

Mites associated with açaí palm trees (*Euterpe oleracea*: Arecaceae) in native and cultivated areas of the state of Pará, eastern Amazon, Brazil

EDNA ANTÔNIA DA SILVA BRITO

edna.silvabrito2@gmail.com

University of Taquari Valley – UNIVATES

IURY SILVA CASTRO

University of Taquari Valley – UNIVATES

ALOYSÉIA CRISTINA SILVA NORONHA

Embrapa Amazônia Oriental

NOELI JUAREZ FERLA

University of Taquari Valley – UNIVATES

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Abstract

The objective was to quantify and analyse the diversity of mites associated with native and cultivated açai palms crops, as well as their distribution in the dry and rainy seasons in the municipalities of Bragança and Augusto Corrêa, state of Pará. Rarefaction curves were generated for diversity values using the statistical programming language R, rarefaction curves for estimates of richness and equitability and analysis of variance with permutations. A total of 2,069 mites from 28 families were sampled, being most representative Phytoseiidae (32.4%), Phytoptidae (13%), Cunaxidae (7.7%), Tetranychidae (5.6%) and Tydeidae (4.9%). Among predators, the most abundant species were *Amblyseius* sp. 1, *Armascirus amazoniensis* Wurlitzer & Silva, *Iphiseiodes zuluagai* Denmark & Muma, *Scutopalus tomentosus* Rocha, Skvarla & Ferla, and the phytophagous mites *Acaphyllisa* sp., *Davisella* sp., *Oligonychus* sp. and *Retracus johnstoni* Keifer. In the rainy season, more mites were sampled ($n = 1,176$) than in the dry season ($n = 893$). The greatest richness was observed in the dry period (73 species) and diversity was also greater in this period. In the municipality of Bragança there was greater richness (78 species) and the cultivated açai trees had greater acarine abundance (74.7%) than the native ones. However, natives had slightly higher wealth (6%) than those cultivated. The diversity and richness of predatory mites show the potential of the Amazon biome to be used in applied biological control.

Introduction

The açai palm trees (*Euterpe oleracea* Mart.: Arecaceae), native to the Brazilian Amazon, has the state of Pará as the largest producer and consumer of the fruit. The gain in fruit production is related to the fact that açai, previously aimed solely at local consumption, has reached new markets and has become a commodity and an important source of income and employment (Menezes et al. 2009). The fruit is consumed by all social classes, making it a product with high market potential, allowing added value, reducing market risks, making the activity competitive, generating employment and income in rural areas (Silva & Da Silva, 2006).

Several organisms reach pest status, causing damage to this palm tree, but there is little information about the presence of mites on this plant. Phytophagous mites with previously reported potential to cause damage to crops belong to the families Eriophyidae, Tarsonemidae and Tetranychidae (Schruff, 1985; Duso & Lillo, 1996). In Brazil, several phytophagous mite species have already been reported in *Euterpe edulis* Martius (Arecaceae): *Brevipalpus phoenicis* (Geijskes), *Brevipalpus* sp., *Tenuipalpus* sp. (Tenuipalpidae) e *Eutetranychus* sp., *Tetranychus* sp., *Oligonychus* sp. and *Schizotetranychus* sp. (Tetranychidae) (Arruda Filho & Moraes, 2002; Rodrigues et al. 2016).

With the increase in commercial crops in the state of Pará, research demands arise to ensure the safe and sustainable development of production (Oliveira et al. 2002). It is necessary, for example, to know the potential organisms that could reach pest status related to this palm tree, affecting survival or production (Santos et al. 2015). The occurrence of mite species in high populations can compromise the productivity of açai groves, and it is important to identify arthropods that cause damage and injuries. In view of this, the need to know and identify the associated acarofauna, highlighting the phytophagous and predatory mites, is justified, aiming to create possibilities for alternative control of pest mites in that crop. This work aimed to understand the acarofauna associated with native açai crops and cultivated in the dry and rainy seasons, as well as their distribution on the plant, in the municipalities of Bragança and Augusto Corrêa, state of Pará.

Materials and methods

Study location and sampling procedure

The study was carried Northeast of the state of Pará. The collections were carried out in commercial areas at Fazenda Alto Arajivu (coordinates 1°10'18.6"S, 46°43'49.3"W), at 41 m altitude and Sítio Jiquiri (1°03'59.8"S 46°44'40.0"W) 16 m above sea level, in areas of natural and commercial açai cultivation in the Bragança (Bragantina microregion) and Augusto Corrêa, in the Sítio Coisas da Roça (1°03'58.91"S 46°66'23.30"W) and Fazenda Bacuri (1°04'11.10"S 46°66'33.82"W) (Fig. 1). Collections took place in Augusto Corrêa, in the dry season, between August, October and December 2021, and in the rainy period, between January, April and June 2022, and in Bragança, the dry period corresponded to August and December and the rainy period, between January and June. The plants measured two to three meters in height, aged between three and eight years.

The region's climate is hot and humid equatorial (Amw'), according to the Köppen classification, characterized by a very rainy season, between December and May, and a dry season, in the other months of the year. The average annual rainfall is 2,500 mm and the relative humidity varies from 80–91%. The average temperature is 27.7 °C, which can vary from 20.4 to 32.8 °C (Martorano et al. 1993).

Sample processing and mite identification

All leaves collected were placed in paper bags, kept in a cooler with Gelox® at a low temperature (ca. 15°C), being sent to the biology laboratory of the Federal Institute of Education of Pará (IFPA) for screening. The mites were observed using a stereomicroscope (Zeiss Stemi 305) and mounted on microscope slides in Hoyer's medium (Jeppson et al. 1975) and placed in a kiln for 10 days at 50–60°C. Species identification was carried out in the Acarology laboratory at Universidade do Vale do Taquari – Univates. The prepared specimens were examined with a phase contrast microscope (Axio Scope. A1-Zeiss), and taxonomic keys. Species identification was carried out in the Acarology laboratory of the University of Vale do Taquari - Univates, using an OMAX 40x -2500x trinocular phase contrast microscope with an OMAX S35180U3-18Mp camera, and taxonomic keys (Baker and Tuttle 1994; Kazmierski 1998; Chant and McMurtry 2007; Mesa et al. 2009; Johann et al. 2013; Skvarla et al. 2014 and Wurlitzer et al. 2020 and others). Specimens proving the mite species collected in the study are deposited at the Museum of Natural Sciences (ZAUMCN) at UNIVATES, Lajeado, Rio Grande do Sul. Environmental data on temperature, relative humidity, atmospheric pressure and precipitation were collected at the National Institute of Meteorology (INMET) and used to explain the ordering generated in the analyses.

Statistical analysis

Data analysis. In order to explore and analyze in detail the variability and composition of these organisms in açai plantations in two municipalities in the state of Pará/Brazil, during the months of mite collection.

Mite abundance by period, municipality and planting. This sample survey quantified and analyzed the diversity of mites in the two aforementioned municipalities (Augusto Corrêa vs. Bragança) during two different periods (dry vs. rainy), in addition to investigating this also in cultivated açai plantations vs. native. As some species may not be determined because they are new species or genera or, even, due to the collection of immature individuals (which make taxonomic identification difficult), throughout this text, the organisms sampled will be treated as species or morphospecies. In this way, a pyramid graph was generated of the total number of mites within each family in order to enable an exploratory analysis of the distribution of these organisms between the two municipalities, the two periods and the two types of açai planting. With this, it is possible to observe particularities and potential contributions of each taxonomic group to the mite community in this context.

Sampling effort and diversity. As part of the analysis in this study refers to the complexity and diversity of species/morphospecies, the sampling effort to collect the greatest taxonomic variability in these localities is important in order to become a representative analysis. Thus, rarefaction curves were generated for Chao1 diversity values with 99 permutations (Chao & Jost, 2015). This metric estimates the richness in a biological sample based on the number of rare and unique species present in the sample, considering species that were observed only once (singular species) and those that were observed twice (dual species), and so on. onwards, to make an estimate of total wealth. This makes this method more robust, especially when there may be many rare species in the sample that may not have been detected in the sample. Therefore, when Chao1 includes unique species in the estimate, it helps to correct biases caused by insufficient sampling (undersampling).

Therefore, the rarefaction curves for observed and extrapolated richness estimates were generated using the 'specpool' function of the vegan package (Oksanen et al. 2018) using the statistical programming language R (Ihaka & Gentleman, 1996; R Development Core Team 2022) for this and subsequent analyses. The calculation for these rarefaction curves and their respective dispersion measures (95% confidence interval) were based on the total abundance of specimens per species/morphospecies collected. They were generated using the 'iNEXT' function of the iNEXT package (Hsieh & Chao, 2016) in R.

