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Araneofauna (Arachnida, Araneae) in conventional and organic crops of watermelon (*Citrullus lanatus*) in northeastern Brazil

Araneofauna (Arachnida, Araneae) en cultivos convencionales y ecológicos de sandía (*Citrullus lanatus*) en el noreste de Brasil

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Abstract: Spiders are considered generalist predators and sensitive to agricultural practices management. This study was conducted between 2011 and 2012 in the coastal tablelands of Piauí (Brazil), where we compared the community of spiders present in conventional crop of watermelon, organic crop and in a natural vegetation area. Sampling took place through two repetitions in the three systems, considering the crop cycle of 45 and 60 days. In each period, spiders were collected utilizing pitfall traps and diurnal and nocturnal manual collection. There were 506 individuals (21 families and 32 species). Seven families were shared by the three systems, being Lycosidae the most abundant in agricultural system and Corinnidae in the natural system. Regarding guild activity, ground runner hunters, stalker hunters and irregular web weavers were the most abundant. There were significant differences in the diversity between agricultural and natural systems. This work constitutes the first record on the spider community in crops of watermelon in Brazil.

Key words: Agroecosystems. Biodiversity. Natural Enemies. Spiders. Predators.

Resumen: Las arañas son consideradas depredadoras generalistas y sensibles a las prácticas de manejo agrícola. El estudio se realizó entre 2011 y 2012 en las llanuras costeras de Piauí (Brasil), donde se compararon las comunidades de arañas presentes en cultivos de sandía (convencional y orgánico) y un área con vegetación nativa. El muestreo se produjo a través de repeticiones en los tres sistemas, teniendo en cuenta el ciclo del cultivo de 45 a 60 días. En cada período, las arañas fueron obtenidas mediante trampas de caída y colecta manual (diurna y nocturna). Se recolectaron 506 individuos (21 familias y 32 especies). Siete familias se compartieron en los tres sistemas, siendo Lycosidae más abundante en los agrícolas y Corinnidae en el ambiente natural. En cuanto a la actividad gremial, las cazadoras corredoras sobre el suelo, las cazadoras al acecho y las tejedoras de telas irregulares fueron las más abundantes. Hubo diferencias significativas en los índices de diversidad entre los sistemas agrícolas y naturales y el número de arañas muestreadas en cada sistema no ha alcanzado una asíntota. Este trabajo constituye el primer aporte sobre la comunidad de arañas en cultivo de sandía para el Brasil.

Palabras clave: Agroecosistemas. Biodiversidad. Enemigos naturales. Arañas. Depredadores.

Introduction

Changes arising from environmental management type in an agroecosystem can reduce the possibility of maintaining a large number of species (Tscharntke *et al*. 2005). In this context, in agricultural ecosystems, more and more studies suggest that the level of internal control is also correlated to biodiversity present, both of plants as animals (Altieri 1999). Thus, the difference between conventional agriculture and ecological agriculture has received increasing interest in recent years (Bengtsson *et al*. 2005). Additionally, intensification of agriculture in last decades contributed to more uniform landscapes, larger fields of monocultures and the increase of the physical disturbance of habitats (Pluess *et al*. 2008).

The management type practiced can exert a strong influence on the abundance, diversity and composition of a large variety of species in an agroecosystem (Barrios *et al*. 2005). As an example, the spiders are among the first predators to recolonize the cultures after management practices due to their high mobility (Oberg and Ekbom 2006). However, unsustainable agricultural practices, such as excessive manuring, indiscriminate and massive use of pesticides, overlapping cycles, among others problems, contribute to the imbalance in these systems (Horne and Mcdermott 2001). These factors have mostly negative effects on the density and diversity of spiders in managed systems (Marc *et al*. 1999).

