Reconquista, Santa Fe and identification keys. In some cases, the species most common, as pest species, were identified a to species level. Because of the large number of unknown insect species, we analyzed these samples at the level of family for most insects and order for most other invertebrates. The species were grouped as beneficial (predators, parasitoids, pollinator) and harmful arthropods (herbivores, carnivores, decomposers).

Data analysis: With individual data for each treatment per replication from pitfall trap and G-Vac were calculated, abundance, r (richness) and (H) diversity indexes Shannon by using the PAST program (Hammer et al., 2012). Data were tested by ANOVA and average were compared by Tukey test ($\alpha \leq 0.05$) using InfoStat/P software (Di Rienzo et al., 2010); data of abundance were ln transformed prior to analyses to

normalize distributions of variance. In the same way the data was used to observe the proportion of beneficial and harmful organisms and to establish differences between the events analyzed throughout study years.

RESULTS AND DISCUSSION

A total of 31,396 arthropods were captured, distributed in 21 orders and 101 families, where 16,026 individuals were found in RR and 15,370 in BR. In both events, for the soil layer, 18,239 individuals sampled and for aerial layer 13,157 individuals. A total of 20,970 beneficial species (RR: 11,788, BR: 9,182) and harmful 10,426 (RR: 4,238, BR: 6,188) were recorded in both events, without discriminating strata (Table 1, here). In accordance with the findings of Whitehouse et al. (2005) where similar taxa were recorded, but in less proportion, possibly because of the sampling period was shorter than this work. The values of abundance, richness and diversity are showed in Table 2. (Table 2, here)

The richness species was similar for both events and layer analyzed, where RR cotton generally obtained the highest richness but there was not significative difference. Coleoptera and Diptera showed highest value of richness in all the events and layers analyzed. Therefore, in the soil layer were for Coleoptera (24 RR and 24 BR), Diptera (24 RR and 23 BR), spiders (16 RR and 14 BR) and Lepidoptera (10 RR and 9 BR), while in the aerial layer the most richness were Coleoptera (26 RR and 28 BR), Diptera (14 RR and 17 BR), Hemiptera (12 RR and 14 BR) and spiders (13 RR and 13 BR).

The most abundant group captured in soil layer was Formicidae (54,4 % RR and 44 % BR), Collembola (6,12 % RR and 4,7 % BR) and Diptera (4,5 % RR and 5 % BR). Considering the aerial layer the most abundant were Aphididae: *Aphis gossypii* Glover (19 % RR and 49,8 % BR), Lygaeidae: *Nyssius simulans* Stal (10,5 % RR and 2,8 % BR), Formicidae (10,4 % RR and 7,6 % BR), Diptera (9,9 % RR and 6,8 % BR) and Thripidae: *Caliothrips brasiliensis* Morgan (8,54% RR and 9,5% BR).

Varieties did not show significant differences for richness and abundance. Diversity was the only index evaluated that showed significant differences between Y1 and Y2 for soil layer.

The Shannon index is sensibly to rare species (Magurran & McGill, 2011), and this may explain the differences found for diversity between years, due to the biggest number of rare species or recorded species only once in the whole sampling period.

The variation of richness and abundance of arthropod in cotton crops is showed in the Figure 1 (a, b) for both layers and sampling date in RR, and Figure 1 (c, d) in BR. With the exception of the first sampling date in BR the abundance was superior in aerial sampling than soil layer, but in the following sampling, in most of cases it was more abundant in soil layer for both varieties. The high abundance in BR in the first study year is related with the presence of aphids in big number, followed by trips. However in RR crops the peak of abundance was registered in the first sampling date of the second year and it was represented mainly by ants (Formicidae).

One of the most abundant groups in soil arthropods correspond to ants are important in ecosystem

functioning, principally for their ability to maintain or restore the soil quality in environments (Lobry de Bruyn, 1999; Samways et al., 2010). The same occurred for the ants in aerial layer in both events. Following in increased abundance was for collembolan, they and other detritivores in pest management is that many are important components of the diets of generalist predators, so their presence could theoretically help maintain within field communities of natural enemies (García & Altieri, 2005). These latter groups are documented as bioindicators of environmental quality by assessing the ecological status of ecosystems (Samways et al., 2010).

