Asian Journal of Research in Crop Science

Volume 8, Issue 4, Page 83-108, 2023; Article no.AJRCS.100223
ISSN: 2581-7167

Biodiversity and Community Structure of Arboreal Foraging Ants (Hymenoptera: Formicidae), Mealybugs (Hemiptera: Sternorrhyncha: Coccoidea) and Host Plants in Douala, Littoral-Cameroon

Yomon Abdel Kayoum [a], Fouelifack-Nintidem Boris [a], Yetchom-Fondjo Jeanne Agrippine [a], Tsekane Sedrick Junior [a], Ngamaleu-Siewe Babell [a], Kenne Edith Laure [a], Moukhtar Mohammadou [a,b,c] and Martin Kenne [a*]

[a] Zoology Unit, Laboratory of the Biology and Physiology of Animal Organisms, University of Douala, PO Box 24157, Douala, Cameroon.
[b] Department of Biological Sciences, Faculty of Science, Laboratory of Applied Zoology, University of Ngaoundere, PO Box 454, Ngaoundere, Cameroon.
[c] Faculty of Medicine and Biomedical Sciences, University of Garoua, PO Box 317, Garoua, Cameroon.

Authors' contributions

This work was carried out in collaboration among all authors. Authors YAK and MK conceived and planned the field investigations and identification of specimens to species level. Authors YFJA, TSJ, NSB and KEL provided their labour during field collection sessions, in the sorting of the collected specimens in morphospecies, in the data entry and helped to carry out statistical data analysis and they contributed to the writing of the final manuscript. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/AJRCS/2023/v8i4191

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://www.sdiarticle5.com/review-history/100223

**Corresponding author: E-mail: medoum68@yahoo.fr, medoum1968@gmail.com;*

Original Research Article

Received: 11/03/2023
Accepted: 16/05/2023
Published: 20/05/2023

ABSTRACT

Aims: Mealybugs are protected on plants by ants for honeydew. They were identified and assemblages were characterized in Douala suburbs (Littoral-Cameroon).
Study Design: Basic information is needed on pest's occurrence for the pest control strategies. We determined host plants and characterized the community structure of mealybugs and foraging ants.
Place and Duration of Study: Field investigations were conducted from March to August 2020 in Douala suburbs in 16 transects (10x1,260 m each) and 126 quadrats (10x10m each).
Methodology: Stems, the underside of leaves, flower buds and fruits were inspected on weeds, plant bases and canopy of trees. Mealybugs and ants were captured. When the plant was highly infested, the average number of insects was determined on 10 randomly chosen plant organs. Abundances were noted and captured specimens were stored in vials containing 70° alcohol, identified to the species level and the community structure was characterized.
Results: A total of 24,640 specimens belonged to 23 families, 54 genera and 85 species were collected in this research. A low species richness, low diversity and low dominance were detected. Assemblage of foraging ants in Yassa functioned according to the brokend-stick model. Scale insects in Ngoma functioned according to Motomura's model. Assemblages of host plants in Lendi, Yassa, global host plants, global scale insects, foraging ants in Lendi and the global settlement, functioned according to the lognormal model. Host plants in Ngoma, scale insects in Yassa, and foraging ants in Ngoma functioned according to Zipf's model while Zipf-Mandelbrot was adapted to scale insects in Lendi suggesting that these communities had sufficient time to develop a complex network of information close to natural environments and presented a fairly regeneration force.
Conclusion: Due to the abundance pest insects, resources are available and once they will be well developed; they will cause plant pathologies and yield loss.

Keywords: Host plants; scale insects; pest insects; assemblage structure; anthropized areas; Douala suburbs.

1. INTRODUCTION

In home gardens, plantations and natural areas, a tripartite association exists between plants (wild, cultivated or ornamental plants species), Sternorrhyncha Hemiptera including Homoptera and arboreal foraging ants. Insect pests of crops production represent a major constraint to the intensification of agricultural production in the tropics. These bio-aggressors include all organisms harmful to crops such as invertebrates including arthropods (insects and mites) and nematodes, protozoa such as bacteria and viruses, fungi, vertebrates such as rodents, birds, and plants or weeds [1].

Plants are targets of animal species among which insects and pathogens occupy a prominent place and because of their trophic behaviour and diversified nesting, they use the plants either as a nesting site, or as a supplying nutrients site, or both at the same time. The consequence is that insects (qualified as pests), directly or indirectly damage plants through associated organisms. Nevertheless, some insects are useful for the plant when they carry out a beneficial activity (pollination and protection against phytophagous and xylophagous insects) while many species are harmful (when they cause pathologies and damage to the plants).

Since ants are not able to feed in the majority of cases directly on plant matter, with the exception of mushroom species of the *Attini* tribe and seed-eating species of the genera *Messor* and *Pogonomyrmex,* they have developed several types of trophobiotic relationships with mealybugs [2]. Ants and scale insects have lived together for a very long time on wild and/or cultivated plants in our gardens, plantations and forests. In this association, ants able to forage in the canopy, are attracted to the sweet faeces (honeydew) produced by mealybugs and these scale insects are protected against predators, to

the point of being exploited as "cash cows" by intervening in their displacement and repositioning on the most tender parts of the plants (buds, young leaves, young thumbs and hollow interior of epiphyte galls). Thus, the presence of ants favours the densities of honeydew-producing insects [3].

Mealybugs are sap-sucking insects capable, through their mouth stylet, of piercing plant tissues and pumping a large quantity of raw sap to exploit a small quantity of water, amino acids and vitamins while rejecting in the form of faeces the excess undigested and enriched in sugar. During this food intake, these insects transmit many bacterial and viral germs to the plant, responsible for plant pathologies.

Colonized plants tolerate very few high densities of mealybugs and the consequences of their presence include the physical deformation of plant organs, the disturbance of plant metabolism, and the decline in plant productivity. The attacked plant dies in the majority of cases, which leads to a huge loss for the farmer. Then mealybugs are specialized sap suckers on many annual and perennial plants, ranked among the major plant pests, not only because they damage plant tissue during sap extraction, but also because they inject toxins or viruses into many economically important plants and many of these direct pest insects are not specific to a host plant, but can attack several neighboring plant species [3].

From an agronomic point of view, cultivated plants must be protected against their aggressors, in order to ensure a good yield of fruits and seeds, essential to satisfy the constantly growing demand in cities and countryside. However, many studies have shown that the success of control programs against plant bio-aggressors must be subject to the availability, for given up-to-date entomological information that can account for their identification and ecology control.

In Cameroon, populations live much more from agriculture and the country has in its southern part, expanses of land and a climate that can be favorable to the proliferation of insect pests. Ants are one of the most important components of the fauna of agro-ecosystems. Their presence can be beneficial because they exert significant predation on many crop pests. However they can also be real pests, seriously degrading the sanitary condition of crops and/or hampering the progress of agricultural activities if the species in question are aggressive towards humans. Throughout the literature, losses due to bio-aggressors during the production and storage of agricultural commodities remain abnormally high, due in particular to the low effectiveness of phytosanitary protection measures for crops when they are implemented.

Most of the studies carried out on the interactions between ants and mealybugs remain fragmented. The other partners involved directly or indirectly in these relationships have been the subject of a limited number of studies. The third most obvious partner, the plant, has rarely been included [3,4]. Ants are true indicators of biodiversity and ecosystem health [5].

The purpose of this study in urban and suburbs of Douala (Cameroon) was to provide to ecologists and entomologists useful basic information concerning the three-components interactions developed in plants, foraging ants and scale insects for a better orientation of operations to control pests of cultivated and ornamental plants. This involved: (1) the determination of the spectrum of host plants parasitized by scale insects (2) the determination of the structure and composition of the plants' associated scale insects, and (3) the determination of the structure and composition of the arboreal foraging ants.