Hill's diversity. Despite being able to analyze different diversity indices (e.g. Shannon-Winner, Simpsons, Margalef) in a particular and individual way, this approach may be biased towards what each of these indices considers in their respective formulas. In other words, each of them focuses on some premises that can give greater relevance to the presence of rare species, others that are more abundant, among other things. Hill's diversity profile is an interesting approach because it allows us to monitor, in a more dynamic way, how each of the mite communities (municipalities, periods, types of planting) behaves when different diversity indices attribute more weight to rare or dominant species (Hill, 1973).

In general, this analysis generates a scale along the x-axis of the graph based on the Renyi index with different orders of magnitude (Hill, 1973). This makes it possible to observe which communities are more diverse and on what scale of magnitude than the others and from what perspective (rarity of species/taxa vs. abundance of species/taxa). Thus, Hill's diversity profile is especially useful for verifying how the relative presence of more abundant species/taxa in comparison to less abundant ones contribute to altering the diversity of the organism community. Therefore, the scale on the x-axis focuses on different aspects of diversity and thus allows a more detailed analysis of the structure of the mite community based on simultaneous data on its richness, its evenness and its sensitivity to dominant species, with the values on the side left side of the graph more sensitive to rare species and the values on the right side are more sensitive to abundant or more common species (Tóthmérész, 1995). This analysis was carried out using the 'renyi' function (hill = TRUE) from the vegan package (Oksanen et al. 2018) in R.

Mite community structure. Species/morphospecies composition is an important factor in evaluating the diversity of organisms in a system or location. In this way, orders based on non-metric multidimensional scaling (NMDS) were generated for each attribute in question (period, municipality and planting) to evaluate the structure of mite communities in those locations. Before that, however, the abundance data was standardized using the 'decostand' function (method = Hellinger) from the vegan package (Oksanen et al. 2018) in R. After that, this amount of standardized data was transformed into a dissimilarity matrix by the Bray-Curtis method using the vegan 'vegdist' function (Oksanen et al. 2018) in R. The arguments used to generate the NMDS were using the 'metaMDS' function (k = 3 dimensions) also from vegan (Oksanen et al. 2018) in R. The quality of the NMDS adjustment was evaluated using the resulting stress value, with values < 0.2 considered adequate.

To test whether the respective mite communities were statistically different from each other, we used an analysis of variance with permutations (n = 99) (PERMANOVA) using the 'adonis2' function in the vegan package (Oksanen et al. 2018) in R. The permutations were stratified according to the collection campaigns (1st, 2nd, 3rd). Additionally, a multivariate homogeneity analysis of group dispersions was carried out using the vegan 'betadisper' function (Oksanen et al. 2018) in R, which calculates the average distance of groups through their centroid, which helps to verify whether the results, significant or not, of PERMANOVA were not actually affected by data dispersion (greater variability within groups than between them).

The final ordering result generated by the NMDS can be affected by both the species/taxa present and ecological factors. Thus, to analyze which species/taxa were the most representative or determinant for the pattern generated by the NMDS ordination and which ecological factors (e.g. temperature, relative humidity, atmospheric pressure and precipitation) would be contributing significantly to those mite community structures, we used the 'envfit' function from the vegan package (Oksanen et al. 2018). This function adjusts environmental vectors in the NMDS to assess how environmental variables can influence community structure. The interpretation of the results from this analysis involves the assessment of the direction and magnitude of the environmental vectors (i.e. coefficient of variation) significant in relation to the dispersion of the samples in the ordination space.

Distribution in the plant. An experimental design was carried out to compare the abundance of mites in plant strata, in the basal, median, apical regions and in the fruit of cultivated vs. native açai palms. As there were at least three collection campaigns (time factor) in the same sampling points, this demonstrates a repetition factor that can generate pseudo-repetitions or non-independence of the data, as it involves sampling organisms in exactly the same

locations. To deal with data of this nature, we adjusted a Generalized Linear Mixed Model (GLMM) in order to evaluate which of the plant substrates would be significantly different from each other. Therefore, to obtain the best model that fits the data, two GLMMs were generated, one with a Poisson error distribution family and the other with negative binomial. These models were generated using the functions *glmer*´ and *glmer.nb*´, respectively from the lme4 package (Bates et al. 2015). Model selection was based on choosing the one with the lowest Akaike Information Criterion (AIC), using the *AICcTab*´ function from the bbmle package (Bolker & R Core Team, 2020).

The structure of these GLMMs was as follows: dependent variable – the number of mites observed; the independent variables – plant substrate (basal, median, apical, fruit) and the type of planting (cultivated vs. native), as well as the interaction between them (substrates * type of planting). The structure of the random effects of these models was nested (1/municipality/period). After that, paired comparisons were made between the different types of substrates and the types of açai planting. For this, the *'emmeans'* function was used, adjusting the p values using the False Discovery Rate (FDR) method, present in the *emmeans* package (Lenth, 2018).

Results

In total, 2,069 mites belonging to 28 families and 87 species/morphospecies were sampled (Table 1). The most representative families were Phytoseiidae (32.4%), Phytoptidae (13%), Cunaxidae (7.7%), Tetranychidae (5.6%) and Tydeidae (4.9%). According to our richness estimates, the quantity of mites sampled throughout this study was satisfactory, considering that the estimated richness was 96 ± 6 s.e.. Thus, the richness found in this work indicates that few species were no longer collected. Environmental variability (temperature and relative humidity) between municipalities and collection periods with the respective quantity of mites collected (Fig. 2). The most abundant species were *Amblyseius* sp.1, *A. amazoniensis*, *Acaphyllisa* sp., *Davisella* sp., *I. zuluagai*, *R. johnstoni*, *S. tomentosus*.

Table 1

Acarofauna collected in the Açaí culture during the Dry and Rainy periods, in the municipalities of Augusto Corrêa and Bragança, state of Pará, Brazil. (N - total number of mites sampled).

Families (N)	Species/morphospecies	Augusto Corrêa				Bragança				N	%
		Dry		Rainy		Dry		Rainy			
		Cultivated	Native	Cultivated	Native	Cultivated	Native	Cultivated	Native		
Acaridae (88)	Immature	0	0	0	0	0	0	1	1	2	0.1
	<i>Rechiacaros</i> sp.	59	0	0	0	2	0	22	0	83	4.0
	<i>Tyrophagus putrescentiae</i>	0	0	0	0	0	3	0	0	3	0.1
Ameroseiidae (1)	<i>Ameroseius</i> sp.	0	0	1	0	0	0	0	0	1	0.0
Ascidae (18)	<i>Asca</i> sp.1	0	0	0	0	1	1	0	1	3	0.14
	<i>Asca</i> sp.3	0	0	0	0	1	0	0	8	9	0.4
	Immature	0	0	0	0	0	3	2	1	6	0.3
Bdellidae (33)	<i>Bdella uckermanni</i>	1	0	16	0	8	0	0	0	25	1.2
	<i>Hexabdella</i> sp. 2	0	0	0	0	5	2	0	0	7	0.3
	<i>Trachymolgus</i> sp.	0	0	0	0	0	1	0	0	1	0.0
Caligonellidae (5)	<i>Neognatus</i> sp.	0	0	2	0	3	0	0	0	5	0.2
Cheyletidae (20)	<i>Cheletomimus</i> (H.) <i>bakeri</i>	0	0	2	0	0	0	0	2	4	0.2
	<i>Cheletomimus</i> (H.) <i>darwin</i>	0	7	0	0	0	4	0	1	12	0.6
	<i>Cheletomimus</i> (H.) <i>duosetosus</i>	0	0	0	0	0	1	0	2	3	0.1
	<i>Cheletomimus</i> (H.) <i>wellsi</i>	0	0	0	0	1	0	0	0	1	0.0
Cunaxidae (159)	<i>Armascirus amazoniensis</i>	3	1	0	0	2	2	26	28	62	3.0
	<i>Cunaxatricha</i> n. sp.	0	0	0	0	3	2	0	0	5	0.2
	<i>Neobonzia</i> sp.	0	0	0	0	2	2	0	0	4	0.2
	<i>Neocunaxoides ovatus</i>	0	0	0	0	2	2	6	10	20	1.0
	<i>Scutopalus tomentosus</i>	0	0	0	0	10	9	32	17	68	3.3
Diptilomiopidae (62)	<i>Davisella</i> sp.	0	0	14	0	0	0	35	13	62	3.0
Eriophyidae (81)	<i>Acaphyllisa</i> sp.	0	0	42	0	2	0	10	27	81	3.9
Erythraeidae (1)	Immature	0	0	0	0	0	0	0	1	1	0.0
Eupalopsellidae (5)	<i>Eupalopsellus</i> sp.	0	0	1	0	1	1	1	1	5	0.2
Eupodidae (27)	<i>N. genus</i>	0	0	0	0	9	1	8	9	27	1.3
Glycyphagidae (16)	<i>Lepidoglyphus</i> sp.	0	0	5	0	0	3	2	6	16	0.8
Iolinidae (67)	<i>Parapronematus</i> sp.	15	0	2	0	6	5	2	1	31	1.5
	<i>Pseudopronematus</i> sp.	0	7	3	0	0	0	22	4	36	1.7
Laelapidae (5)	<i>Pseudoparasitus</i> sp.	0	0	0	0	0	0	1	1	2	0.1
	Immature	0	0	0	0	2	0	0	1	3	0.1
Olagamasidae (5)	Olagamasidae Immature	0	0	0	0	2	0	0	3	5	0.2
Oribatida (99)	Oribatida	7	4	1	0	81	0	2	4	99	4.8
Parholaspididae (1)	Immature	0	0	0	0	0	0	1	0	1	0.0