In the aerial layer, the biggest abundance of *A. gossypii* in BR match with founded by Hagenbucher et al., (2010), who argue that when caterpillars feed on plant structure induce a defense system producing terpenoids which in certain way control phloem-feeding insects (aphid and whitefly), because of that Bt crops would benefit this kind of pest. On the other hand, the high abundance of aphids in crops plays an important role in agricultural since they serve as hosts or prey for a variety of parasitoids and predators (Lawo et al., 2009). Nevertheless, the cotton blue disease that is transmitted by *A. gossypii* in non resistance varieties can cause economically important losses in cotton crop if controls are not implemented (Corrêa et al., 2005).

Wellings & Dixon (1987) studying population aphids in crop plants concluded that the impact of natural enemies and climatic conditions on aphid populations are variable; especially temperature and wind are critical to outbreak. This coincides with the results, where predators are not as abundant in the early stages of the crop (Thorbek & Bilde, 2004) coupled with weather conditions that conditioned the population as occurred in the third year of studies.

Other abundant group in the aerial layer was *N. simulans*, which population increased in RR for the third year of study. This is coincident with an increase of its presence in recent years in Argentina, mainly on no tillage crops due this provides a favorable habitat for the proliferation of this, and other species (Molinari & Gamundi, 2010).

The high abundance and species richness obtained every year show that the crop provides favourable conditions for the establishment of arthropods in both events. No application of insecticide and herbicides possibly helped arthropods diversity can develop and behave naturally. However the variations that occur crops would be associated with the phenological development stage of the crop, as well as

Table 1. Abundance of all organism identified in cotton varieties during three years of sampling and the number of individuals found at each site, including their role (B: beneficial; H: harmful). * = Corresponds a superfamily category only in two groups; msp.= morphospecies. Beneficial (i. e.: predators, parasitoids, pollinator), Harmful (i.e.: herbivores, carnivores, decomposers)

Phylum	Class	Order	Family	Genus/ msp.	Role	Sampling method					
						Pitfall		G-Vac			
						Non Bt crop (RR)	Bt crop (BR)	Non Bt crop (RR)	Bt crop (BR)		
Mollusca	Gastropoda	Pulmonata			H	7	2	6	15		
	Malacostraca	Isopoda			H	0	1	0	0		
Arthropoda											
	Chilopoda	Lithobiomorpha			H	1	0	0	0		
	Diplopoda	Polydesmida			H	29	27	0	0		
	Arachnida	Araneae	Anyphaenidae		B	0	2	7	10		
			Araneidae		B	10	6	18	30		
			Clubionidae		B	1	0	0	0		
			Corinnidae		B	14	18	1	0		
			Caponiidae		B	1	0	0	0		
			Gnaphosidae		B	2	2	0	0		
			Linyphiidae		B	13	10	0	1		
			Lycosidae		B	188	746	1	5		
			Miturgidae		B	7	1	4	6		
			Oxyopidae		B	5	2	23	10		
			Phliodromidae		B	5	4	12	18		
			Trechaleidae		B	0	0	2	8		
			Salticidae		B	9	10	4	10		
			Tetragnathidae		B	0	0	3	3		
			Theridiidae		B	11	7	5	5		
			Thomisidae		B	4	0	78	38		
			Titanoecidae		B	3	3	0	1		
			Zodariidae		B	0	1	0	0		
				Acari			H	104	35	3	2
					Tetranychidae	<i>Tetranychus sp.</i>	H	0	0	4	0
Hexapoda	Coleoptera				B	6	10	8	16		
			Cicindelidae	<i>Cicindela sp.1</i>	B	1258	893	0	0		
				<i>Cicindela sp.2</i>	B	5	4	0	0		
			Carabidae		B	66	85	0	0		
				<i>Calosoma</i>							
				<i>argentinensis</i>	B	9	9	0	0		
				<i>Gallerita collaris</i>	B	1	0	0	0		
				<i>Lebia concinna</i>	B	1	0	0	0		
				<i>Callida sp.</i>	B	3	0	0	0		
				<i>Listroderes sp.</i>	H	0	1	0	0		
				Staphylinidae		B	160	154	0	0	
				Scarabaeidae		B	232	341	2	4	
				Elateridae		H	65	41	0	1	
				Lampyridae		B	3	5	2	2	
				Melyridae	<i>Astylus atromaculatus</i>	H	3	5	55	12	
				Nitidulidae		B	84	147	0	0	
				Coccinellidae		B	3	4	18	28	
					<i>Coleomegilla</i>						
					<i>quadrifasciata</i>	B	0	0	2	0	
					<i>Cycloneda sanguinea</i>	B	0	0	7	6	
			<i>Eriopsis connexa</i>	B	9	5	39	35			
			<i>Harmonia axyridis</i>	B	0	0	1	1			
			<i>Hippodamia convergens</i>	B	1	1	0	1			
			<i>Hyperaspis festiva</i>	B	0	2	30	20			
			<i>Scymnus argentinicus</i>	B	0	1	36	19			