Spiders are considered common and very abundant predators in agroecosystems and they may significantly limit the pest populations and therefore, their impact (Chatterjee *et al*. 2009). These arthropods are at high trophic levels, no presenting host specificity, acting on the top of food chain of invertebrates, consuming all life stages of pest (Coddington *et al*. 1991; Sunderland 1999). Moreover, they can be found in most microhabitats, which makes the group one of the most diverse in the world (Wise 1993), being recorded more than 44.000 species distributed in 114 families (Platnick 2015).

As potential predators, the spiders have a functional complementarity in prey capture (Díaz *et al.* 2005) and organize themselves into guilds relatively well defined (Dias *et al.* 2010; Cardoso *et al.* 2011). Therefore, the identification of possible functional roles of spiders, their composition and factors influencing the structure of their community are essential in studies on the arthropod fauna in agroecosystem

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(Uetz *et al.* 1999). Thus, management success in a given agroecosystem depends essentially on the maintenance of their associated biodiversity.

In Brazil, studies about the fauna of spiders in agroecosystem have been conducted in cultures of cane sugar (Rinaldi *et al*. 2002), rubber trees (Rinaldi and Ruiz 2002), orange (Morais *et al*. 2007), tangerine (Ott *et al*. 2007) and rice (Rodrigues *et al*. 2008), but no study was carried out to do a characterization of spider communities on cultivation of watermelon for the country. This cultivation represents a production of 2,163,501 tons, according to Food and Agriculture Organization of the United Nations Statistics Division, putting Brazil in five place in world production (FAOSTAT, 2013). The aim of this study was to determine the composition, abundance, richness and functional attributes (guilds) of spiders present in watermelon crops under conventional and organic systems, having as control an area of natural vegetation adjacent to agricultural areas in the northern state of Piauí, Brazil.

Materials and methods

Study area. The study was conducted in the region of coastal tablelands of Piauí (03º05'S 41º47'W), between the years 2011 and 2012, municipality of Parnaíba, Piauí, northeastern Brazil (Fig. 1). The region is located to 40 m above sea level, with an average temperature of 27 ºC, relative humidity around 75%, annual average evaporation of 400 mm (Lima *et al*. 2008) and seasonal vegetation of tablelands (Fernandes *et al*. 1996). Sampling was conducted in three areas containing one hectare (ha) each one: (1) organic cultivation of watermelon –ORGA; (2) conventional cultivation of watermelon–CONV; and (3) natural vegetation - NATU.

The ORGA system, with three years of adoption, was so named because of management with the use of green manures, aspig bean (*Canavalia ensiformis* (L.) DC.), velvet bean (*Mucuna aterrima* (Piper Tracy) Holland), sunn hemp (*Crotalaria juncea* L.), pearl millet (*Pennisetum glaucum* (L.) R. Br.), cowpea (*Vignaun guiculata* (L.) Walp.), maize (*Zea mays* L.) and sunflower (*Helianthus annuus* L.). These manures were arranged in the system before planting the seedlings of watermelon and bio-fertilizers aerobic (manure + grass + leucaena) and anaerobic (manure + wood ash + vegetative material of banana (*Musa* spp.)) applied fortnightly. In the CONV system with six years of adoption, were applied via chemical inputs foundation (200 kg P_2O_5) and fertirrigation (120 kg of N + 120 kg of K_2O + Ca + B) The NATU system is characterized as a forestal area with a large concentration of litter on the ground and was considered as control area for ORGA and CONV systems. In each system of watermelon cultivation (ORGA and CONV), the seeds were sown at a spacing of 0.90 cm between plants and 2 m between rows. The crop was irrigated with a drip line lateral per row of plants and drippers spaced every 5 m. The NATU system was kept without artificial irrigation.

Spider sampling. Two sampling methods were used: (1) pitfall traps for invertebrates and (2) manual samplings (diurnal and nocturnal) time of 30 minutes each. The pitfall traps consisted of cups 500 ml buried in the ground, containing 200 ml of preservative liquid (sodium chloride solution to 10% + droplets detergent) kept in activity during five days in the field. These were arranged forming a "X", with one trap in the center and four in each edges, distant about 1 m one from another and connected by a plastic device 15 cm in height. The set of five traps were considered as one sample. Four samples were taken place in the areas of watermelon cultivation ORGA and CONV, two at 40 days and two at 60 days of cultivation, and four samples in the NATU system. Four diurnal manual samples and four nocturnal manual samples were performed in each system (CONV, ORGA and NATU), realized without delimitation of area and with a standardized time of 30 minutes.