Families (N)	Species/morphospecies	Augusto Corrêa				Bragança				N	%
		Dry		Rainy		Dry		Rainy			
		Cultivated	Native	Cultivated	Native	Cultivated	Native	Cultivated	Native		
Phytoptidae (268)	<i>Retracus johnstoni</i>	0	0	150	0	3	3	82	30	268	13.0
Phytoseiidae (677)	<i>Amazoniaseius imparisetosus</i>	0	0	0	0	0	2	0	3	5	0.2
	<i>Amblydromalus</i> sp.	0	0	0	0	0	0	0	1	1	0.0
	<i>Amblydromalus itacoatiarensis</i>	24	2	0	0	7	0	3	15	51	2.5
	<i>Amblyseius</i> n. sp.1	0	6	0	0	9	18	15	99	147	7.1
	<i>Amblyseius</i> n. sp.2	11	4	9	0	22	15	7	8	76	3.7
	<i>Amblyseius</i> n. sp.3	0	14	0	0	30	58	0	34	136	6.6
	<i>Amblyseius</i> n. sp.6	0	0	0	0	1	12	0	9	22	1.1
	<i>Amblyseius largoensis</i>	0	0	11	0	0	1	0	0	12	0.6
	<i>Amblyseius tamatavensis</i>	0	0	0	0	1	0	0	0	1	0.0
	<i>Euseius alatus</i>	0	1	0	0	0	0	0	0	1	0.0
	<i>Euseius inouei</i>	1	0	0	0	0	2	1	0	4	0.2
	<i>Iphiseiodes quadripilis</i>	0	0	0	0	0	2	0	0	2	0.1
	<i>Iphiseiodes zuluagai</i>	1	5	1	0	42	8	0	0	57	2.8
	<i>Leonseius regularis</i>	0	1	0	0	0	13	1	0	15	0.7
	<i>Metaseiulus (M.) ferlai</i>	0	0	0	0	0	1	0	0	1	0.0
	n. genus sp.1	0	0	0	0	0	1	0	2	3	0.1
	<i>Paraphytoseius orientalis</i>	0	0	0	0	0	1	0	0	1	0.0
	<i>Phytoscutus sexpilis</i>	1	0	0	0	0	0	0	0	1	0.0
	<i>Proprioseiopsis neotropicus</i>	0	2	0	0	0	0	1	2	5	0.2
	<i>Typhlodromips</i> n. sp.	0	0	0	0	0	1	0	2	3	0.1
	<i>Typhlodromips mangleae</i>	21	1	0	0	8	0	0	6	36	1.7
	<i>Typhlodromus (T)</i> n. sp.	0	0	0	0	8	1	0	0	9	0.4
	Immature	0	0	0	0	19	17	19	33	88	4.3
Stigmaeidae (17)	<i>Agistemus brasiliensis</i>	1	0	4	0	1	0	0	1	7	0.3
	<i>Agistemus</i> n. sp.1	0	1	0	0	0	4	0	0	5	0.2
	<i>Zetzellia quasagistemus</i>	0	0	0	0	0	1	0	0	1	0.0
	Immature	0	0	1	0	0	0	2	1	4	0.2
Tarsonemidae (15)	<i>Ceratarsonemus</i> sp.	0	0	0	0	0	1	0	3	4	0.2
	<i>Tarsonemus</i> sp.2	1	0	0	0	0	0	0	0	1	0.0
	<i>Xenotarsonemus</i> sp.1	0	0	0	0	0	0	0	1	1	0.0
	<i>Xenotarsonemus</i> sp.2	0	0	0	0	0	0	0	3	3	0.1
	<i>Xenotarsonemus</i> sp.3	0	0	3	0	0	0	0	3	6	0.3
Tenuipalpidae (90)	<i>Brevipalpus yothersi</i>	0	0	37	0	0	0	0	0	37	1.8
	<i>Brevipalpus</i> sp.1	2	1	12	0	0	0	0	0	15	0.7
	<i>Tenuipalpus</i> sp.1	0	3	0	0	0	7	0	0	10	0.5
	Immature	0	0	26	0	0	2	0	0	28	1.4

Families (N)	Species/morphospecies	Augusto Corrêa				Bragança				N	%
		Dry		Rainy		Dry		Rainy			
		Cultivated	Native	Cultivated	Native	Cultivated	Native	Cultivated	Native		
Tetranychidae (115)	<i>Oligonychus</i> sp.	3	1	0	0	54	9	0	15	82	4.0
	<i>Tetranychus urticae</i>	12	0	0	0	2	0	0	1	15	0.7
	<i>Tetranychus</i> aff. <i>palmarum</i>	5	1	0	0	11	0	1	0	18	0.9
Triophyteidae (42)	<i>Triophyteus lebruni</i>	10	0	2	0	0	0	2	17	31	1.5
	<i>Triophyteus</i> sp.	5	0	0	0	1	0	1	0	7	0.3
	Triophyteidae Immature	2	0	2	0	0	0	0	0	4	0.2
Tuckerellidae (47)	<i>Tuckerella ornata</i>	0	0	18	0	15	0	0	14	47	2.3
Tydeidae (101)	<i>Brachytydeus formosa</i>	1	0	38	0	0	1	0	1	41	2.0
	<i>Pretydeus</i> sp.1	0	1	0	0	0	1	0	2	4	0.2
	<i>Pretydeus</i> sp.2	0	0	0	0	0	0	0	2	2	0.1
	<i>Pseudolorryia</i> sp.1	1	0	0	0	0	1	0	14	16	0.8
	<i>Pseudolorryia</i> sp.2	0	0	0	0	10	0	0	0	10	0.5
	<i>Tydeus</i> sp.1	5	0	0	0	1	0	0	1	7	0.3
	<i>Tydeus</i> sp.2	0	0	0	0	7	0	0	0	7	0.3
	Immature	0	0	0	0	14	0	0	0	14	0.7
Winterschmidtidae (4)	<i>Oulenzia</i> sp.	3	0	0	0	0	0	0	0	3	0.1
	Immature	1	0	0	0	0	0	0	0	1	0.0
		Augusto Corrêa				Bragança					
		Dry		Rainy		Dry		Rainy			
		Cultivated	Native	Cultivated	Native	Cultivated	Native	Cultivated	Native		
Diversity											
	Richness	25	19	25	0	40	42	28	50		
	Abundance	196	63	403	0	409	225	308	465		
	Dominance	0.14	0.10	0.18	0.00	0.09	0.10	0.12	0.08		
	Shannon-Wiener	2.47	2.55	2.27	0.00	2.93	2.95	2.52	3.10		
	Uniformity	0.47	0.68	0.39	0.00	0.47	0.46	0.44	0.44		
	Equitability	0.77	0.87	0.71	0.00	0.79	0.79	0.76	0.79		

Mite abundance and diversity. The data indicate that more mites were sampled in the rainy period ($n = 1,176$) than in the dry period ($n = 893$), or around 32% more mites in the rainiest and most humid period than in the hottest period (Fig. 3A, Table 1). Despite a greater abundance of mites in the rainy season, greater richness was observed in the dry season with 73 species, while in the rainy season there were 65, that is, in the dry season 12.3% more species/morphospecies were sampled than in the rainy season. (Fig. 3B). Due to the abundance of mites collected throughout this study in açai crops, it was observed that both periods, the richness was similar between them and, possibly, there was a very efficient and satisfactory sampling of the diversity of mites in açai crops (Fig. 3B).

Regarding the Hill diversity profile, the dry period was more diverse, presenting higher values along the entire x axis for the Hill diversity order parameters (Fig. 3C). However, the pattern of Hill's diversity profile was similar between both periods. This suggests that although the mite community in açai crops is more diverse in the dry season, the rainy season was not far behind. This highlights similar dynamics between both mite communities, whether when less abundant (rare) species are more important for this estimate, when the scale moves to the left, that is, when more abundant taxa gain greater relevance moving towards the right. of the scale on the x-axis.