Table 1(continuation). Abundance of all organism identified in cotton varieties during three years of sampling and the number of individuals found at each site, including their role (B: beneficial; H: harmful). * = Corresponds a superfamily category only in two groups; msp.= morphospecies. Beneficial (i. e.: predators, parasitoids, pollinator), Harmful (i.e.: herbivores, carnivores, decomposers)

Phylum	Class	Order	Family	Genus/ msp.	Role	Sampling method			
						Pitfall		G-Vac	
						Non Bt crop (RR)	Bt crop (BR)	Non Bt crop (RR)	Bt crop (BR)
			Lagriidae	<i>Lagria sp.</i>	H	3	0	0	1
			Mordellidae		H	2	0	0	1
			Anthicidae		H	0	2	48	6
			Chrysomelidae		H	7	3	0	9
				<i>Colaspis sp.</i>	B	0	1	0	0
				<i>Cyrtes sp.</i>	H	0	0	6	1
				<i>Diabrotica significata</i>	H	1	0	9	7
				<i>Diabrotica speciosa</i>	H	1	2	24	19
				<i>Epitrix sp.</i>	H	0	2	9	3
			Curculionidae		H	17	24	32	9
				<i>Pantomorus sp.</i>	H	2	0	0	0
			Scolytidae		H	1	2	0	0
		Diptera			B	473	395	561	512
				<i>msp. 1</i>	B	8	0	0	0
				<i>msp. 2</i>	B	12	16	16	30
				<i>msp. 3</i>	B	0	1	0	0
				<i>msp. 4</i>	B	0	1	0	0
				<i>msp. 5</i>	B	0	1	0	0
			Asilidae		B	0	1	0	0
			Calliphoridae		H	20	8	0	0
			Cecidomyiidae		H	11	62	19	27
			Chironomidae		B	1	0	0	0
			Culicidae		H	38	30	573	338
			Dolichopodidae		B	7	15	81	87
			Drosophilidae		B	2	0	0	1
			Muscidae		H	44	21	0	0
			Muscoidea(*)		H	8	8	32	11
			Mycetophilidae		H	4	0	0	0
			Oestridae		B	1	0	0	0
			Otitidae		H	1	0	0	0
			Phoridae		B	10	0	0	2
			Rhagionidae		B	1	0	0	0
			Sarcophagidae		H	1	0	0	0
			Scenopinidae		B	0	1	0	0
			Sciaridae		H	54	35	0	0
			Syrphidae		B	0	2	4	2
			Tabanidae		H	0	1	6	9
			Tachinidae		B	118	103	0	0
			Tephritidae		H	0	4	6	9
			Tipulidae		H	3	4	4	3
		Hemiptera			H	3	1	7	11
			Anthocoridae	<i>Orius insidiosus</i>	B	2	1	25	31
			Gelastocoridae		B	3	9	0	0
			Geocoridae	<i>Geocoris callosulus</i>	B	2	0	78	24
			Largidae		H	0	2	0	0
			Lygaeidae		H	5	3	1	2
				<i>Coryzus sp.</i>	H	0	0	1	0
				<i>Lygaeus alboomatus</i>	H	0	0	0	1
				<i>Nysius simulans</i>	H	24	16	596	209
			Nabidae	<i>Nabis punctipennis</i>	B	0	2	4	2
			Miridae		H	0	0	2	3