The spiders were identified to species level or recognized in morphospecies when specific identification was not achieved. The voucher specimens were deposited in the Coleção de História Natural da Universidade Federal do Piauí-CHNUFPI (Natural History Collection of Federal University of Piauí), in Floriano, Piauí, Brazil (curator E.F.B. Lima). Spiders were classified in guilds according to Uetz *et al*. (1999), Dias *et al*. (2010) and Cardoso *et al*. (2011).

Data analysis. To evaluate the efficiency of sampling methods and to compare the species richness observed in each system we constructed rarefaction curves based on the number of individuals with 500 randomizations. We performed a species richness estimation using the nonparametric estimators Jackknife 1, Jackknife 2, ACE, ICE, Chao 1, Chao 2 and Bootstrap using the software EstimateS, version 8.0 (Colwell 2006). The choice of the best estimator of the species richness was obtained by the observation of the curve more similar to observed curve and greater tendency to stability (Toti *et al*. 2000). In this case, we present only the results of estimators Jackknife1 for the CONV and ORGA systems, and Chao 1 for NATU system.

The diversity of each system was determined by application of diversity index of Shannon-Wiener diversity index (H'), based on the proportion of the abundant species and of the evenness index of Pielou (J'), expressed by the ratio between observed diversity and maximum expected diversity (Magurran 1988). The nonparametric tests of Mann-Whitney (U) and Kruskal-Wallis (H) were used to compare the differences between species richness and total abundance per sampling method, as well as between the sampling methods for each studied system, using the software BioEstat 5.0 (Ayres *et al*. 2007).

Cluster analysis (UPGMA) was performed to assess patterns in the spider community composition between the systems, using Jaccard (qualitative) and Morisita-Horn (quantitative) the similarity coefficient. To check statistical differences between the species composition given for both indices we applied ANOSIM (one way), with Bonferroni correction for repeated testing. This procedure is a test based on permutation to detect differences between groups of multivariate samples (Clarke and Warwick 2001). To determine the percentage of the similarity of spider community between systems and which species contributed most to this variation we used a SIMPER analysis (similarity percentage). Analyses of diversity and similarity (Jaccard, Morisita, ANOSIM and SIMPER) were performed using the software PAST version 2.17 (Hammer *et al*. 2001).

Results

Composition of spider communities. In this study, we collected 506 spiders of 32 species. The ORGA system of watermelon presented the highest number of spiders (n = 253), followed by NATU system (n = 134) and CONV system (n = 119). The adults represented 44% of the total reported spiders (n = 221) being the most abundant males than females (n_{male} = 135, 61% versus n_{female} = 86, 39%) (Table 1). Considering the most abundant species for each system, *Steatoda* sp. with 26 individuals (39%) was the most abundant species for CONV watermelon system, while for ORGA system and NAT system the species most abundant was *Leprolochus oeiras* (Lise, 1994) with 35 individuals (33%) and subfamily spiders of Corinninae with 11 individuals (22%), respectively.

Guilds composition. The spider families sampled in the three treatments were grouped into seven guilds according to their functional attributes. There was a predominance of hunter spiders (86%) compared to web weaver spiders (14%). Among the hunters, the ground runner hunters (77%) and stalker hunters (14%) were predominated, while the foliage runner hunters and ambusher hunters showed abundances lower than 10%. With respect to the weavers, the most abundant guilds were the irregular web weavers (84%), while orb web weavers and sheet web weavers represented less than 10% each. The guild with the highest number of individuals was ground runner hunters (n = 330), which constituted the major guild in the three studied systems, mainly represented by Lycosidae in both ORGA and CONV systems (71% and 64% respectively) and Corinnidae (46%) in the NATU system (Table 2).