2. MATERIALS AND METHODS

2.1 Study Site

The field surveys were carried out from March to August 2020 in three localities located in the suburbs of the city of Douala (Cameroon) [Lendi (4°7'29.00"N, 9°46'31.00"E; 8 m a.s.l.), Ngoma (4°6'51.00"N, 9°47'17.00"E; 18 m a.s.l.) and Yassa (3°59'29.00"N, 9°48'37.00"E; 36 m a.s.l.)]. These localities were situated 13.4, 13.8 and 15.8 km from Douala-Bonanjo (4°2'7.16"N, 9°41'45.01"E) respectively. Lendi and Ngoma are close to each other (1.82 km) and they are on the other hand quite far from Yassa (17.6 and 16.3 km respectively). The average temperature in Douala and its suburbs is 26.2°C and the average annual rainfall reaches 3,702 mm [6]. Air temperature and relative humidity were recorded using a hygrothermometer suspended 1.5 m above the ground.

They were selected on the basis of the availability of four types of plant cover: (1) monoculture [*Manihot esculenta* (Euphorbiaceae), *Abelmoschus esculentus* (Malvaceae), *Ipomea batatas* (Convolvulacae), *Theobroma cacao* (Sterculiaceae), *Solanum scabrum* (Solanaceae) and *Zea mays* (Poaceae)], (2) mixed cropping plots, (3) one to two-years old fallows, and (4) home gardens around houses.

The methodology of the study used an inventory of plants infested by scale insects as well as foraging ants collecting honeydew produced by scale insects, and to link the presence of ants and scale insects with the various crop damage. The prevailing climate in Douala and suburbs is tropical characterized by two seasons: (1) a rainy season from April to October of the same year with maximum precipitation in September and (2) a dry season from November to March of the following year with minimum precipitation in January.

Sixteen transects of 10x1,260 m each were delimited in the three localities (10 transects in Lendi and three transects in Ngoma and Yassa respectively). Each transect was subdivided into 126 quadrats of 10x10m each overlapping four vegetation types (total: 2,016 quadrats divided into 1,260 in Lendi, 378 in Ngoma and Yassa respectively). Ten quadrats (total: 160) were randomly selected per transect (100 in Lendi and 30 in Ngoma and Yassa respectively). When a selected quadrat was occupied by a house, it was replaced with the neighboring available open-site quadrat. Twenty nine plots were divided into 9 plots of monoculture, 9 plots of food polyculture and 11 plots of two- to three-years old fallows (three plots of monoculture and three plots of food polyculture in Lendi, Ngoma and Yassa respectively; five plots of fallows in Lendi and three plots of fallows in Ngoma and Yassa respectively).

In each quadrat, plants were inspected by seven collaborators, from the ground surface for weeds and plant bases to the top of the canopy of the tall trees for the presence of mealybugs and foraging ants. All the mealybugs parasitizing the grasses and the base of the plants were counted. When the plant was highly infested, the average number of mealybugs or ants was determined on a sample of 10 aeral plant organs randomly chosen on the same plant.

2.2 Sample Design and Species Identification

In each quadrat, plants carrying scale insects were identified. Plants mealybugs and foraging ant workers were collected, using a mouth aspirator or the soft claws. Captured insects were stored in labelled test-tubes containing 70% alcohol.

Ants from each vegetation type were pooled and stored in labelled plastic tubes as above and the same thing was done for mealybugs. The work was carried out only once during the rainy season. Plants that supported scale insects were identified using keys and illustrated catalog [7-20]. Ant workers and scale insects were first sorted in morphospecies, compared to the reference collection available in the laboratory, identified to the species level and confirmed using taxonomic keys [21].

In order to consider recent developments in the taxonomy of Formicidae and Hemipterans and the native range origin of identified species, recent reports and check lists were consulted [22-28]. Identifications were confirmed by comparing specimens with the identified ones provided in the past by Danièle Matile-Ferrero and Barry Bolton as reported in our previous publications [29-31], duplicates being kept in the reference collection in our laboratory.

2.3 Statistical Analysis

A species data matrix of absolute abundances was constructed for each site and for each species, the mean value and the variance of abundances were determined. The number of species by taxa (order, family, subfamily and genus) was determined at each site and the relative abundance (percentages) was calculated from the overall total number of the collected specimens. Statistics are given in term of percentage of occurrence for qualitative modalities, or mean ± standard error (se) for quantitative series. Comparison of two relative abundances was set up using the two binomials Fisher's exact-test and the two-sided p-value was recorded (StatXact-3 software) while two means (± se) were compared using Student t-test when normality and equal variance tests passed, or Mann-Whitney rang sum test (for independent series) or Wilcoxon rang sum test (for dependent series) when at least one of the above conditions did not pass.

Simultaneous comparison of several percentages was set up using either Fisher-Freeman-Halton test from StatXact software 3.1 (one of the best procedures tests highly recommended for nonparametric analysis of unordered tables), or the non-parametric Kruskal-Wallis's test from SigmaStat software 2.0® because when considering the number of species as a metric/response variable, sample units being different, uneven variability could occur between sampling sites.

Several mean values were simultaneously compared using the parametric ANOVA test followed by the Mann-Whitney pairwise test when normality and equal variance tests passed. Otherwise the nonparametric Kruskall-Wallis rang sum test (normality and equal variance tests failed) was used and post-hoc analysis was done using Dunn's procedure (SigmaStat software). Regression equations were tested using ANOVA procedure and parameters were compared to the null value using the student t-test.

For the biodiversity analysis, the number of species by order, family, subfamily and genus was determined and relative abundances were determined. The percentage of plants attacked by scale insects was determined from 20 plants selected per plot. Ant workers observed in the presence of mealybugs were collected and listed.

For the analysis of alpha diversity the following statistics were determined using PAST 3.05 software: the species richness (S), the absolute abundance of the i^{th} species n_i, the sample size n (sum of all n_i), the maximum abundance nmax, the percentage of the i^{th} species $(n_i/n)*100$, Margalef species richness index $Mg = (S-1)/\ln(n)$ with $0 \leq Mg < +\infty$ (Mg = 0 for a very low species richness), the richness ratio $d = S/n$ with with $0 \leq d \leq 1$ (d = 0 for a very low species richness), the Shannon-Weaver diversity index H', Shannon-Weaver maximum diversity index $H'_{max} = \ln(S)$, Simpson's diversity index D (H' = 0 or D = 0 for a highly low species diversity, Pielou's evenness index $J = H'/Hmax$ with $0 \leq J \leq 1$ (J = 0 for a lowly even assemblage). Hill's first-order diversity number $N_1 = eH'$ which represents the number of simply abundant species and Hill's second-order diversity number $N_2 = 1/D$ which represents the number of codominants. Rare species were then easily identified. The Berger-Parker dominance index $I_{BP} = n_{max}/n$ with $0 \leq I_{BP} \leq 1$ (I_{BP} = 0 for not dominated assemblage by few species). The true theoretical species richness was estimated using the non-parametric estimator index Chao1 and the sampling effort was estimated by the relation (S/Chao1)*100.

The comparison of the species richness was made by the Saunders's species rarefaction method from PAST 3.05 software and pairwise comparison of the species diversities of Shannon and Simpson was set up using the student's t test. The Whittaker rank-frequency diagram was used to illustrate the shape of the species abundance distribution (SAD). The goodness of fit of each SAD to a theoretical model was assessed by calculating the Pearson correlation between the logarithms of the numbers and the ranks of the species and interpreted as follows: (1) r <-0.95 for poor quality adjustment; (2) r ≈ -0.95 for approximate fit; (3) r ≈ -0.98 for a satisfactory fit; and (4) r ≥-0.99 for excellent fit. SADs were adjusted to five theoretical models using the package vegan of R 3.0.1. software: (1) the broken-stick (BS), (2) the geometric (GM), (3) the lognormal (LN), (4) the Zipf (Z) and (5) the Zipf-Mandelbrot (ZM). The best fitted model was selected by referring to the lowest value of the Akaike Information Criterion (AIC) or the Bayesian Information Criterion (BIC) [32]. Parameters of the selected model were determined.