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Phylum	Class	Order	Family	Genus/ msp.	Role	Sampling method			
						Pitfall		G-Vac	
						Non Bt crop (RR)	Bt crop (BR)	Non Bt crop (RR)	Bt crop (BR)
				<i>Horcias nobilellus</i>	H	0	0	13	14
				<i>Creontiades pallidus</i>	H	1	0	7	2
			Pentatomidae		H	0	0	0	1
				<i>Dichelops furcatus</i>	H	0	0	1	0
				<i>Edessa mediatibunda</i>	H	0	0	3	1
				<i>Nezara viridula</i>	H	0	0	2	1
				<i>Piezodorus guildinii</i>	H	0	1	2	2
			Reduviidae		H	0	1	0	0
			Tingidae		H	5	1	0	1
		Hymenoptera			B	13	36	10	2
			Apidae	<i>Apis mellifera</i>	B	1	0	0	0
			Braconidae		B	2	3	7	5
			Chalcidoidea(*)		B	19	8	121	133
			Eulophidae	<i>Euplectrus sp.</i>	B	0	0	7	33
			Formicidae		B	5718	3465	587	567
			Halictidae		B	2	0	1	0
			Ichneumonidae		B	0	0	7	4
			Megachilidae		B	1	0	0	0
			Mutillidae		H	21	14	0	0
			Mymaridae		B	2	0	2	0
			Platygasteridae		B	2	0	0	0
			Pompilidae		B	4	1	0	0
			Vespidae		B	10	5	2	0
		Homoptera	Cicadellidae		B	122	84	628	428
				msp. 1	H	23	12	0	0
			Delphacidae		H	6	1	7	10
			Membracidae		H	0	0	6	2
			Aleyrodidae	<i>Bemisia tabaci</i>	H	0	0	38	15
			Cercopidae		H	8	7	4	6
				<i>Tomaspis sp.</i>	B	1	0	0	0
			Aphididae		H	110	80	1076	3734
		Lepidoptera		msp. 1	H	0	25	0	11
			Cosmopterigidae		H	0	0	0	1
			Gelechiidae		B	3	2	5	16
			Noctuidae	<i>Alabama argillacea</i>	H	33	9	46	15
				<i>Spodoptera frugiperda</i>	H	216	181	60	86
				<i>Spodoptera latifascia</i>	H	1	1	0	0
				<i>Anticarsia gemmatalis</i>	H	6	5	0	0
				<i>Pseudaletia adultera</i>	H	0	6	0	0
				<i>Heliothis zea</i>	H	1	0	0	0
			Pyalidae		H	2	0	1	1
			Pyraustidae	<i>Loxostege bifidalis</i>	H	3	3	0	0
		Collembola			B	644	370	0	0
		Dermoptera	Forficulidae	<i>Doru lineare</i>	B	19	11	3	0
		Mecoptera			B	0	0	0	2
		Neuroptera	Chrysopidae	<i>Chrysoperla externa</i>	B	0	0	1	5
		Odonata	Libellulidae		B	1	0	3	0
		Orthoptera	Gryllidae		H	46	53	1	1
				<i>Anurogryllus sp.</i>	H	1	1	1	0
			Gryllotalpidae	<i>Scapteriscus sp.</i>	H	0	4	0	0
			Acrididae		H	49	60	6	10

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						Pitfall		G-Vac		
						Non Bt crop (RR)	Bt crop (BR)	Non Bt crop (RR)	Bt crop (BR)	
				<i>Dichroplus sp.</i>	H	11	9	0	0	
			Blattidae		B	11	8	1	0	
			Mantidae		B	1	3	0	0	
			Phasmatidae		H	1	0	0	0	
			Tettigoniidae		H	0	0	0	2	
			Raphidioptera		B	0	1	0	0	
			Thysanoptera Thripidae		H	35	35	483	712	
			Trichoptera		B	1	0	0	0	
TOTAL							10369	7870	5657	7500

environmental conditions, rainfall were more abundant during the crop cycle in the first two study years, compared with the third which was driest during the first 60 days.

Comparing the values of beneficial and harmful species (Fig. 2), in three years, and events analysed, the beneficial have high abundance what harmful arthropods. Only one date sampling a high abundance of harmful arthropods was recorded in the first year of sampling (BR), probably due to the aphids population exhibited outbreaks, which affected the crop at the time. Significant differences were observed between groups in most date sampling, in the three years and events.

We detected high abundance of beneficial arthropods for both cotton varieties throughout the entire sample period in these studies; similarly to Whitehouse et al., (2005), who compared communities for transgenic Bt and conventional cotton, showing that genetically modified crops, may allow to be host for larger amounts of beneficial arthropods, fostering a large decrease for insecticide applications and avoiding new pest to be develop in the current conditions such us as the case of bollworms and *Helicoverpa armigera* Hübner.

Bt crops generate indirect effects due to reducing broad spectrum insecticide applications allowing the increasing of natural enemies and these are those that would control the secondary pest (Kos et al., 2009). This is shown by decreasing the dominant groups in the presence of BR event, and corresponds to that reported by several studies (Whitehouse et al., 2005; Lawo et al., 2009; Naranjo, 2009; Romeis et al., 2012) who claim that reducing insecticide favors diversity of arthropods and for the maintenance and more uniform distribution of the species. Moreover, the cotton plants have a high structural diversity, with a complex architecture

and canopy development, promoting greater diversity and associated species richness, being some groups of arthropods highly dependent on the structure of the vegetation (Uetz et al., 1999; Heitholt, 1999).