The ordination of the mite community composition in relation to the period showed a satisfactory NMDS fit (stress = 0.10, non-metric fit $[R^2] = 0.98$). PERMANOVA analysis indicated a significant difference in the structure of the mite community between the dry and rainy periods ($F(1, 72) = 3.85$, $R^2 = 0.05$, P

= 0.01. Figure 3D). Despite the statistical significance, the coefficient of determination (R^2) was quite low, requiring caution when interpreting the proportion of variability explained by the NMDS. No statistical difference was observed in the homogeneity of dispersion between these groups ($F(1,71) = 0.94$, $P = 0.32$), indicating that the PERMANOVA result was not influenced by variability within the groups.

Out of a total of 87 acarine species, 11 of them played a significant role in the NMDS ordination (Table 2. Figure 3D), highlighting the importance of these species/morphospecies. Regarding the four ecological factors, it was observed that three of them had a significant contribution to this ordering (Fig. 3D). Thus, temperature ($R^2 = 0.24$, $P = 0.001$), relative humidity ($R^2 = 0.11$, $P = 0.015$) and atmospheric pressure ($R^2 = 0.11$, $P = 0.008$) were relevant in determining the community structure according to the NMDS.

Table 2
Mite species with significant contribution to the NMDS ordination based on community structure in the dry and rainy periods (Fig. 2D).

Species/morphospecies	p-value
Ascidae Immature	0.01
<i>Bdella uckermanni</i>	0.01
<i>Armascirus amazoniensis</i>	0.01
<i>Neocunaxoides ovatus</i>	0.03
<i>Scutopalus tomentosus</i>	0.03
<i>Davisella</i> sp.	0.03
<i>Lepidoglyphus</i> sp.	0.04
<i>Retracus johnstoni</i>	0.01
<i>Amblyseius</i> n. sp1	0.04
<i>Brevipalpus</i> sp.1	0.02
<i>Tuckerella ornata</i>	0.02

Mite abundance and diversity. The data indicate that in Bragança there was greater abundance ($n = 1,407$), while Augusto Corrêa contributed a total of 662 individuals (Fig. 4A). Bragança recorded more than twice the acarine abundance than Augusto Corrêa, making a percentage 112, 39% higher. Similarly, Bragança presented a greater richness, totaling 78 species, while Augusto Corrêa presented 48 species (Fig. 4B). This represents a percentage difference of 62.5% more mite species in Bragança. The rarefaction curve shows that a slightly greater sampling effort in Bragança could collect some more species, not collected in this study, while the Augusto Corrêa rarefaction curve practically achieved a satisfactory sampling despite having collected fewer individuals and presenting lower richness. (Fig. 4B).

Hill's diversity profile indicates antagonistic situations when rare species/morphospecies or abundant species/morphospecies are considered. For example, when rare species are more important for this estimate, Bragança presents greater diversity in the mite community, indicating that the greater number of individuals collected in this location may have contributed to increasing the structural complexity of the community, contributing species/morphospecies that would be difficult to collect. with a smaller number of individuals (Fig. 4C). However, when observing the Shannon-Wiener index (exponential of entropy) represented by the number one, on the x axis, both municipalities present a very similar diversity to each other. From this point, towards the right of the graph, when more abundant species/taxa are more relevant, the acarine community of Augusto Corrêa becomes more diverse than that of Bragança. Therefore, unlike the diversity profile between periods (dry vs. rainy), where the difference in diversity was less pronounced, in the case of municipalities, the differences were marked to the point where the diversity of the mite community changed. Thus, when more abundant species/morphospecies have greater weight in the analysis of Hill's diversity profile, municipalities assume an opposite role than when rare species are considered.

The ordination of the mite community composition in relation to the municipality also presented a satisfactory fit in the NMDS (stress = 0.10, non-metric adjustment [R^2] = 0.98). PERMANOVA analysis revealed significant differences in the structure of the mite community between Augusto Corrêa and Bragança ($F(1, 72) = 3.86$, $R^2 = 0.05$, $P = 0.01$. Figure 4D). Again, the coefficient of determination (R^2) was quite low, indicating that the variability explained by the NMDS in comparison with the analysis between periods must be analyzed with caution since other factors, not analyzed in this work, may help to explain the difference in mite community between the two municipalities. No statistically significant differences were found in dispersion homogeneity within groups ($F(1,71) = 3.55$, $P = 0.053$). Therefore, the results indicate that PERMANOVA was not affected by intra-group variability.

Analyzing the 87 species/morphospecies, we observed that 13 of them played a significant role in the ordination of the NMDS (Table 3. Figure 4D). When we consider ecological factors, again, temperature ($R^2 = 0.24$, $P = 0.001$), relative humidity ($R^2 = 0.11$, $P = 0.009$) and atmospheric pressure ($R^2 = 0.11$, $P = 0.009$) showed significance for this analysis.

Table 3
Mite species with significant contribution to the NMDS ordination based on community structure in Augusto Corrêa and Bragança (Fig. 4D).

Species/morphospecies	p-value
Ascidae Immature	0.01
<i>Bdella uckermanni</i>	0.02
<i>Neognatus</i> sp.	0.04
<i>Armascirus amazoniensis</i>	0.03
<i>Neocunaxoides ovatus</i>	0.03
<i>Scutopalus tomentosus</i>	0.02
<i>Lepidoglyphus</i> sp.	0.03
<i>Retracus johnstoni</i>	0.02
<i>Amblyseius</i> n. sp1	0.03
<i>Brevipalpus</i> sp.1	0.01
Tenuipalpidae Immature	0.02
<i>Tuckerella ornata</i>	0.02
<i>Brachytydeus formosa</i>	0.03

Abundance and diversity by cultivation. The results demonstrate that cultivated açai palm trees had a greater number of mites ($n = 1,316$) than native ones ($n = 753$) (Fig. 5A, Table 1). Therefore, the cultivated açai trees analyzed in this study had a 74.7% higher percentage of mites than those of native ones. However, native plantations showed slightly greater richness ($n = 70$, or 6%) than those cultivated ($n = 66$). In the case of the rarefaction curve, the data indicate that, although there is a need for a relatively small sampling effort for native açai plantations and a slightly larger one for cultivated ones, in relation to the abundance of mites to be collected (Fig. 5B). It also suggests that wealth will not increase drastically, suggesting that the sampling effort for this work was sufficient.

Contrary to Hill's diversity profiles presented previously, this one related to the type of açai planting (cultivated vs. native) suggests that the most discordant diversity parameter was species/morphospecies richness (parameter zero on the x-axis) (Fig. 5C). Therefore, we can assume that both mite communities behave practically the same in both types of plantations, remembering, however, that in cultivated plantations the mite abundance was much greater (74.7%) than in native ones.

The ordination of the mite community composition in relation to the type of açai cultivation presented a satisfactory fit in the NMDS (stress = 0.10, non-metric adjustment $[R^2] = 0.98$). PERMANOVA analysis revealed significant differences in mite community structure between cultivated and native plantings ($F(1, 72) = 2.89$, $R^2 = 0.03$, $P = 0.01$. Figure 5D). Here, the coefficient of determination (R^2) was slightly lower, indicating again that the variability explained by the NMDS, together with the analyzes between periods and municipalities, must be analyzed with caution as other factors, not analyzed in this work, can help to explain the difference in the mite community between the two types of açai planting. Statistically significant differences were found in dispersion homogeneity within groups ($F(1,71) = 4.15$, $P = 0.037$) suggesting that PERMANOVA may have been affected more by variability within groups than between the two crop types of açai.

Analyzing the 87 taxa, we observed that 14 of them played a significant role in the ordination of the NMDS (Table 4. Figure 5D). When we consider ecological factors, again, temperature ($R^2 = 0.28$, $P = 0.002$), relative humidity ($R^2 = 0.11$, $P = 0.009$) and atmospheric pressure ($R^2 = 0.11$, $P = 0.007$) showed significance.

Table 4
Mite species with significant contribution to the NMDS ordination based on community structure in Augusto Corrêa and Bragança (Fig. 5D).