ORGA system showed the greatest guild richness (six), and the second most representative guild was the stalker hunters, mainly represented by Oxyopidae (87%). Besides, ambusher hunters, mainly represented by Thomisidae (67%) were registered solely for this system. In NATU system, the second guild most representative was foliage runner hunters, composed mainly by Miturgidae (62.5%). In CONV system, which showed the lowest richness of guilds, Theridiidae (71%) family was dominant in irregular web weaver guild that was the second most representative.

Spider diversity. The species accumulation curves did not reach an asymptote in none of the sampled systems. The NATU system presented the greatest number of species (Sobs = 16 ± 1.55) compared to the CONV (Sobs = 11 ± 2.57) and ORGA (Sobs = 13 ± 1.72) systems. Furthermore, the curves of richness estimators have not reached stability. The estimators that most nearly of observed richness were Jackknife 1 in the CONV (16.5 ± 2) and ORGA (17.58 ± 2.12) systems and Chao 1 in the NATU (17.67 ± 2.13) system. According to the distribution of species by system, the abundance was higher in the ORGA system (n = 105), followed by CONV (n = 66) and NATU (n = 50) systems, without any significant difference in relation to the collection method, both to richness (U = 4.050; df = 2; p (bilateral) < 0.0001) as to individuals number (U = 4.631; df = 2; p (bilateral) < 0.0001). The pitfall method was more efficient (n = 177) than manual collection method (n = 44).

There were significant differences between the diversity of NATU system when compared to the CONV and ORGA systems. Indices of diversity and evenness demonstrated that the NATU system had higher diversity (H' = 2.447) compared to the ORGA system (H' = 1.809) and CONV system (H' = 1.738). Although, the ORGA system presents the greater number of individuals, these belonged largely to *L. oeiras*. NATU system had fewer individuals, however were evenly distributed among species. The results of ANOSIM showed that the composition of spider communities was significantly different between the systems (R = 0.2013; p < 0.001). NATU system differed both in species richness and in abundance with CONV (R = 0.003) and ORGA systems (R = 0.0276), showing the separation of them from NATU system in the dendrogram (Fig. 2). The highest percentage of contribution to separation between NATU and CONV systems was due of *Steatoda* sp. with 32.4%, while the largest contribution to dissimilarity between NATU and ORGA systems was produced by *L. oeiras* with 16.3%. One Lycosidae species (morpho sp. 3) contributed more to the similarity between the ORGA and CONV systems.

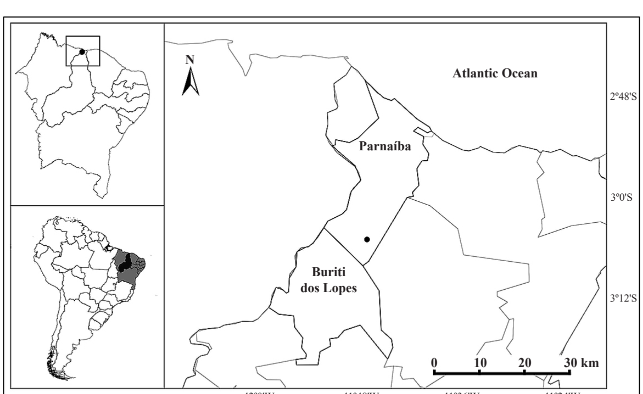

Figure 1. Geographic location of the sampling areas, municipality of Parnaíba, Piauí state, northeastern Brazil.

Discussion

Of the 21 families, four represented 72% of total spiders collected (Corinnidae, Lycosidae, Theridiidae and Zodariidae). These results corroborate with the study of Almada *et al*. (2012), which showed that only four spider families constitute 95% of the spider community in cotton crops in Argentina. Besides, the presence of Lycosidae and Theridiidae families coincides with study of Young and Edwards (1990) for North American crops. However, the results of this study differ from European agricultural systems (Nyffeler and Sunderland 2003), where the spider fauna is largely dominated by Linyphiidae. That family is also mentioned by Haddad *et al*. (2004, 2006) as household spiders most abundant in the soil environment, as well as in the tree layer of pistachio orchards in South Africa.