Almada et al. (2012) compared the community spiders in cotton Bt crop and conventional cotton crop in North Santa Fe were not observed difference significative between crops only the spiders abundance were increased in Bt crops, indicating that these crops did not affect the population of spiders and that it is an effective tool for inclusion in the biological control of pests of agricultural importance. This is in accordance with our studies support where arthropods communities not shown difference between events Bt and not Bt, promoting the inclusion of these crops as suitable tools for IMP.

Our results show that the community of arthropods reaches the highest peak of abundance and richness during the third moment of sampling coinciding with the stage of flowering and maturation of bolls, mainly represented by pollinators and predators. The above is consistent with the findings of other authors (Musser & Shelton, 2003; Romeis et al., 2008), who claim that crops with new technologies allow to integrate IPM (Integrated Pest Management), generating more feasible control and conducive to the preservation of biodiversity due to the adoption of Bt cotton event may help meet the expected reduction in insecticide use.

However, an important part of a Bt crop management is to maintain efficacy includes planting non-Bt cotton as border rows to Bt cotton is currently recommended as a step towards delaying the development of resistance in bollworms to Bt proteins. This corresponds to one of the conditions and other mechanisms for the maintenance and preservation of biodiversity and the environment, which make the appropriate tools the advancement of IPM.

Table 2. Diversity index of arthropods for soil (Pitfall) and aerial (G-Vac) stratum, by variety (BR and RR) and by study year (Y1: 2009/10, Y2: 2010/11 and Y3: 2011/12). Means in each column followed by the same letter are not significantly different ($p \leq 0.05$)

Variety /year	Richness (r)		Abundance		Diversity Shannon (H)							
	G-Vac	Pitfall	G-Vac	Pitfall	G-Vac	Pitfall						
BR	30	a	34	a	833	a	874	a	1,78	a	1,74	a
RR	30	a	37	a	613	a	1168	a	1,82	a	1,76	a
Y1 (2009/10)	35	a	40	a	1148	a	1305	a	1,89	a	1,47	a
Y2 (2010/11)	29	a	35	a	540	a	1008	a	1,80	a	2,01	b
Y3 (2011/12)	26	a	32	a	481	a	750	a	1,72	a	1,78	ab
CV %	21,4		15,9		11,5		7,6		27,4		16,0	