Species/morphospecies	p-value
Ascidae Immature	0.01
<i>Bdella uckermanni</i>	0.01
<i>Neognatus</i> sp.	0.02
<i>Armascirus amazoniensis</i>	0.01
<i>Neocunaxoides ovatus</i>	0.02
<i>Scutopalus tomentosus</i>	0.01
<i>Davisella</i> sp.	0.02
<i>Retracus johnstoni</i>	0.02
<i>Amblyseius</i> n. sp1	0.01
<i>Brevipalpus yothersi</i>	0.03
<i>Brevipalpus</i> sp.1	0.03
Tenuipalpidae Immature	0.04
<i>Tuckerella ornata</i>	0.01
<i>Brachytydeus formosa</i>	0.04

Distribution in the plant. There was a difference in the number of mites collected between the different types of açaí planting (Table 5, Figure 6). Furthermore, our data indicate that there is a significant difference in the number of mites collected on the different açaí substrates (Table 6, Figure 7). The observed difference was detected between the basal substrates of cultivated açaí palms (higher quantity) and the apical substrate and native fruit (lower quantity). There was also a difference between the median substrate of cultivated açaí trees (larger quantity) with the same apical substrate and the fruit of native açaí trees (smaller quantity) and, finally, the median substrate (more mites) with the fruit of native açaí trees (less mites) (Fig. 7). However, there was no significant interaction between the types of plantations (Table 6).

Table 5
Results of the generalized linear mixed model (negative binomial) comparing the number of mites found on açaí plants.

Type of planting	Substrate	Average	Standard deviation
Cultivated	Basal	40	14
Native	Basal	27	18
Cultivated	Median	37	20
Native	Median	34	25
Cultivated	Apical	26	19
Native	Apical	17	19
Cultivated	Fruit	23	19
Native	Fruit	13	13

Table 6
Results of the generalized linear mixed model (negative binomial) comparing the number of mites found on açaí plants.

Fixed effects	χ^2	G.L.	p-value	
Type of planting	4.72	1	0.029*	
Substrate	17.3	3	< 0.001***	
Substrate: Type of planting	1.03	3	0.791	
Aleatory effects	Variance	D.P.		
Municipality	0.000	0.000		
Period	0.271	0.521		
Model selection	AICc ¹	dAICc ²	G. L ³	Peso ⁴
Negative binomial GLMM (chosen model)	633.4.	0.0	11	1
GLMM Poisson	1102.2	468.8	10	< 0.001
G.L.: degrees of freedom; p-value; probability of finding z values by chance. ¹ AIC estimate; ² Differences between AICs; ³ Degrees of freedom; ⁴ Weight of AICs.				

Discussion

This is the first study carried out in the Bragantina microregion of Northeast Pará, reporting the fauna and diversity of mites in açaí palm trees in native and cultivated areas, in two municipalities in the state of Pará. To date, little is known about the distribution, dynamics and effects of predatory and phytophagous mites in cultivated açaí crops and in natural environments. It is known that the quality and production of açaí can be impacted by the presence of phytophagous mites.

The majority of species and specimens collected belonged to the families Phytoseiidae, Phytoptidae, Cunaxidae, Tetranychidae and Tydeidae. Phytoseiid mites present variations in lifestyle, with specialization in the use of food sources, and mites of the genera *Amblyseius* and *Typhlodromus* are commonly reported as predators of tetranychid mites (McMurtry & Croft, 1997). Species of both genera were identified in the present study. *Amblyseius* sp. 1 was the most abundant species in natural systems and in the rainy season, followed by *Amblyseius* sp. 3 and sp. 2. These mites are predominant in the North region, where environmental factors such as temperature and relative humidity interfere with the structure of the mite community, as their occurrence was greater during the period of greater precipitation. In previous studies carried out on *Elais guineensis* Jacq. (Arecaceae), in the state of Amazonas, during the rainy season, mites of the genus *Amblyseius* were reported in greater abundance during the period (Cruz et al., 2019). These results also confirm those found in coconut trees on the coast of Bahia (Lawson-Balagbo et al. 2008). The genus *Amblyseius* houses a great diversity of species that are natural enemies of several organisms (Amaral, 2017). The cunaxid mites *S. tomentosus* and *A. amazoniensis* were also common. In areas with cultivated systems and during the dry period, *Amblyseius* sp. 2, *Amblyseius* sp.3 and *I. zuluagai* were the most abundant species. The latter species has also been reported in Bahia in *Cocos nucifera* L., *E. oleracea* and *E. guineensis* (Arecaceae) (Souza et al., 2015).

Among the phytophagous mites, mites from the families Phytoptidae, Tetranychidae, Tenuipalpidae and Eriophyidae stood out. Thus, as in other studies, phytophagous mites were found in a group of Arecaceae plants in Brazil, the most diverse of which have been representatives of the superfamily Eriophyoidea (Flechtmann 1994, 1998; Flechtmann & Santana, 1997; Santana & Flechtmann, 1998; Santana et al. 1994; Gondim Jr. et al. 2000; Rodrigues et al. 2016). Tetranychidae are strictly phytophagous and have great potential to reduce the production of economically important crops, mainly due to their high reproductive potential (Rodrigues et al. 2016).

Among the phytophagous mites identified in açaí palm trees, the following stood out: *T. ornata*, *B. yothersi*, *Brevipalpus* sp.1, *Brevipalpus* sp.2, *Ceratarsonemus* sp., *Tarsonemus* sp.2, *Xenotarsonemus* sp.1, *Xenotarsonemus* sp.2 and *Xenotarsonemus* sp.3. Specimens of *T. ornata* were lodged in the cracks of açaí fruits. The Tenuipalpidae were in the fruit stalk and continued to be present in many fallen fruits. Mites from the families Bdellidae, Eupodidae, Phytoseiidae, Stigmaeidae and Tydeidae were also collected from the fruits.

The greatest richness was observed in the dry period with 73 species, while in the rainy period it was 65 species. In relation to the types of açaí cultivation, the highest number of mites was found in the basal part of the leaflets in cultivated açaí, while in native açaí groves the highest average number of mites found was in the middle part of the leaflets. As for diversity, the dry period was more diverse compared to the rainy period. The greatest abundance of Phytoseiidae mites was found in the dry period. Thus, as in a similar survey in the state of Pará reported by De Alfaia et al. (2023), which shows a positive association between Phytoseiidae and temperature, as higher temperatures increase the prevalence of these mites.

The municipality of Bragança presented greater richness, with 62.5% more species than Augusto Corrêa. Cultivated açaí palm trees also had a greater abundance, 74.7% greater than in native ones. However, native açaí trees presented a greater species/taxa richness (6%) than those cultivated. In this way, biological control can occur naturally in this type of system because it is more diverse, as already reported in some studies (e.g. McMurtry & Croft, 1997; Easterbrook et al. 2001; Wright & Chambers, 1994), where the Predatory mites, as they have high potential as biological control agents, can be used as part of an integrated pest management program (IPM). Knowing the diversity of mites in açaí palm trees, especially in natural environments and in planted areas, is fundamental for integrated pest management and could contribute to supporting future research into the control of organisms with the potential to cause

damage to this crop. Therefore, it is essential to know and prevent outbreaks of these organisms that can cause damage and protect the crop from possible damage.

Declarations

Author Contribution

Edna A. da Silva Brito - Coleta e escrita do artigo
Iury Silva Castro - Identificação dos ácaros
Aloyzeia Noronha - Identificação de ácaros
Noeli Juarez Ferla - Identificação e Tradução

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Figures

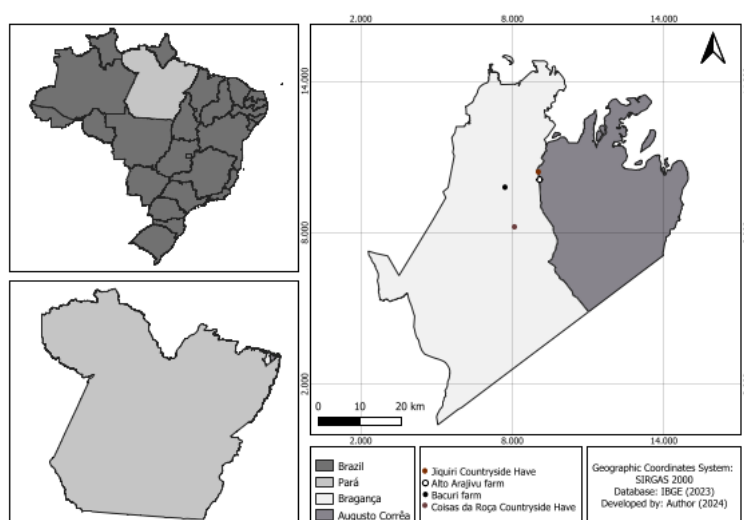


Figure 1

Location of açaí cultivations evaluated in the municipalities of Bragança and Augusto Corrêa, in the Northeast of Pará, Pará, Brazil.