For the beta diversity analysis, the presence/absence data matrix permitted us to determine the overall species covariance using the Schluter's procedure [33]. Between species correlations were determined using the Kendall's tau coefficient. The dissimilarity between sampling sites was evaluated using the Bray-Curtis index.

3. RESULTS

3.1 Inventory of Host Plant Species

A total of 1,616 plants were found bearing mealy bug individuals [488 plants (30.2%) in Lendi, 456 plants (28.2%) in Ngoma and 672 plants (41.6%) in Yassa] (Table 1). These plants belonged to 15 orders, 20 families, 26 genera and 30 species.

Table 1. List and abundance of plant species bearing scale insects in the studied localities

		Study sites			
Order /Familly	**Species**	**I (%)**	**II (%)**	**III (%)**	**Global (%)**
Arales Juss. ex Bercht. & J. Presl, 1820					
Araceae	*Colocasia esculenta* (L.) Schott, 1832 *	-	1 (0.0)	1 (0.0)	2 (0.1)
Asterales Lindl. (1833)					
Asteraceae	*Ageratum conyzoides* L., 1753 §	149 (9.2)	-	-	149 (9.2)
	Chromolaena odorata (L.) R. M. King & H. Rob., 1970 §	53 (3.3)	-	34 (2.1)	87 (5.4)
	Vernonia amygdalina Delile Sch.Bip. ex Walp., 1843 *	17 (1.1)	2 (0.1)	-	19 (1.2)
Caryophyllales Perleb (1826)					
Amaranthaceae	*Amaranthus viridis* L., 1763 *	1 (0.0)	-	-	1 (0.0)
Cyperales Wettst., (1911)					
Poaceae	*Zea mays* L., 1753 *	-	-	36 (2.2)	36 (2.2)
Magnoliales Bromhead (1838)					
Annonaceae	*Annona muricata* L., 1753 *	-	-	28 (1.7)	28 (1.7)
Malpighiales Mart. (1835)					
Euphorbiaceae	*Alchornea cordifolia* (Schumach. & Thonn.) Müll. Arg., 1865 §	40 (2.5)	8 (0.5)	31 (1.9)	79
	Macaranga grandifolia (Blanco) Merr. §	-	-	31 (1.9)	31 (1.9)
	Manihot esculenta Crantz, 1766 *	27 (1.7)	355(22.0)	-	382 (23.6)
Phyllanthaceae	*Bridelia micranta* (Hochst.) Baill., 1862 §	-	-	55 (3.4)	55 (3.4)
Malvales Juss. ex Bercht. & J. Presl (1820)					
Malvaceae	*Abelmoschus esculentus* (L.) Moench, 1794 *	-	-	164(10.1)	164 (10.1)
	Hibiscus sabdariffa L., 1753 *	-	-	1 (0.0)	1 (0.0)
Sterculiaceae	*Theobroma cacao* L., 1753 *	-	-	65 (4.0)	65 (4.0)
Myrtales Rchb. (1828)					
Myrtaceae	*Psidium guajava* L., 1753 *	-	2 (0.1)	-	2 (0.1)
Pandanales Lindl. (1833)					
Pandanaceae	*Pandanus fascicularis* Lam., 1785 *	4 (0.2)	1 (0.0)	-	5 (0.3)
Poales Small (1903)					
Poaceae	*Saccharum sinense* Roxb., 1815 *	16 (1.0)	32 (2.0)	25 (1.5)	73 (4.5)
Rosales Bercht. & J. Presl					
Moraceae	*Ficus* sp. L., 1753 §	-	-	62 (3.8)	62 (3.8)
Urticaceae	*Cecropia peltata* Linnaeus, 1759 §	-	-	5 (0.3)	5 (0.3)

Table 1 (continue)

		Study sites			
Order /Familly	**Species**	**I (%)**	**II (%)**	**III (%)**	**Global (%)**
Sapindales Juss. ex Bercht. & J.Presl (1820)					
Anacardiaceae	*Mangifera indica* L., 1753 *	-	-	5 (0.3)	5 (0.3)
Burseraceae	*Dacryodes edulis* (G. Don) H. J. Lam, 1932 *	14 (0.9)	-	-	14 (0.9)
Solanales Juss. ex Bercht. & J.Presl (1820)					
Convolvulacae	*Ipomea batatas* (L.) Lam., 1793 *	-	1 (0.0)	-	1 (0.0)
Solanaceae	*Capsicum annum* L., 1753 *	-	-	1 (0.0)	1 (0.0)
	Solanum incanum L., 1753 *	-	-	49 (3.0)	49 (3.0)
	Sl. nigrum L., 1753 *	-	-	23 (1.4)	23 (1.4)
	Sl. scabrum Mill., 1768 *	30 (1.9)	-	-	30 (1.9)
	Sl. torvum Sw., 1788 §	-	-	30 (1.9)	30 (1.9)
Urticales Juss. ex Bercht. & J.Presl (1820)					
Urticaceae	*Musanga cecropioides* R. Br. ex Tedlie, 1819 §	-	-	3 (0.2)	3 (0.2)
Zingiberales Griseb. (1854) (13.2%)					
Musaceae	*Musa* ×*paradisiaca* L., 1753 *	23 (1.4)	54 (3.3)	23 (1.4)	100 (6.2)
	Musa sp. L., 1753 *	114 (7.1)	-	-	114 (7.1)
	Total	**488(30.2)**	**456(28.2)**	**672(41.6)**	**1,616(100.0)**

*I: Lendi; II: Ngoma; III: Yassa; * cultivated plant; §: wild or weed plant species*

The most abundant order was Malpighiales (33.8% of total abundance) (4.1% in Lendi, 22.5% in Ngoma and 7.2% in Yassa) followed by Asterales (15.8%) (13.6% in Lendi, 0.1% in Ngoma and 2.1% in Yassa), Malvales (14.2%) in Yassa, Zingiberales (13.2%) (8.5% in Lendi, 3.3% in Ngoma and 1.4% in Yassa) Solanales (8.3%) (1.9% in Lendi, 0.06% in Ngoma and 6.4% in Yassa), Poales (4.5%) (1.0% in Lendi, 2.0% in Ngoma and 1.6% in Yassa), Rosales (4.1% in Yassa), Cyperales (2.2% in Yasa). The other orders were rare (0.1% of Caryophytales in Lendi, 1.7% of Magnoliales in Yassa, 0.1% of Myrtales in Ngoma, 0.3% of Pandanales in Lendi (0.2%) and in Ngoma (0.06%), 1.2% of Sapindales (0.9% in Lendi and 0.3% in Yassa) and 0.2% of Urticales in Yassa.

The most abundant family was Euphorbiaceae (30.4% of total abundance) (4.1% in Lendi, 22.5% in Ngoma and 3.8% in Yassa) followed by Asteraceae (15.8%) (13.6% in Lendi, 0.1% in Ngoma and 2.1% in Yassa), Musaceae (13.2%) (8.5% in Lendi, 3.3% in Ngoma and 1.4% in Yassa), Malvaceae (10.2% exclusively in Yassa), Solanaceae (8.2%) (1.9% in Lendi and 6.4% in Yassa), Poaceae (6.7%) (1.0% in Lendi, 2.0% in Ngoma and 3.7% in Yassa), Sterculiaceae (4.0% exclusively in Yassa), Moraceae (3.8% exclusively in Yassa), Phyllanthaceae (3.4% exclusively in Yassa), Annonaceae (1.7% exclusively in Yassa). The other families were rare and represented each by less than 1% of the overall abundance (0.9% for Burceraceae, 0.3% for Anacardiaceae, Pandanaceae and Urticaceae respectively, 0.1% for Amaranthaceae, Araceae, Convolvulacaeae and Myrtacaeae respectively) (Table 1).