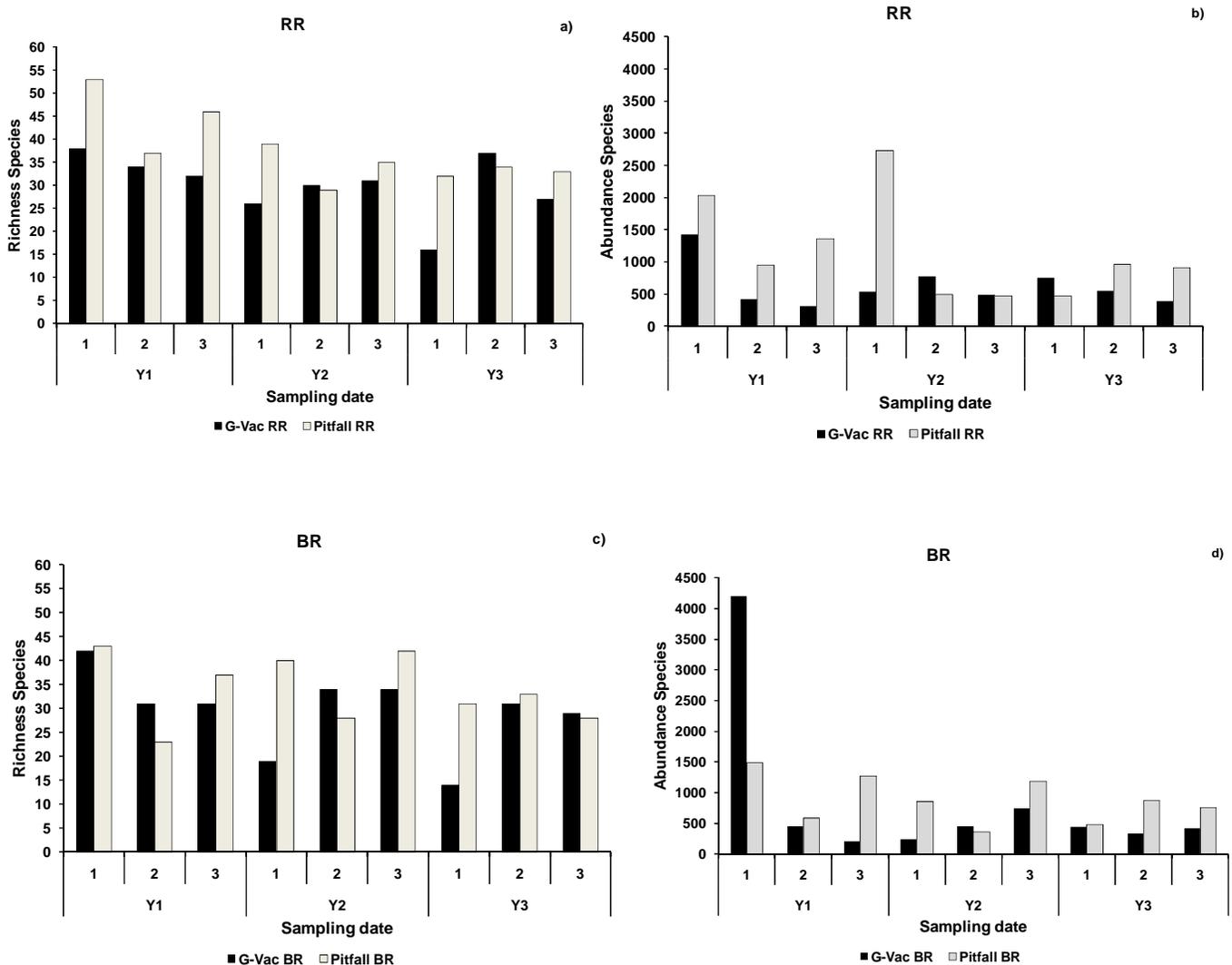


Figure 1. Arthropods variation for soil and aerial stratum at 30, 60 and 90 days after emergence (1, 2 and 3, respectively) during 3 years of study (Y1: 2009/10, Y2: 2010/11 and Y3: 2011/12) for a) richness and b) abundance in RR (G2000); c) richness and d) abundance in BR (NuOpal).

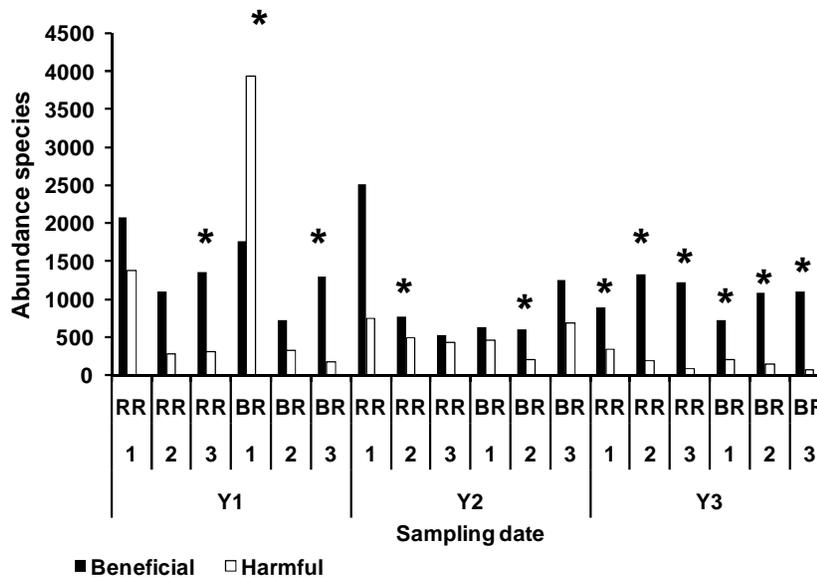


Figure 2. Beneficial and harmful arthropods in each events (BR, RR) during 3 years of study (Y1: 2009/10, Y2: 2010/11 and Y3: 2011/12). * = Means in each column significantly different between beneficial and harmful arthropods ($p \leq 0.05$).

The present study proposed that is necessary new research concerning the behavior and the biocology of non-target organisms on Bt and non Bt cotton crop, as well as investigate the effects of different transgenic cotton varieties production systems on dynamics of non-target insects under cultivation conditions Santa Fe.

CONCLUSIONS

This work constitutes the first record on the arthropods diversity in single-trait events (non Bt) and stacked trait events (Bt) cotton crops in Argentina.