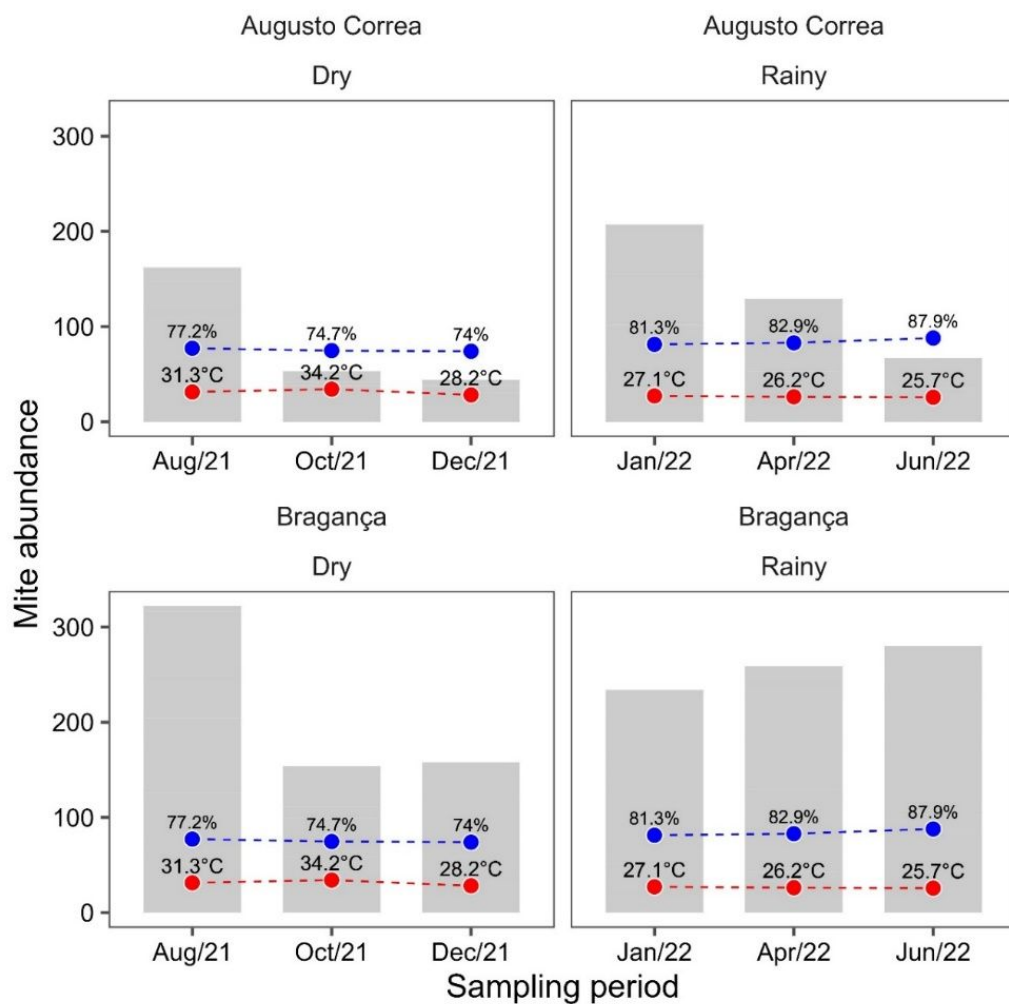


Figure 2

Mite abundance, temperature (°C) and relative air humidity (%) observed in açai cultivation in the dry and rainy seasons in the municipalities of Bragança and Augusto Corrêa, state of Pará, Brazil.

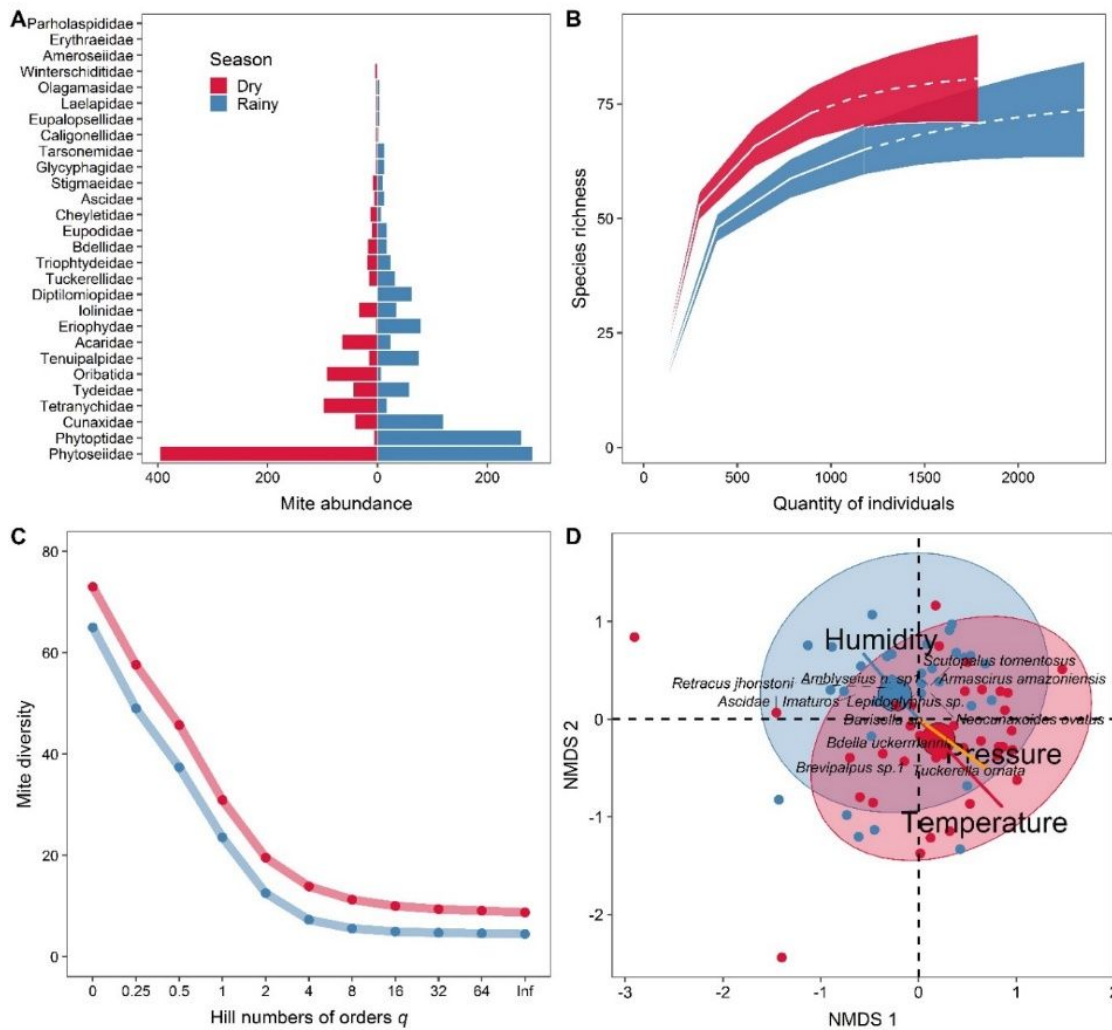


Figure 3

Comparative analysis of the mite community in the dry and rainy periods: abundance, richness, diversity and community structure. (A) Total number of mites sampled between the dry and rainy periods. The y-axis shows the mite families, while the x-axis shows the abundance of mites organized according to the absolute quantity collected per period. The left side of the pyramid represents the dry season, and the right side represents the rainy season. (B) Species rarefaction curves with 95% confidence intervals. Observed species richness values are shown as solid lines, while dashed lines indicate extrapolation. (C) Hill diversity profile. The y-axis denotes diversity lato sensu, while the x-axis shows the gradual change in this diversity for both mite communities. Some diversity indices on the x-axis can be inferred: 0 = species richness; 1 = Shannon-Wiener index (entropy exponential); 2 = Simpson index; and inf = Berger-Parker index. This continuum of values on the x-axis reflects the contributions of rare vs. rare species. abundant. Thus, the left side of the x-axis indicates that the diversity found is more sensitive to rare species, while on the right side of the x-axis, the abundance of species has more weight (greater equability; common species have more weight). (D) Non-metric multidimensional scaling (NMDS) plot differentiating mite community composition. Larger dots indicate group centroids and smaller dots represent sampling sites. The environmental variables 'temperature' and 'humidity' contributed significantly to the pattern of this ordering. (Note: the colors are according to the sampling period, with red being *dry* and blue *rainy*).