The most species-rich order was Solanales (6 species, 20.0%) followed by Malpighiales (4 species, 13.3%), Asterales and Malvales (3 species, 10.0% respectively). Musaceae, Rosales and Sapindales each had two species (6.7% respectively). Arales, Caryophytalles, Cyperales, Magnoliales, Myrtales, Pandanales, Poales and Urticacae were rarely represented with only one species each (3.3% respectively). The most species-rich family was Solanaceae (5 species, 16.7%) followed by Asteraceae and Euphorbiaceae (3 species, 10.0% respectively), Malvaceae, Musaceae, Poaceae and Urticaceae (2 species, 6.7% respectively).

The 12 rare families (3.3% each) were Araceae, Amaranthaceae, Anacardiaceae, Annonaceae, Burceraceae, Convolvulaceae, Moraceae, Myrtaceae, Pandanataceae, Poaceae, Phyllanthaceae, Sterculiaceae.

Five species (16.7%) were found in Lendi, two species (6.7%) in Ngoma, 15 species (50.0%) in Yassa, three species (10.0%) simultaneously in Lendi and Ngoma, one species (3.3 %) in Lendi and Yassa, one species (3.3 %) in Lendi and Yassa and three species (10.0%) simultaneously in the three localities. The most recorded plant was *Manihot esculenta* (Malpighiales: Euphorbiaceae) (23.6%) followed by *Abelmoschus esculentus* (Malvales: Malvaceae) (10.1%), *Ageratum conyzoides* (Asterales: Asteraceae) (9.2%), *Musa* sp. (Zingiberales: Musaceae) (7.1%), *Mu.* ×*paradisiaca* (Zingiberales: Musaceae) (6.2%), *Chromolaena odorata* (Asterales: Asteraceae) (5.4%), *Alchornea cordifolia* (Malpighiales: Euphorbiaceae) (5.4%), *Saccharum sinense* (Poales: Poaceae) (4.5%), *Theobroma cacao* (Malvales: Sterculiaceae) (4.0%), *Ficus* sp. (Rosales: Moraceae) (3.8%), *Bridelia micranta* (Malpighiales: Phyllanthaceae) (3.4%), 3.0% of *Solanum incanum* (Solanales: Solanaceae), 1.9% respectively for *Zea mays* (Cyperales: Poaceae) (2.2%), *Macaranga grandifolia* (Malpighiales: Euphorbiaceae), *Sl. scabrum* and *Sl. torvum* (Solanales: Solanaceae), 1.7% for *Annona muricata* (Magnoliales: Annonaceae), 1.4% for *Sl. nigrum* (Solanales: Solanaceae), 1.2% of *Vernonia amygdalina* (Asterales: Asteraceae) (see Table 1).

Other species were rare [0.9% of *Dacryodes edulis* (Sapindales: Burceraceae), 0.3% respectively of *Pandanus fascicularis* (Pandanales: Pandanaceae), *Cecropia peltata* (Urticales: Urticaceae), *Mangifera indica* (Sapindales: Anacardiaceae), 0.2% of *Musanga cecropioides* (Urticales: Urticaceae), and 0.1% respectively of six species [*Amaranthus viridis* (Caryophytalles: Amaranthaceae), *Capsicum annum* (Solanales: Solanaceae), *Colocasia esculenta* (Arales: Araceae), *Hibiscus sabdariffa* (Malvales: Malvaceae), *Ipomea batatas* (Solanales: Convulvulaceae) and *Psidium guajava* (Myrtales: Myrtaceae)] (see Table 1). Twenty one cultivated plants (70.0%) were recorded [*Ab. esculentus*, *Am. viridis*, *An. muricata*, *Ca. annum*, *Co. esculenta*, *Da. edulis*, *Hi. sabdariffa*, *Ipomea batatas*, *Ma. indica*, *Mn. esculenta*, *Mu.* ×*paradisiaca*, *Musa* sp., *Pa. fascicularis*, *Ps. guajava*, *Sa. sinense*, *Sl incanum*, *Sl. nigrum*, *Sl. scabrum*, *Th. cacao*, *Vernonia amygdalina*, *Zea mays*], nine wild plants and weeds (30.0%) [*Ageratum*

conyzoides, *Alchornea cordifolia*, *Br. micranta*, *Ce. peltata*, *Ch. odorata*, *Ficus* sp., *Mc. grandifolia*, *Mu. cecropioides* and *Sl. torvum*]. The abundance distribution of the host plants was concave, suggesting a predominance of a few species in each locality (Fig. 1A; 2A, 2D and 2G).

3.2 Inventory of Scale Insects

A total of 15,935 mealybugs was collected [2,588 scale insects (16.2%) in Lendi, 6,408 scale insects (40.2%) in Ngoma and 6,939 scale insects (43.5%) in Yassa] (Table 2). These scale insects belonged to the order Hemiptera, to two families [Coccidae (74.2% divided into 13.1% in Lendi, 26.2% in Ngoma and 34.9% in Yassa) and Pseudococcidae (25.8% divided into 3.1% in Lendi, 14.1% in Ngoma and 8.7% in Yassa)], 12 genera, 16 identified species and two undetermined species (Table 2).

The species-rich family was Pseudococcidae [11 species (61.1%) divided into one species (5.6%) in Ngoma, five species 27.8% in Yassa, one species (5.6%) simultaneously in Lendi and Ngoma, four species (22.2%) simultaneously in the three sampling sites] and Coccidae showed seven species (38.9%) divided into 5.6% respectively in Ngoma, Yassa, Lendi and Yassa, Lendi and Ngoma, all three sites and two species (11.1%) simultaneously in Ngoma and Yassa (Table 3).

Ceroplastes sp. was the most represented (26.8%) followed by *Coccus* sp. (13.5%), *Pulvinaria* sp. (10.8%), *Coccus celatus* (9.4%), *Inglisia conchiformis* (= *Vitrococcus conchiformis*) (7.9%), *Paracoccus marginatus* (6.5%), *Pulvinaria elongata* (5.3%), 3.3% respectively for *Ferrisia virgata* and *Saccharicoccus saccharis*, 3.2% of morphospecies 1, 3.1% of *Rastrococcus invadens* (3.1%), 1.1% respectively of morphospecies 2 and *Planococcus citri*.

Phenacoccus manihoti was recorded (3.0%) (Table 3). Other species were rare (0.9% for *Stictococcus formicarius*, 0.5% for *Coccus viridis*, 0.1% for *Pseudococcus viburni* = *Pseudococcus affinis* and 0.03% for *Pseudococcus longispinus* (Table 3).

These scale insects were recorded at the base of plants (case of sugar cane and banana plants), on the underside of leaves, on the small branches of fruit trees, at the level of the flower buds of weeds, on the flowers, fruits, berries and pods. The abundance distribution of the collected scale insects was concave, suggesting a predominance of a few species and an abundance of rare species (Fig. 1B) and the same shape was noted in each study locality (Fig. 2B, 2E and 2H).