According to the results obtained in three cotton seasons, the abundance and richness of arthropods in the crop were not affected by GM cotton varieties except for the diversity index which showed differences between first and second year.

These results demonstrated the requirement of continuing studies related to diversity of arthropods in GM cotton varieties, which are important for the sustainable development of agriculture and to be part of the IPM suitably.

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REFERENCES

Almada, M.S., M.A. Sosa & A. González. 2012. Araneofauna (Arachnida: Araneae) en cultivos de algodón (*Gossypium hirsutum*) transgénicos y

convencionales en el norte de Santa Fe, Argentina. *Revista de Biología Tropical*. 60: 611-623.

ArgenBio. 2014. Cultivos aprobados y adopción. Disponible en: <http://www.argenbio.org/index.php?action=cultivos&opt=5>. Último acceso: Julio 2014.

Corrêa, R.L., T.F. Silva, J.L. Simões-Araújo, P.A. V. Barroso, M.S. Vidal & M.F.S. Vaslin. 2005. Molecular characterization of a virus from the family Luteoviridae associated with cotton blue disease. *Archives of Virology*. 150: 1357-1367.

Di Rienzo, J.A., F. Casanoves, M.G. Balzarini, L. Gonzalez, M. Tablada & C.W. Robledo. 2010. Grupo InfoStat, FCA, Universidad Nacional de Córdoba, Argentina.

Erwin, T.L. 1982. Tropical forests: their richness in Coleoptera and other arthropod species. *Coleopterists Bulletin* 36:74-75.

García, M.A. & M.A. Altieri. 2005. Transgenic Crops: Implications for Biodiversity and Sustainable Agriculture *Bulletin of Science, Technology & Society*. 25 (4): 335-353

Gardiner, M.M., D.A. Landis, C. Gratton, D. Difonzo, M. O'neal, J.M. Chacon, M.T. Wayo, N.P. Schmidt, E.E. Mueller, & G.E. Heimpel. 2009. Landscape diversity enhances biological control of an introduced crop pest in the north-central USA. *Ecological Applications* 19: 143-154.

Hagenbucher, S., D.M. Olson, I. Ruberson, F.L. Wäckers & I. Romeis. 2010. Reduced foliage herbivory in bt cotton benefits phloem-feeding insects. *International biosafety of genetically modified organisms*. ISBGMO. Buenos Aires. pp. 158-159. Disponible en: <http://www.isbgmo.info/11th%20symposiumbuenos%20aires%20%20Argentina.pdf>. Último acceso: Septiembre de 2013.