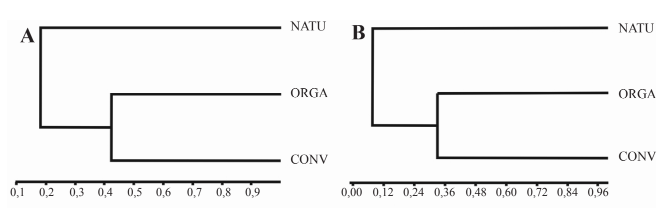

Figure 2. Cluster analysis (UPGMA) by similarity using species/morphospecies sampled in the systems: Watermelon conventional (CONV), organic (ORGA) and natural area (NATU) in Parnaíba-PI, northeastern Brazil: A: Coefficient of Morisita-Horn B: Coefficient Jaccard.

Table 1. Families and species/morphospecies and abundance of adults collected in watermelon cultivation and natural area in Parnaíba, Piauí, Brazil. CONV: System Watermelon conventional; ORGA: Organic watermelon system and NATU: natural vegetation system.

Families	Species/morphospecies	CONV	ORGA	NATU	Total
Araneidae	*Alpaida* sp.	1	0	0	1
Araneidae	*Metazygia* sp.	0	0	1	1
Ctenidae	*Centroctenus* sp.	0	0	2	2
Corinnidae	*Abapeba* sp.	0	0	2	2
Corinnidae	*Corinna* sp.	0	0	4	4
Corinnidae	Corinninae sp.	0	0	11	11
Corinnidae	*Falconinna gracilis* (Keyserling, 1891)	1	3	0	4
Corinnidae	*Mazax* sp.	0	1	0	1
Hahniidae	Morpho sp.	0	0	3	3
Lycosidae	Morpho sp. 1	1	0	0	1
Lycosidae	Morpho sp. 2	6	16	0	22
Lycosidae	Morpho sp. 3	12	30	0	42
Lycosidae	Morpho sp. 4	0	3	0	3
Linyphiidae	Morpho sp. 1	0	2	0	2
Miturgidae	*Cheiracanthium inclusum* (Hentz, 1847)	1	0	0	1
Miturgidae	*Teminius* sp. 1	1	1	0	2
Miturgidae	*Teminius* sp. 2	0	1	0	1
Oonopidae	*Neoxyphinus termitophilus* (Birabén, 1953)	0	0	2	2
Oonopidae	Oonopinae sp.	0	0	1	1
Oxyopidae	*Oxyopes* sp.	0	3	0	3
Pholcidae	*Ibotyporanga* sp.	0	0	1	1
Pholcidae	*Mesabolivar* sp.	2	0	0	2
Pholcidae	*Mesabolivar* aff. *spinulosus* (Mello-Leitao, 1939)	2	0	0	2
Salticidae	Morpho sp. 1	1	1	1	3
Salticidae	Morpho sp. 2	0	1	2	3
Salticidae	Morpho sp. 3	0	0	3	3
Theridiidae	*Steatoda* sp.	26	8	0	34
Theridiidae	Morpho sp. 1	0	0	5	5
Tetragnathidae	Morpho sp. 1	0	0	1	1
Zodariidae	*Cybaeodamus* sp.	12	0	0	12
Zodariidae	*Epicratinus* sp.	0	0	2	2
Zodariidae	*Leprolochus oeiras* (Lise, 1994)	0	35	9	44
Total		66	105	50	221

As suggested by Armendano and González (2010) in alfalfa cultivation in Argentina, spider hunters stood out in relation to weavers. However, differently of these authors which pointed out the predominance of ambusher hunters, the present study showed greatest contribution of ground runner hunters. Lee and Kim (2001) separated spiders in two guilds – builder of webs and hunters – considering the hunter spiders as the most effective predator. For Lang *et al*. (1999), wandering spiders has proven to play an important role in the control of herbivores populations in cultivated fields.