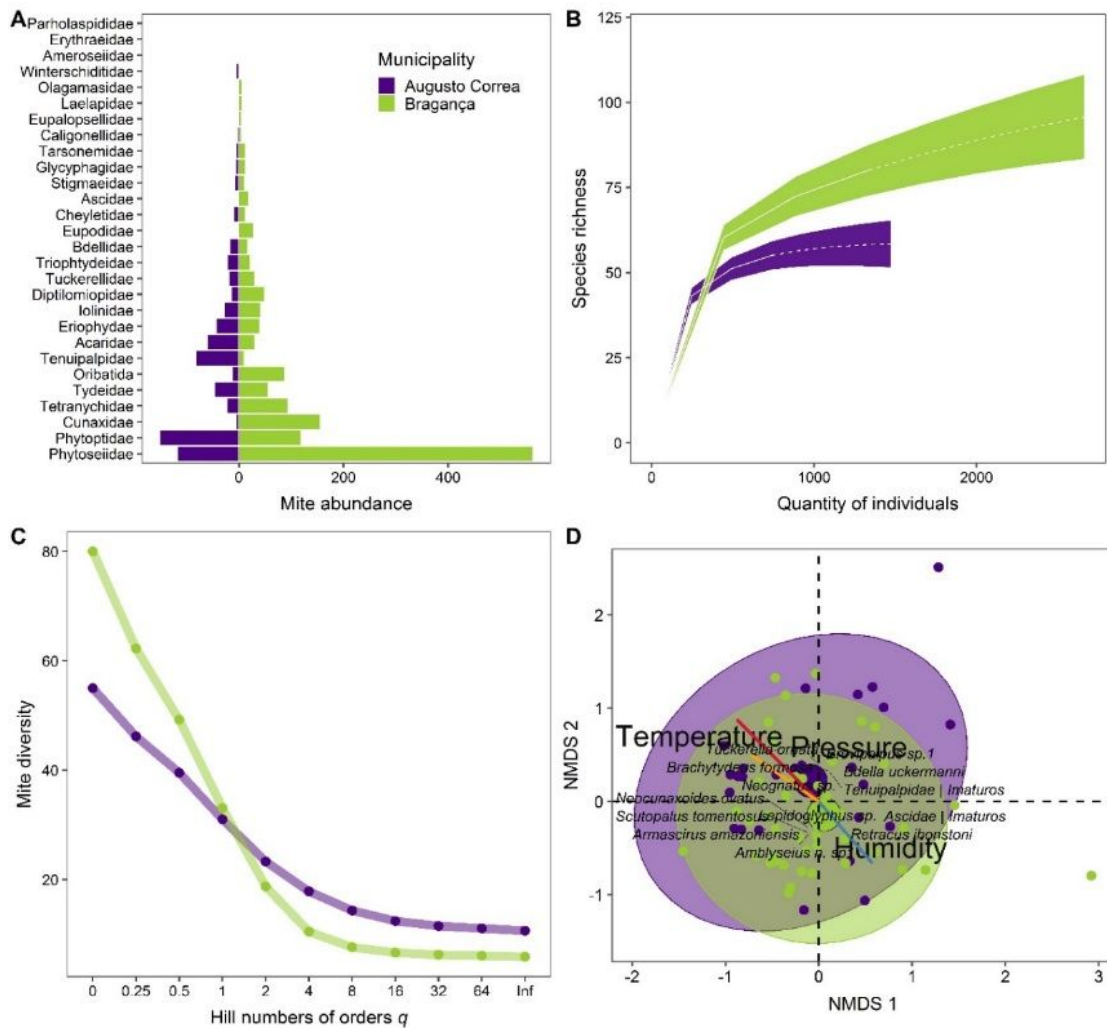


Figure 4

Comparative analysis of the mite community in the municipalities of Augusto Corrêa and Bragança, Pará, Brazil: abundance, richness, diversity and structure. (A) Total number of mites sampled among the municipalities of Augusto Corrêa vs. Bragança. The y-axis shows the mite families, while the x-axis shows the abundance of mites organized according to the absolute quantity collected per period. The left side of the pyramid represents the municipality of Augusto Corrêa and the right side represents the municipality of Bragança. (B) Species rarefaction curves with 95% confidence intervals. Observed species richness values are shown as solid lines, while dashed lines indicate extrapolation. (C) Hill diversity profile. The y-axis denotes diversity lato sensu, while the x-axis shows the gradual change in this diversity for both mite communities. Some diversity indices on the x-axis can be inferred: 0 = species richness; 1 = Shannon-Wiener index (entropy exponential); 2 = Simpson index; and inf = Berger-Parker index. This continuum of values on the x-axis reflects the contributions of rare vs. rare species. abundant. Thus, the left side of the x-axis indicates that the diversity found is more sensitive to rare species, while on the right side of the x-axis, the abundance of species has more weight (greater equability; common species have more weight). (D) Non-metric multidimensional scaling (NMDS) plot differentiating mite community composition. Larger dots indicate group centroids and smaller dots represent sampling sites. The environmental variables 'temperature' and 'humidity' contributed significantly to the pattern of this ordering. (Note: the colors are according to the sampling period, being purple for *Augus* → *C* or *rêa* and *greenf* or Bragança).

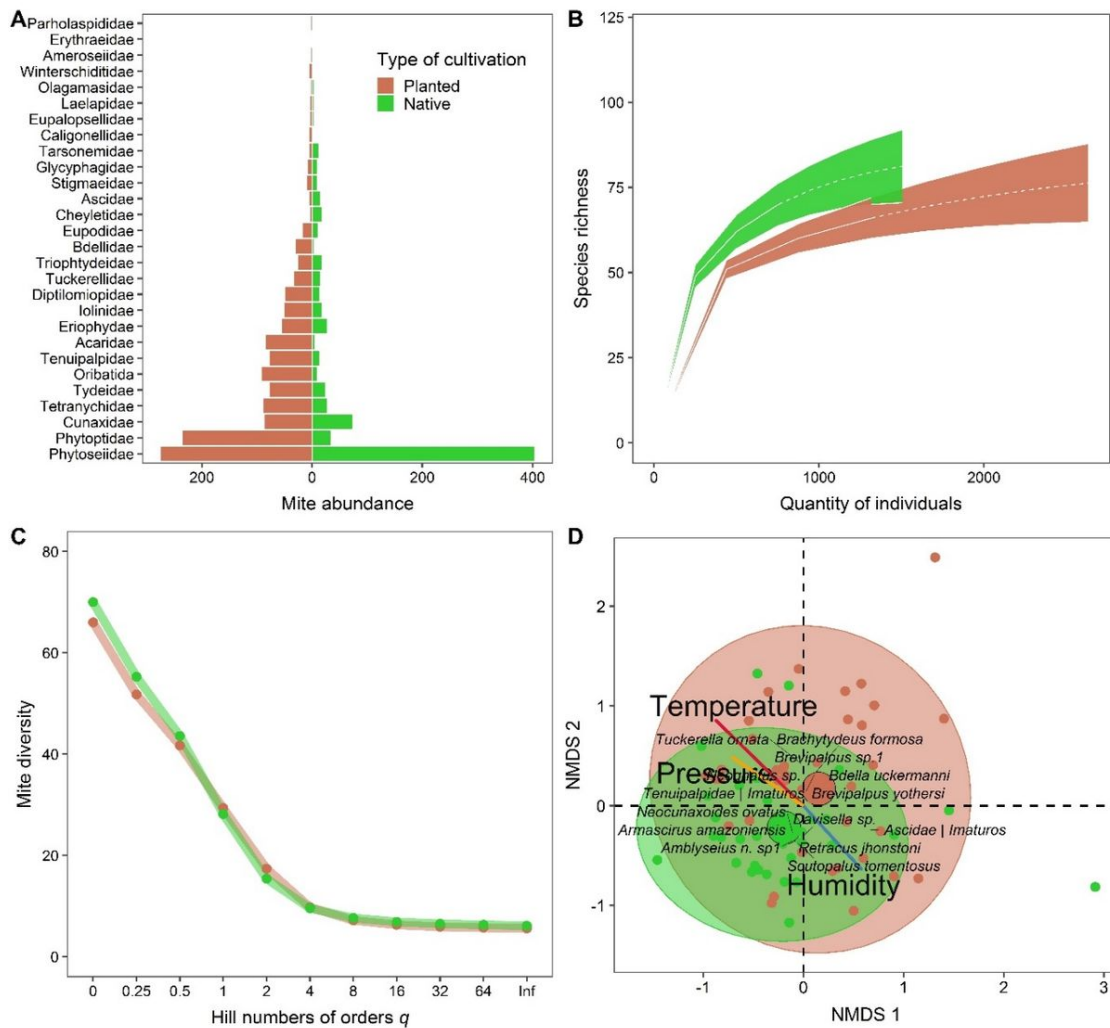


Figure 5

Comparative analysis of the mite community in cultivated and native açai plantations, Pará, Brazil: abundance, richness, diversity and structure. (A) Total number of mites sampled among crop types. The y-axis shows the mite families, while the x-axis shows the abundance of mites organized according to the absolute quantity collected by type of crop. The left side of the pyramid represents cultivated crops and the right side represents native crops. (B) Species rarefaction curves with 95% confidence intervals. Observed species richness values are shown as solid lines, while dashed lines indicate extrapolation. (C) Hill diversity profile. The y-axis denotes diversity lato sensu, while the x-axis shows the gradual change in this diversity for both mite communities. Some diversity indices on the x-axis can be inferred: 0 = species richness; 1 = Shannon-Wiener index (entropy exponential); 2 = Simpson index; and inf = Berger-Parker index. This continuum of values on the x-axis reflects the contributions of rare vs. rare species. abundant. Thus, the left side of the x-axis indicates that the diversity found is more sensitive to rare species, while on the right side of the x-axis, the abundance of species has more weight (greater equability; common species have more weight). (D) Non-metric multidimensional scaling (NMDS) plot differentiating mite community composition. Larger dots indicate group centroids and smaller dots represent sampling sites. The environmental variables 'temperature' and 'humidity' contributed significantly to the pattern of this ordering. (Note: the colors are according to the sampling period, being light brown for 'cultivated açai' and green for 'native açai').