3.3 Inventory of Arboreal Foraging Ants

A total of 12,126 foraging ant workers were seen collecting honeydew produced by scale insects [3,426 individuals (28.3%) in Lendi, 3,940 individuals (32.5%) in Ngoma and 4,760 specimens (39.3%) in Yassa] (Table 4). Insects belonged to the Hymenoptera order, Formicidae family, five subfamilies (Dolichoderinae, Formicinae, Myrmicinae, Ponerinae and Pseudomyrmecinae), 16 genera and 37 species (Table 4). Myrmicinae was the most abundant subfamily (73.4%) [13.5% in Lendi, 31.9% in Ngoma and 28.1% in Yassa] followed by Formicinae (21.1%) [11.9% in Lendi, 0.6% in Ngoma and 8.6% in Yassa], Dolichoderinae (4.0%) [1.9% in Lendi and 2.2% in Yassa], Ponerinae (1.0%) exclusively in Lendi and Pseudomyrmecinae was rare (0.4%) exclusively in Yassa (Table 4). The most species-rich subfamily was Myrmicinae (23 species, 62.2%) followed by Formicinae (nine species, 24.3%), Dolichoderinae (three species, 8.1%), Ponerinae and Pseudomyrmecinae were rare (2.7%) (Table 4).

The species abundance distribution (SAD) of the foraging ants was concave, suggesting a predominance of a few species and a high number of rare species (Fig. 1C). The similar results were noted in each study locality (Fig. 2C, 2F and 2I). The most represented species was *Pheidole megacephala* (33.0%) followed by *Crematogaster (Nematocrema) stadelmanni* (7.1%), *Odontomachus troglodytes* (6.3%), *Paratrechina longicornis* (5.6%), *Crematogaster kohli* (4.6%), *Myrmicaria opaciventris* (4.5%), *Camponotus (Tanaemyrmex) brutus* (4.0%), 3.7% for *Atopomyrmex mocquerysi* and *Solenopsis geminata* respectively, 2.4% for *Monomorium pharaonis*, 2.2% for *Anochetus katonae, Monomorium schultzei* and *Tetramorium anxium* respectively. We recorded 2.1% for *Te. minusculum*, 2.0% for *Tapinoma luteum*, 1.6% for *Monomorium floricola* and *Nesomyrmex catalaucoides* = *Leptothorax catalaucoides* respectively, 1.1% for *Tapinoma melanocephalum* and *Pheidole* sp. respectively and 1.0% for *Hypoponera* sp.

Table 2. Matrix of the species richness, diversity, evenness and dominance indexes

	Assemblages											
	A. Host plants				**B. Scale insects**				**C. Arboreal foraging Ant workers**			
Indexes	**I**	**II**	**III**	**Global**	**I**	**II**	**III**	**Global**	**I**	**II**	**III**	**Global**
Sample size n (%)	488	456	672	1,616	2,588	6,408	6,939	15,935	3,426	3,940	4,760	12,126
Richness S (%)	12	9	20	30	8	11	14	18	24	18	19	37
n_{max}	149	355	164	382	1,259	2,066	4,277	4,277	761	2,644	1,045	3,999
Margalef Mg	1.777	1.307	2.918	3.925	0.891	1.141	1.470	1.757	2.826	2.053	2.126	3.829
Richness ratio d = S/n	0.025	0.020	0.030	0.019	0.003	0.002	0.002	0.001	0.007	0.005	0.004	0.003
Chao1	12	10	23	32	8	11	14	18	24	18	19	37
Sample effort (%)	100.0	90.0	87.0	93.8	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Shannon-Weaver H'	2.007	0.7928	2.528	2.705	1.509	1.914	1.478	2.350	2.722	1.388	2.441	2.725
H'_{max}	2.485	2.197	2.996	3.401	2.079	2.398	2.639	2.890	3.178	2.890	2.944	3.611
Simpson D	0.179	0.625	0.107	0.098	0.306	0.187	0.403	0.130	0.092	0.465	0.109	0.134
Hill's $N_1 = e^{H'}$	7	2	13	15	5	7	4	10	15	4	11	15
Hill's N_2= 1/D	6	2	9	10	3	5	2	8	11	2	9	7
Hill's ratio N_2/N_1	0.753	0.724	0.748	0.680	0.723	0.788	0.565	0.737	0.716	0.537	0.802	0.490
Pielou's evenness J	0.808	0.361	0.844	0.795	0.726	0.798	0.560	0.813	0.857	0.480	0.829	0.755
Berger-Parker I_{BP}	0.305	0.779	0.244	0.236	0.487	0.322	0.616	0.268	0.222	0.671	0.220	0.330
Student test)	**H' index**		**D index**		**H' index**		**D index**		**H' index**		**D index**	
I *vs.* II	t=18.6; df=855.5; $p=6.9x10^{-65}$*		t=-15.6; df=576.9, $p=7.2x10^{-46}$*		t=-18.9; df=4,205.2; $p=7.6x10^{-77}$*		t=15.3;df=3,263.6, $p=3.3x10^{-51}$*		t= 47.6; df=6437.4; p=0*		t=-38.3; df=4497.4 ; $p=9.0x10^{-278}$*	
I *vs.* III	t=-10.4; df=1,017.5; $p=3.9x10^{-24}$*		t=6.14; df=859.5; $p=1.3x10^{-9}$*		t=1.26; df=6,591.7; p=0.208 ns		t=-10.01; df=6,771.6; $p=2.0x10^{-23}$*		t= 15.3; df=6,794.3; $p=4.6x10^{-52}$*		t=-5.3; df=6,775.0; $p=1.0x10^{-7}$*	
II *vs.* III	t=-28.4; df=775.7; $p=6.3x10^{-122}$*		t=18.7; df=505.7; $p=6.6x10^{-60}$*		t=22.62; df=11,524.0; $p=7.7x10^{-111}$*		t=-30.84; df=9,061.7; $p=1.1x10^{-198}$*		t=-40.1; df=5,583.1; $p=1.9x10^{-309}$*		t=37.1; df=4,252.7; $p=1.6x10^{-261}$*	

*I: Lendi; II: Ngoma; III: Yassa; * significant difference (p<0.05)*

Table 3. List and abundance of scale insects hosted by 1,616 plants in the studied localities

	Study sites			
Family/Species	I (%)	II (%)	III (%)	Total (%)
Coccidae				
Ceroplastes sp.	-	-	4,277 (26.8)	4,277 (26.8)
Coccus celatus	1,259 (7.9)	-	236 (1.5)	1,495 (9.4)
Co. viridis	-	80 (0.5)	-	80 (0.5)
Coccus sp.	-	2,066 (13.0)	86 (0.5)	2,152 (13.5)
Inglisia conchiformis	262 (1.6)	839 (5.3)	154 (1.0)	1,255 (7.9)
Pulvinaria elongata	-	44 (0.3)	807 (5.1)	851 (5.3)
Pulvinaria sp.	574 (3.6)	1,140 (7.2)	-	1,714 (10.8)
Pseudococcidae				
Ferrisia virgata	51 (0.3)	317 (2.0)	164 (1.0)	532 (3.3)
Undetermined 1	176 (1.1)	224 (1.4)	116 (0.7)	516 (3.2)
Undetermined 2	73 (0.5)	79 (0.5)	26 (0.2)	178 (1.1)
Paracoccus marginatus	41 (0.3)	1,001 (6.3)	-	1,042 (6.5)
Phenacoccus manihoti	-	483 (3.0)	-	483 (3.0)
Planococcus citri Risso, 1813	-	-	170 (1.1)	170 (1.1)
Pseudococcus longispinus	-	-	4 (0.03)	4 (0.03)
Ps. viburni	-	-	21 (0.1)	21 (0.1)
Rastrococcus invadens (	-	-	490 (3.1)	490 (3.1)
Saccharicoccus saccharis	152 (1.0)	135 (0.8)	246 (1.5)	533 (3.3)
Stictococcus formicarius	-	-	142 (0.9)	142 (0.9)
Total	**2,588(16.2)**	**6,408(40.2)**	**6,939(43.5)**	**15,935 (100.0)**

I: Lendi; II: Ngoma; III: Yassa

Seventeen species were rare [*Anochetus africanus, Camponotus (Tanaemyrmex) roubaudi, Ca. acvapimensis, Ca. maculatus, Crematogaster scutellaris, Cr. smichdti, Cr. striatula, Monomorium bicolor, Pheidole albidula, Ph. darwini, Polyrhachis laboriosa, Solenopsis orbuloides, Tapinoma lugubre, Tetramorium aculeatum, Te. ataxium, Te. camerunense* and *Tetraponera* sp.] (Table 4).