In the three systems studied, ground runner hunters were the guild most representative, with 72% in ORGA, 59% in CONV, and 58% in NATU system. Lycosidae family was the most abundant in agricultural systems here studied (CONV and ORGA), being considered by Schmidt and Rypstra (2010), as the group more successful in agroecosystems. This result corroborates with the study of Avalos *et al*. (2013) in cultivation of citrus at Argentina, which showed this family was the most abundant. In NATU system, Corinnidae was most abundant due perhaps to the concentration of leaf litter in this area. According to Carvalho and Avelino (2010), these spiders are abundant in areas with a concentration of leaf litter being characterized by Silva and Coddington (1996) as hunter spiders seeking prey in various microhabitats, such as under rocks and logs.

In CONV system, the irregular web weavers were the second most important guild of the system, mainly represented by Theridiidae. According to Turnbull (1973) for the construction of webs, different from hunters, they need to wait for food and cannot venture out looking for prey.

Similarly, Galvis and Daza (2005), in a study conducted in cultivation of transgenic cotton and conventional in Colombia, and Bambaradeniya and Edirisinghe (2001) in rice cultivation in Sri Lanka, observed that Theridiidae was the family with the largest number of individuals. This fact indicates that the system presented here is depleted relative to spider fauna, since overall this family does not have specificity by habitat (Azevedo *et al*. 2002).

ORGA system, that presented a major number of guilds, had the stalker hunters as the second most important guild with 16%, mainly represented by Oxyopidae. The presence of these spiders in this system is possibly related to the higher and denser vegetation available by the green manure, resulting in herbaceous vegetation. According to Ott *et al*. (2007), herbaceous vegetation is an essential factor for spiders Oxyopidae, due to the increase of places to hunting and shelter. Similar records were obtained in soybean crop in Argentina, where the species most abundant of herbaceous crop belonged to this family (Beltramo *et al*. 2006). In this system was also registered the exclusivity of ambusher hunters, represented mainly by Thomisidae. Armendano and González (2010) and Almada *et al*. (2012) showed that in Argentina, Thomisidae was very abundant in herbaceous layer in alfalfa and cotton crops.

The second guild most abundant in NATU system was the foliage runner hunters with 19%, being represented mainly by Miturgidae. These spiders according to Dias *et al*. (2010) are excellent hunters with their hunting activity and captures mainly at night, though the genera sampled in this work can be found during the day. This family according to Cunha *et al*. (2012) presents a good distribution in closed areas/coastal tablelands and according to Perez-Guerrero *et al*. (2009) was the most abundant family in cotton cultivation under ecological system of production. The natural area, associated with an increased concentration of leaf litter, tends to have more available resources for foraging, fostering an environment where each individual can explore a source of equal quality.

Table 2. Composition, abundance and richness of species/morphospecies of all spider families associated with the watermelon cultivation and natural area, grouped by guilds in Parnaíba-PI, Brazil. N: total abundance; CONV: watermelon conventional system; ORGA: watermelon organic system; NATU: natural vegetation system.

Guilds	CONV	ORGA	NATU	N	%
Ground runner hunters					
Corinnidae	4	10	36	50	9.88
Ctenidae	0	0	7	7	1.38
Gnaphosidae	0	0	9	9	1.77
Lycosidae	45	130	6	181	35.77
Oonopidae	0	0	4	4	0.79
Zodariidae	21	42	23	86	16.99
Stalker hunters					
Oxyopidae	0	40	0	40	7.90
Salticidae	1	6	14	21	4.15
Scytodidae		0	0	1	1
Foliage runner hunters					
Anyphaenidae	0	2	0	2	0.39
Miturgidae	6	6	15	27	5.33
Sparassidae	0	0	2	2	0.39
Ambusher hunters					
Philodromidae	0	1	0	1	0.19
Thomisidae	0	5	0	5	0.98
Irregular web-weavers					
Theridiidae	29	8	9	46	9.09
Pholcidae	12	0	1	13	2.56
Orb web-weavers					
Araneidae	1	1	1	3	0.59
Tetragnathidae	0	0	2	2	0.39
Uloboridae	0	0	1	1	0.19
Sheet web-weavers					
Hahniidae	0	0	3	3	0.59
Linyphiidae	0	2	0	2	0.39
Total	119	253	134	506	100%