- Hammer, O., D.A.T. Harper & P.D. Ryan.** 2012. PAST (Paleontological Statistics) version 2.16. Software package for education and data analysis. *Paleontología Electrónica* 4:1-9. Disponible en: <http://folk.uio.no/ohammer/past/>. Último acceso: Septiembre 2013.
- Heitholt, J.J.** 1999. Cotton: Factors associated with assimilation capacity flower production, boll set, and yield. En: *Crop yield, Physiology and processes*. Smith, L.D. & C. Hamel (Eds.). Stoneville, EEUU. pp. 235-269.
- Isaacs, R., J. Tuell, A. Fiedler, M. Gardiner & D. Landis.** 2009. Maximizing arthropod-mediated ecosystem services in agricultural landscapes: the role of native plants. *Frontiers in Ecology and the Environment* 7 (4): 196-203.
- Kos, M., J.J.A. van Loon, M. Dicke, & L.E.M. Vet.** 2009. Transgenic plant as vital components of integrated pest management. *Trends in Biotechnology* 27(11): 621-627.
- Lawo, N.C., F.L. Wäckers & J. Romeis.** 2009. Indian Bt Cotton varieties do not affect the performance of cotton aphids. *PLoS ONE* 4(3): e4804. Doi:10.1371/journal.pone.0004804.
- Lobry de Bruyn, L.A.** 1999. Ants as bioindicators of soil function in rural environments. *Agriculture Ecosystems & Environment*. 74: 425-441.
- Losey, J.E., & M. Vaughan.** 2006. The economic value of ecological services provided by insects. *BioScience* 56: 311-323.
- Magurran, A.E. & McGill, B.J.** 2011. Biological Diversity. *Frontiers in Measurement and Assessment*. Oxford University Press, New York. 345 pp.
- Marvier, M., C. McCreedy, J. Regetz, & P. Kareiva.** 2007. A meta-analysis of effects of Bt cotton and maize on nontarget invertebrates. En: *Integration of Insect-resistant genetically modified crops within IPM programs*. Romeis, J., A.M. Shelton, & G.G. Kennedy. Ed. Springer. USA. pp. 159-194.
- Molinari, A.M. & J.C. Gamundi.** 2010. La "chinche diminuta" *Nysius simulans* en soja. Para mejorar la producción 45: 117-119.
- Musser, F.R. & A.M. Shelton.** 2003. Bt Sweet corn and selective insecticides impacts on pests and predators. *Journal of Economic Entomology* 96 (1): 71-80.
- Naranjo, S.E.** 2009. Impacts of Bt crops on non-target invertebrates and insecticide use patterns. *CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources* 11: 1-23.
- Naranjo, S.E., J.R. Ruberton, H.C. Sharma, L. Wilson & K. Wu.** 2008. The present and future role of insect-resistant genetically modified cotton in IPM. En: *Integration of Insect-resistant genetically modified crops within IPM programs*. Romeis, J., A.M. Shelton, & G.G. Kennedy. Ed. Springer, USA. pp. 159-194.
- Pereyra, F.** 2003. Ecoregiones de la Argentina. Servicio Geológico Minero Argentino, Buenos Aires, Argentina. 182 pp.
- Qaim, M., E.J. Cap, & A. de Janvry.** 2003. Agronomics and sustentability of Transgenic Cotton in Argentina. *AgBioForum* 6 (1&2): pp. 41-47. Disponible en: <http://www.argenbio.org/adc/uploads/pdf/transgenic.pdf>. Último acceso: Agosto 2013.
- Romeis, J., D. Bartsch, F. Bigler, M.P. Candolfi, M.M.C. Gielkens, S.E. Hartley, R.L. Hellmich, J.E. Huesing, P.C. Jepson, R. Layton, H. Quemada, A. Raybould, R.I. Rose, J. Schiemann, M.K. Sears, A.M. Shelton, J. Sweet, Z. Vaituzis, & J.D. Wolt.** 2008. Assessment of risk of insect-resistant transgenic crops to nontarget arthropods. *Nature Biotechnology* 26 (2): 203-210.
- Romeis, J., S. Hagenbucher, D.M. Olson, J. Ruberson & F.L. Wäckers.** 2012. Reduced foliage herbivory in Bt cotton benefits phloem-feeding insects. The 12th International Symposium on Biosafety of genetically modified organisms. pp. P 2.46. Disponible en: <http://www.isbgmo.com/abstracts>. Último acceso: Octubre 2013
- Samways, M.J., M.A. McGeoch, & T.R. New.** 2010. Insects conservation: A handbook of approaches and methods. *Techniques in Ecology and Conservation Series*. Oxford University Press Inc., New York. 441 pp.
- Thomazoni, D., P.E. Degrande, P.J. Silvie & O. Faccenda.** 2010. Impact of bollgard genetically modified cotton on the biodiversity of arthropods under practical field conditions in Brazil. *African Journal of Biotechnology* 9 (37): 6167-6176.
- Thorbeck, P. & T. Bilde.** 2004. Reduced numbers of generalist arthropod predators after crop management. *Journal of Applied Ecology*. 41: 526-538.
- Trigo, E.J.** 2011. Quince años de cultivos Genéticamente Modificados en la agricultura Argentina. *ArgenBio*, 2011. 52 pp. Disponible en <http://www.argenbio.org/bfiles/fckimg/resumen%20ejecutivo.pdf>. Último acceso: Junio 2013.
- Uetz, G.W., J. Halaj & A.B. Cady.** 1999. Guild structure of spiders in major crops. *Journal Arachnology*. 27: 270-280.
- Wellings, P.W. & A.F.G. Dixon.** 1987. The role of weather and natural enemies in determining aphid outbreaks. En: *Insect Outbreaks*. P. Barbosa & J.C. Schultz (Eds.), New York: Academic Press. pp. 313-346.
- Whitehouse, M.E.A., L.J. Wilson & G.P. Fitt.** 2005. A Comparison of Arthropod Communities in Transgenic Bt and Conventional Cotton in Australia. *Environmental Entomology*. 34: 1224-1241.
- Xingyuan, Men., G. Feng, L. Xianghui & E.N. Yardim.** 2003. Diversity of Arthropod Communities in Transgenic Bt Cotton and Nontransgenic Cotton Agroecosystems. *Environmental Entomology* 32(2): 270-275.