3.4 Species Abundances

A total of 1,616 host plants were recorded (median: 30 plants, mean ± se: 54 ± 14 plants, 30 species) (see Table 1), divided into 488 plants in Lendi (median: 25 plants, 41 ± 13 plants, 12 species, 40.0%), 456 plants in Ngoma (median: 2 plants, 51 ± 39 plants, 9 species i.e. 30.0%) and 672 plants in Yassa (median: 29 plants, 34 ± 8 plants, 20 species, 66.7%). The difference in the mean values and the median values were not significant (one-way ANOVA: $F_{(2; 38)} = 0.225$, $p = 0.800$; Kruskall-Wallis test: $H = 1.846$, $df = 2$, $p = 0.397$, respectively). Five species (16.7%) were exclusively in Lendi [*Ageratum conyzoides*, *Amaranthus viridis, Dacryodes edulis, Musa* sp. and *Solanum scabrum*], two species (6.7%) were exclusively in Ngoma [*Ipomea batatas* and *Psidium guajava*], 15 species (50.0%) were exclusively in Yassa [*Abelmoschus esculentus, Annona muricata, Bridelia micranta, Capsicum annum, Cecropia peltata, Ficus sp., Hibiscus sabdariffa, Macaranga grandifolia, Mangifera indica, Musanga cecropioides, Solanum incanum, Sl. nigrum, Sl. torvum, Theobroma cacao* and *Zea mays*]. The only one species (3.3%) *Chromolaena odorata* was recorded simultaneously in Lendi and Yassa.

Three species (10.0%) [*Manihot esculenta, Pandanus fascicularis* and *Vernonia amygdalina*] were recorded simultaneously in Lendi and Ngoma. The only one species (3.3%) *Colocasia esculenta* was recorded simultaneously in Ngoma and Yassa. Three species (10.0%) [*Alchornea cordifolia, Musa ×paradisiaca* and *Saccharum sinense*] were recorded simultaneously in the three study sites. This makes for cosmopolitan species 252 plants (15.6%). Then the percentage of host plant species found exclusively in a single site was significantly high compared to that of cosmopolitan host plant species (Fisher exact test: $\chi^2 = 42.23$, $df = 1$, $p = 2.8x10\text{-}10$). Percentages varied significantly between the three study sites (Fisher-Freeman-Halton test: $\chi^2 = 2{,}520.4$, $df = 58$, $p<0.001$). A significant difference was noted between Lendi and Ngoma ($\chi^2 = 868.57$, $df = 14$, $p<0.001$), Lendi and Yassa ($\chi^2 = 1{,}170.5$, $df = 27$, $p= <0.001$) and between Ngoma and Yassa ($\chi^2 = 1{,}245.5$, $df = 24$, $p= <0.001$).

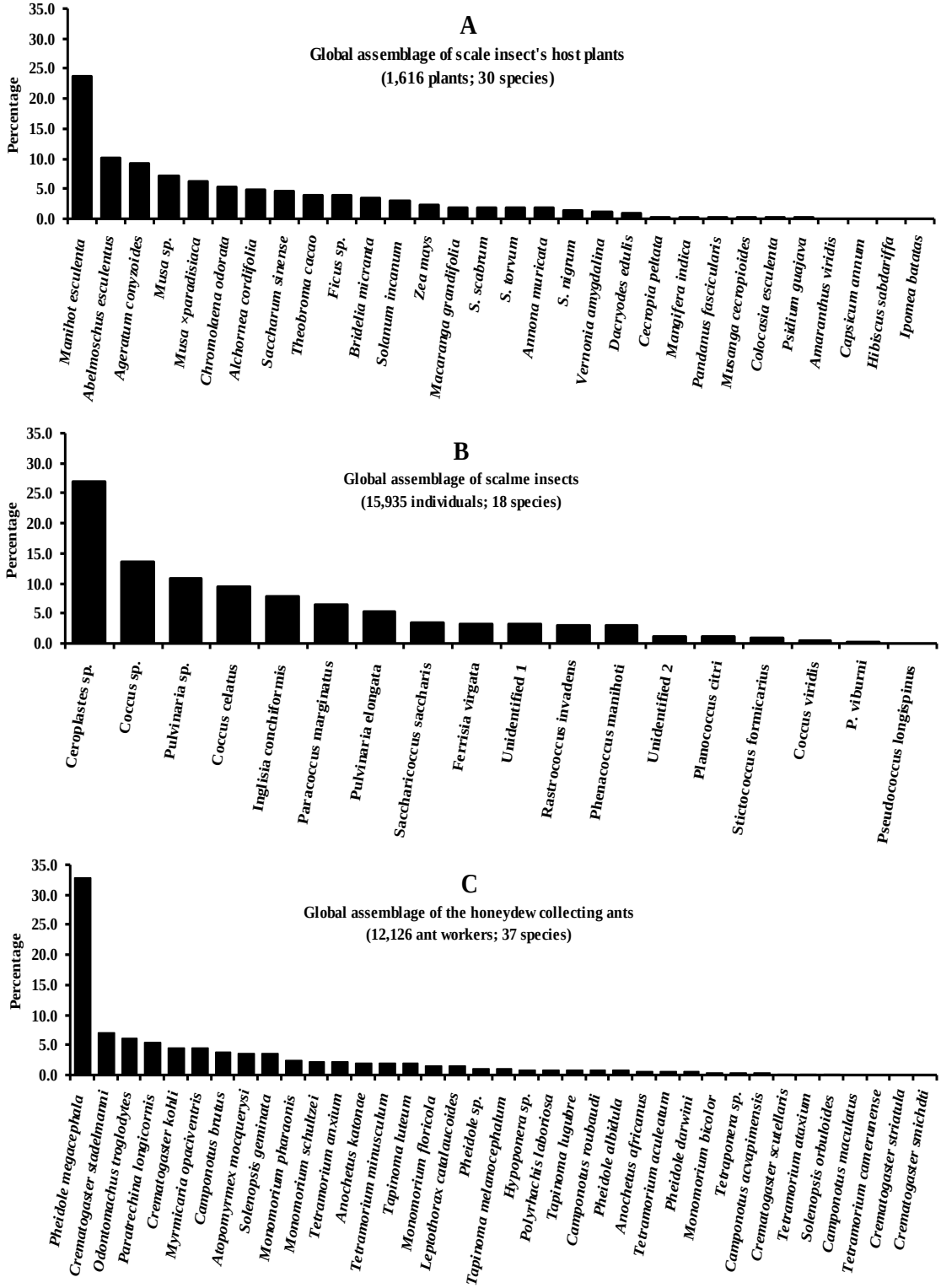

Fig. 1(A-C). Global species abundance distribution (SAD) of the scale insects, host plants and the honeydew collecting ants