The absence of asymptotic estimates in this study is directly related to the fact that the number of rare species remained stable and high. These attributes can indicate a performance realistic of the estimative calculations (Toti *et al*. 2000), despite being in an agricultural area. These estimates are related to high incidence of a large number of rare or less frequently species. According to Santos (2003), this situation is typical of tropical regions, where it is unlikely to achieve accumulation species curves.

Uetz and Unzicker (1976) observed that manual collection method, added few species to spider community in comparison with the pitfall trap, corroborating our results, in which it was identified that pitfall method captured higher number of exclusives species (n = 18) compared to manual method (n = 5). Carvalho *et al*. (2010) also pointed out similar results, although the two methods used by these authors are similar with respect to unique species, the pitfall trap contributed more to exclusivity.

The spider community, according to Wise (1993), is highly sensitive to environmental changes acting on the structure of habitats, causing significant changes in the distribution pattern of theirs species. However, there are some spiders that can tolerate certain environmental factors, in contrast to others which are less flexible to these changes, showing that each species has a different response according to environment characteristics (Foelix 1996). In this study we found some morphospecies (specially from Lycosidae), which seem not to be affected by disturbances, because they occur with a great abundance in areas with management pressure, contributing to the spider community composition observed between CONV and ORG systems as can be showed in the dendrogram (Fig. 2). Some species of Lycosidae, according to Schmidt and Rypstra (2010), are strictly related to habitat structure, being more active, especially when colonizing unoccupied habitats and avoid intraguild competition, being even more successful in agroecosystems highly disturbed due their role of good colonizers.

Comparison of these systems through the diversity index showed that CONV system has an araneofauna less diverse followed of ORGA and NATU systems. The diversity index assigns weight to rare species and expressed the importance of the relative abundance of each species (Magurran 1988). These observations may be likely related to lower variability in CONV environments, since the dominance of one species *Steatoda* sp. affected the values of uniformity and contributed to the separation of this system from the NATU. Although the diversity of species of ORGA system has been low compared to NATU one, this system showed the greatest number of individuals. However the species *L. oeiras* was dominant, affecting the uniformity between species and separated this system of the NATU.

In general, the agricultural systems studied here present different species compared to NATU. This fact has a relationship among the specialist species of spiders, since they can live in different environments. In addition, several studies have reported that spiders are sensitive to changes in habitat structure, including its complexity and ground cover (Wise 1993). Thus, it can be inferred that habitats most heterogeneous in structures as in NATU system leads to more variety in terms of the species diversity in comparison to ORGA and CONV systems. According to Langellotto and Denno (2004), structural complexity with in agricultural habitats is known to be an important factor of influence on dynamic population of spiders, and following to Bell *et al*. (2001) that both the vegetation structures as well as the layer of leaf litter determine the microclimatic conditions which are important for the spiders. Still, there is a need to assess the ecology of these species, because little is known about the natural history of Neotropical spiders (Peres *et al*. 2007). This work is the first constitution to the spider community in cultivated watermelon to Brazil. The data here presented show that the maintenance of agricultural systems under organic management without soil disturbance and presence of green manure, give a considerable advantage in terms of abundance, but not in relation to the species diversity of spiders. However, a greater number of predators, by itself, is important to prevent the proliferation of pests. The key is to identify the type of biodiversity desirable to maintain and / or increase ecological services and thus determine the best practices that will stimulate the desired components of biodiversity.

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