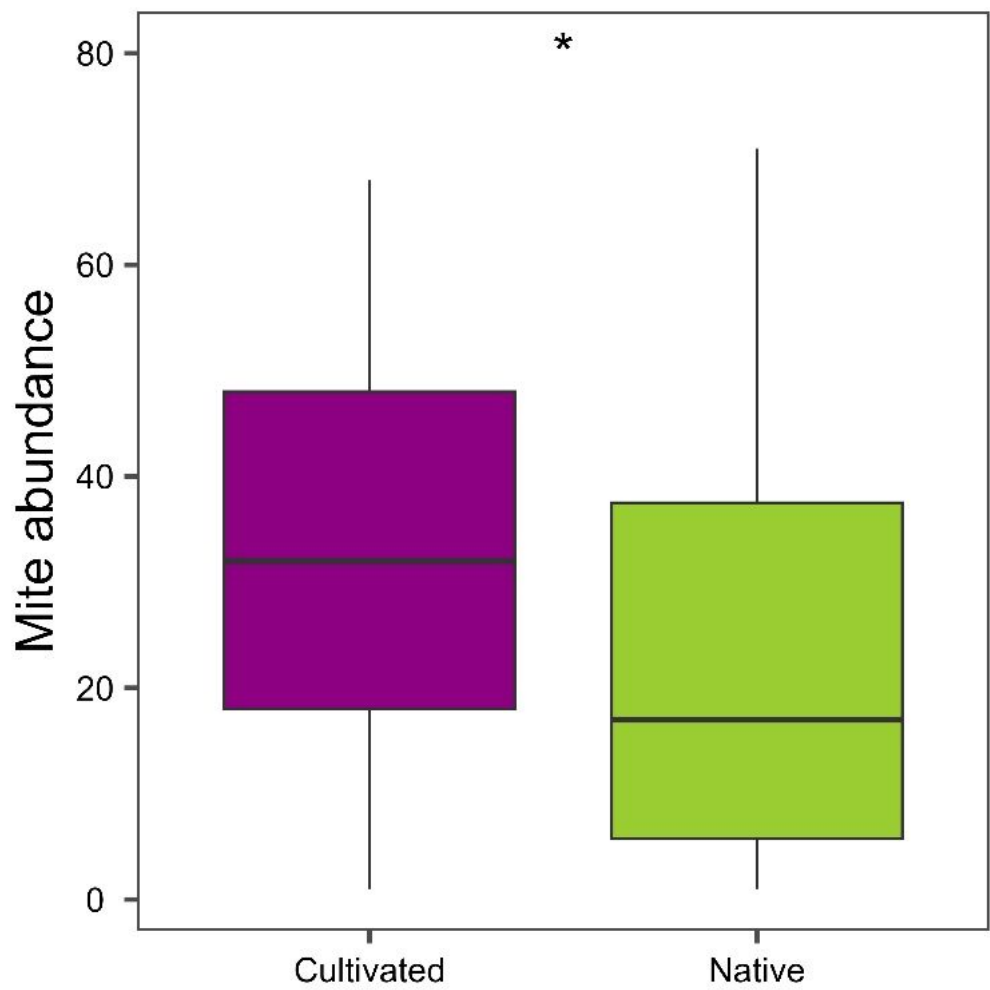


Figure 6

Comparison of the number of mites collected on cultivated and native açai plants. Notes: asterisk indicates significant difference (< 0.05).

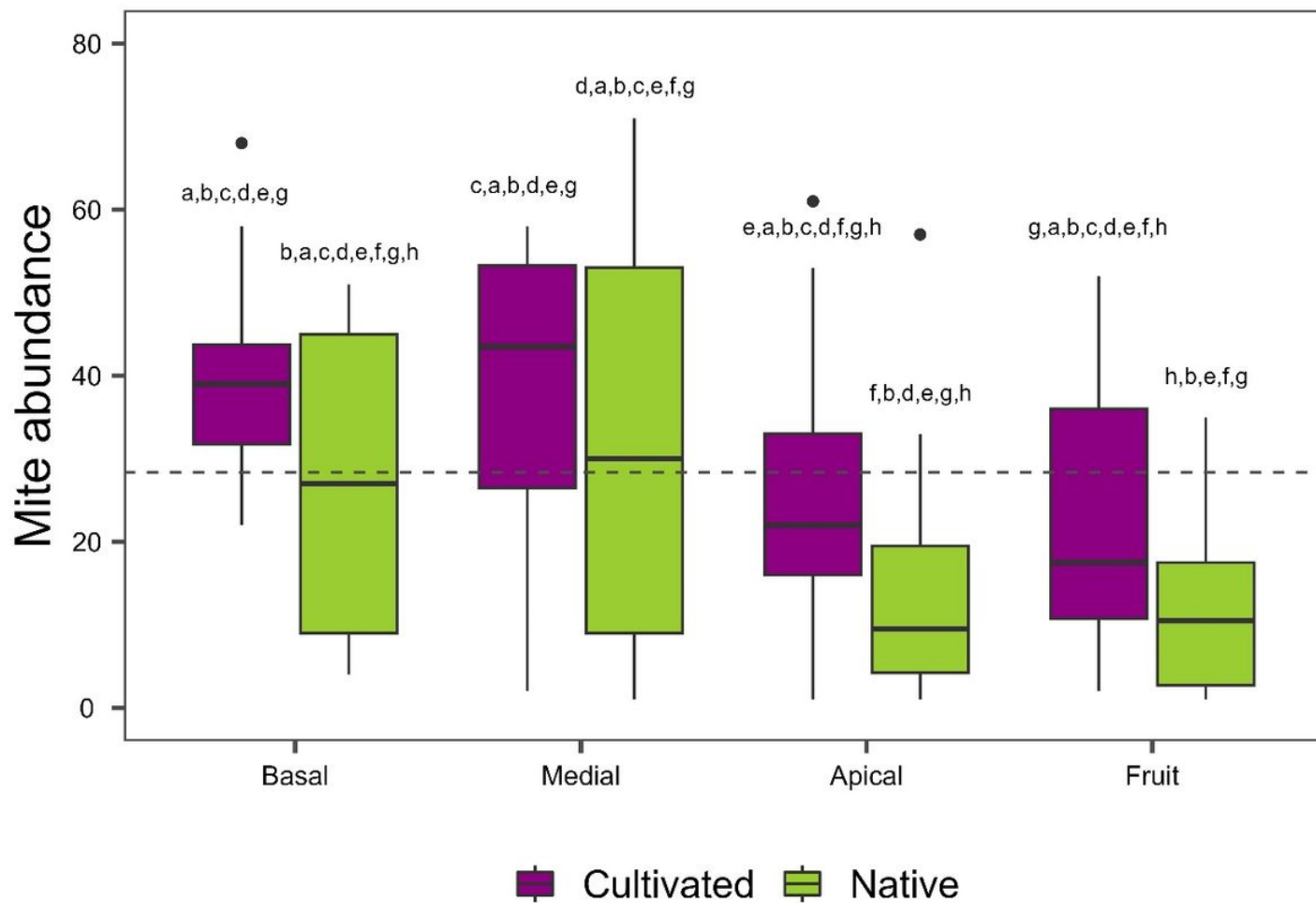


Figure 7

Comparative analysis of the number of mites collected according to the plant substrate of cultivated and native açai plants. Notes: dashed line indicates the general average number of mites; the letters above the boxplots indicate a significant difference when they are different between them and a non-significant difference when they are the same between them (they are repeated).