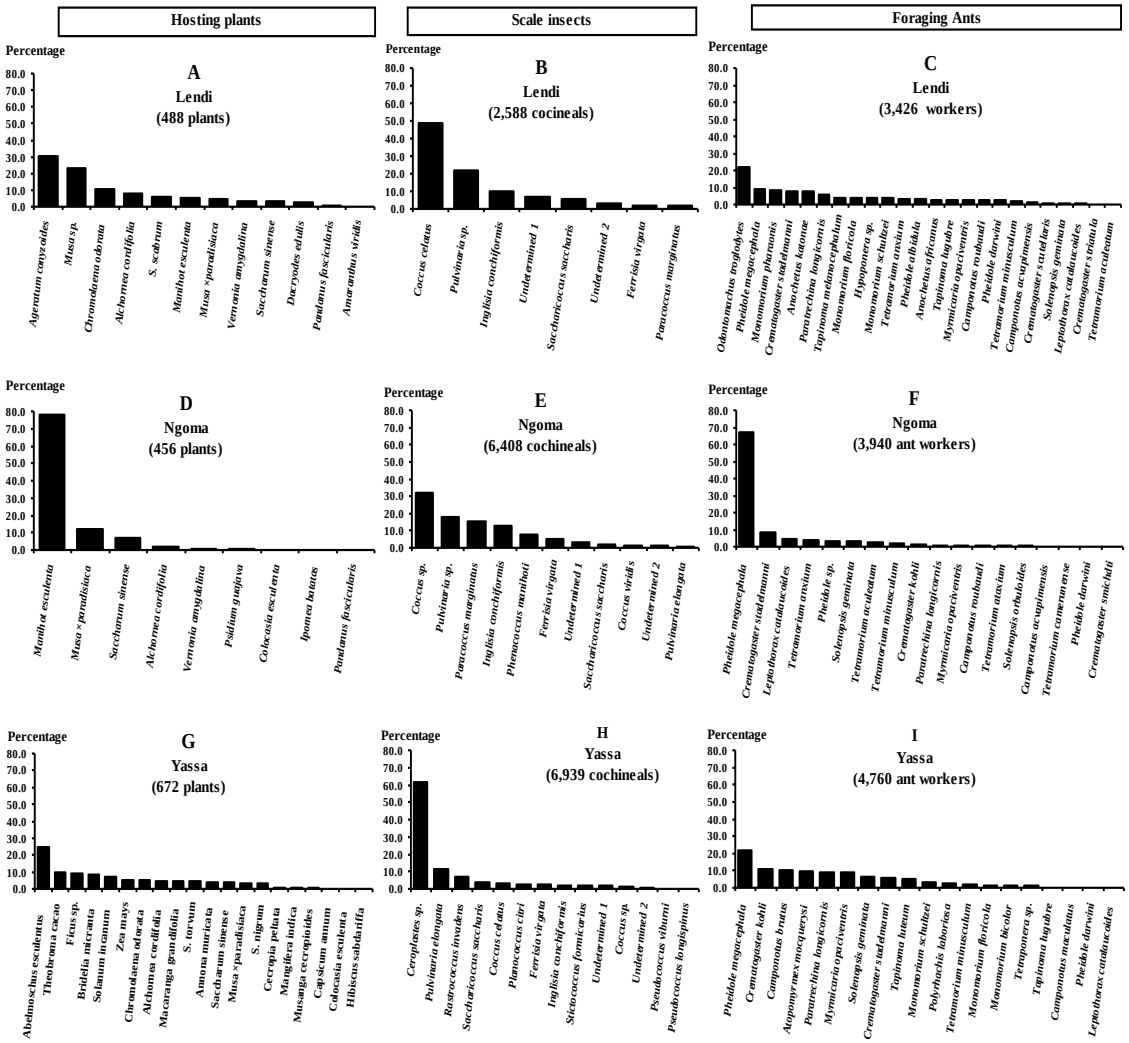

Fig. 2(A-I). Species abundance distribution (SAD) of the scale insects, host plants and the honeydew collecting ants in each study locality

A total of 15,935 scale insects were recorded (median: 524 scale insects, mean ± se: 885 ± 248 scale insects, 18 species) (see Table 3), divided into 2,588 individuals in Lendi (median: 164 individuals, 324±147 individuals, eight species, 44.4%), 6,408 scale insects in Ngoma (median: 217 scale insects, 583 ± 190 scale insects, 11 species, 61.1%) and 6,939 scale insects in Yassa (median: 159 individuals, 496 ± 296 individuals, 14 species, 77.8%). The difference in the mean values and the median values were not significant (one-way ANOVA: $F_{(2; 30)} = 0.223$, $p = 0.801$; Kruskall-Wallis test: $H = 1.521$, $df = 2$, $p = 0.467$, respectively). No species was recorded exclusively in Lendi. Two species (11.1%) [*Coccus viridis* and *Phenacoccus manihoti*] were recorded exclusively in Ngoma and six species (33.3%) [*Ceroplastes* sp., *Planococcus citri, Pseudococcus longispinus, Ps. viburni, Rastrococcus invadens* and *Stictococcus formicarius*] were recorded exclusively in Yassa.

Two species (11.1%) [*Paracoccus marginatus* and *Pulvinaria* sp.] were recorded simultaneously in Lendi and Ngoma, The only one species (5.6%) *Coccus celatus* was recorded simultaneously in Lendi and Yassa. Two species (11.1%) [*Coccus* sp. and *Pulvinaria elongata*] were recorded simultaneously in Ngoma and Yassa and finally five species (27.8%) [*Ferrisia virgata*, Pseudococcidae undetermined 1, Pseudococcidae undetermined 2, *Inglisia conchiformis* and *Saccharicoccus saccharis*] were found simultaneously in the three study sites. This maked for cosmopolitan species 3,014 scale insects (18.9%). Then the percentage of scale insects found exclusively in a single site

was significantly high compared to that of cosmopolitan species (Fisher exact test: χ^2= 0.008, df = 1, p = 0.018). Percentages varied significantly between the three study sites (Fisher-Freeman-Halton test: χ^2 = 21,909.0, df = 34, p<0.001). A significant difference was noted between Lendi and Ngoma (χ^2 = 5,572.5, df = 11, p <0.001), Lendi and Yassa (χ^2 = 7,968.5, df = 15, p <0.001), Ngoma and Yassa (χ^2 = 14,821.0, df = 17, p <0.001).

Table 4. List and abundance of ants collecting honeydew produced by scale insects in the studied localities

	Study sites			
Sous-famille/Species	I (%)	II (%)	III (%)	Total (%)
Dolichoderinae				
Tapinoma lugubre	93 (0.8)	-	15 (0.1)	108 (0.9)
Ta. luteum	-	-	248 (2.0)	248 (2.0)
Ta. melanocephalum	133 (1.1)	-	-	133 (1.1)
Formicinae Latreille, 1802				
Anochetus africanus	94 (0.8)	-	-	94 (0.8)
A. katonae	265 (2.2)	-	-	265 (2.2)
Camponotus acvapimensis	35 (0.3)	12 (0.1)	-	47 (0.4)
Ca. (Tanaemyrmex) brutus	-	-	484 (4.0)	484 (4.0)
Ca. maculatus (Fabricius)	-	-	12 (0.1)	12 (0.1)
Ca. (Tanaemyrmex) roubaudi	83 (0.7)	24 (0.2)	-	107 (0.9)
Odontomachus troglodytes	761 (6.3)	-	-	761 (6.3)
Paratrechina longicornis	206 (1.7)	32 (0.3)	437 (3.6)	675 (5.6)
Polyrhachis laboriosa	-	-	108 (0.9)	108 (0.9)
Myrmicinae				
Atopomyrmex mocquerysi,	-	-	452 (3.7)	452 (3.7)
Crematogaster stadelmanni	266 (2.2)	332 (2.7)	265 (2.2)	863 (7.1)
Cr. kohli	-	43 (0.4)	517 (4.3)	560 (4.6)
Cr. scutellaris	31 (0.3)	-	-	31 (0.3)
Cr. smichdti	-	1 (0.008)	-	1 (0.008)
Cr. striatula	3 (0.02)	-	-	3 (0.02)
Monomorium bicolor	-	-	58 (0.5)	58 (0.5)
Mo. floricola	131 (1.1)		67 (0.6)	198 (1.6)
Mo. pharaonis	295 (2.4)	-	-	295 (2.4)
Mo. schultzei	122 (1.0)	-	150 (1.2)	272 (2.2)
Myrmicaria opaciventris	84 (0.7)	31 (0.3)	432 (3.6)	547 (4.5)
Leptothorax catalaucoides	12 (0.1)	180 (1.5)	1 (0.008)	193 (1.6)
Pheidole albidula	101 (0.8)	-	-	101 (0.8)
Ph. darwini	80 (0.7)	6 (0.05)	3 (0.02)	89 (0.7)
Ph. megacephala	310 (2.6)	2,644 (21.8)	1,045 (8.6)	3,999 (33.0)
Pheidole sp.	-	135 (1.1)	-	135 (1.1)
Solenopsis geminata	20 (0.2)	117 (1.0)	309 (2.5)	446 (3.7)
So. orbuloides	-	15 (0.1)	-	15 (0.1)
Tetramorium aculeatum	1 (0.008)	92 (0.8)	-	93 (0.8)
Te. anxium	103 (0.8)	164 (1.4)	-	267 (2.2)
Te. ataxium	-	23 (0.2)	-	23 (0.2)
Te. camerunense	-	8 (0.07)	-	8 (0.07)
Te. minusculum	72 (0.6)	81 (0.7)	104 (0.9)	257 (2.1)
Ponerinae				
Hypoponera sp.	125 (1.0)	-	-	125 (1.0)
Pseudomyrmecinae				
Tetraponera sp.	-	-	53 (0.4)	53 (0.4)
Total	**3,426 (28.3)**	**3,940 (32.5)**	**4,760 (39.3)**	**12,126 (100.0)**

I: Lendi; II: Ngoma; III: Yassa

A total of 15,935 foraging ants were recorded (median: 133 workers, mean ± se: 328 ± 109 workers, 37 species) (see Table 4), divided into 2,436 workers in Lendi (median: 98 workers, 143 ± 33 workers, 24 species i.e. 64.9%), 3,940 ants in Ngoma (median: 38 workers, 219 ± 144 workers, 18 species i.e. 48.6%) and 4,760 ants in Yassa (median: 150 workers, 251 ± 61 workers, 19 species i.e. 51.4%). The difference in the mean values and the median values were not significant (one-way ANOVA: $F_{(2;\ 57)} = 0.534$, p = 0.589; Kruskall-Wallis test: H = 4.00, df = 2, p = 0.135, respectively). Nine species (24.3%) [*Anochetus africanus, A. katonae, Odontomachus troglodytes, Crematogaster scutellaris, Cr. striatula, Hypoponera* sp., *Monomorium pharaonis, Pheidole albidula* and *Tapinoma melanocephalum*] were recorded exclusively in Lendi while five species (13.5%) [*Crematogaster smichdti, Pheidole* sp., *Solenopsis orbuloides, Tetramorium ataxium* and *Te. camerunense*] were noted exclusively in Ngoma. Seven species (18.9%) [*Atopomyrmex mocquerysi, Camponotus (Tanaemyrmex) brutus, Ca. maculates, Monomorium bicolor, Polyrhachis laboriosa, Tapinoma luteum* and *Tetraponera* sp.] were noted exclusively in Yassa. Four species (10.8%) [*Camponotus acvapimensis, Ca. (Tanaemyrmex) roubaudi, Tetramorium aculeatum* and *Te. anxium*] were found simultaneously in Lendi and Ngoma while three species (8.1%) [*Monomorium floricola, Mo. schultzei* and *Tapinoma lugubre*] were found in Lendi and Yassa. One species (2.7%) *Crematogaster kohli* was recorded simultaneously in Ngoma and Yassa.

Eight ant species (21.6%) were cosmopolitan [*Crematogaster (Nematocrema) stadelmanni, Leptothorax catalaucoides, Myrmicaria opaciventris, Paratrechina longicornis, Pheidole darwini, Ph. megacephala, Solenopsis geminata* and *Tetramorium minusculum*]. Making for cosmopolitan species 7,069 workers (58.3%). The percentage of ants in a single site was high compared to that of cosmopolitan species (Fisher exact test: $\chi^2 = 24.58$; df = 1; p = 1.8x10-6). Percentages varied between sampling sites (Fisher-Freeman-Halton test: χ^2 = 13,009.0; df = 72; p<0.001). A significant difference was noted between Lendi and Ngoma (χ^2 = 5,965.5; df = 29; p= <0.001), Lendi and Yassa (χ^2 = 6,426.6; df = 31; p= <0.001), Ngoma and Yassa (χ^2 = 5,133.6; df = 27; p= <0.001).

3.5 Community Structure

In the case of host plants, although values of the Margalef index are high, assemblages exhibited low species richness (richness ratios being in all cases close to zero) (see Table 2A). Considering Chao1 estimator, the sampling effort was maximum (100%) at Lendi and the species diversity was high, Shannon-Weaver indices being close to the maximum values (Table 2A). The number of codominants was high and close to that of simply abundant species (Hill ratio close to the unity), assemblages were highly even and lowly dominated by a few species (low values of the Berger-Parker index) (Table 2A). In the case of scale insects, Chao1 estimator showed in all cases a maximum sampling effort (100%) and a high species diversity (Shannon-Weaver indices close to the maximum values) (see Table 2B). Moreover, the number of codominants was high and close to that of simply abundant species, explaining a Hill ratio close to unity, the highly even assemblages and the low values of the Berger-Parker dominance index (see Table 2B). In the case of the foraging ants, the sampling effort was maximum (100%) in all cases and the species diversity was high (Shannon-Weaver indices close to the maximum values) (see Table 2C). The number of codominants was high and close to that of simply abundant species, explaining a Hill ratio close to the unity, the highly even level of the assemblages and the low values of the Berger-Parker dominance index (see Table 2C). In the study sites, assemblages were highly even (Pielou's index close to unity) except assemblages of host plants and ant workers in Ngoma and that of scale insects in Yassa whose values were close to the median value (see Table 2). Low species dominance by a few species was noted (values close to the median value) except assemblages of host plants and ant workers in Ngoma and that of scale insects in Yassa whose values were high and close to unity (see Table 2).

The individual rarefaction curves plotted for host plants, scale insects and foraging ants approached the saturation plateaus with similar slopes. The curve observed in Ngoma in host plants (Fig. 3A) and ant workers (Fig. 3C), that recorded in Lendi in scale insects (Fig. 3B) were situated faraway below that of the other communities, suggesting the lowest species richness at Ngoma (cases of host plants and foraging ant workers) and at Lendi (case of the scale insects) and the highest species richness

were recorded in other study sites. Then for a standard sample of 441 plants, the global settlement appeared most riched [$E(S_{n=441})$ = 25 ± 1 species], followed by the settlement recorded in Yassa [$E(S_{n=441})$ = 19 ± 1 species], by that recorded in Lendi [$E(S_{n=441})$ = 12 ± 0 species] while the settlement in Ngoma was the least riched [$E(S_{n=441})$ = 9 ± 0 species]. For a standard sample of 2,401 scale insects, the global settlement appeared most riched [$E(S_{n=2,401})$ = 17 ± 1 species], followed by the settlement in Yassa [$E(S_{n=2,401})$ = 14 ± 0 species], by that recorded in Ngoma [$E(S_{n=2,401})$ = 11 ± 0 species] while the settlement in Lendi was the least riched [$E(S_{n=2,401})$ = 8 ± 0 species]. For a standard sample of 3,301 ant workers, the global settlement appeared most riched [$E(S_{n=3,301})$ = 36 ± 1 species], followed by the settlement recorded in Yassa [$E(S_{n=3,301})$ = 19 ± 0 species], by that recorded in Lendi [$E(S_{n=3,301})$ = 24 ± 0 species] while the settlement recorded in Ngoma was the least rich [$E(S_{n=3,301})$ = 18 ± 0 species].

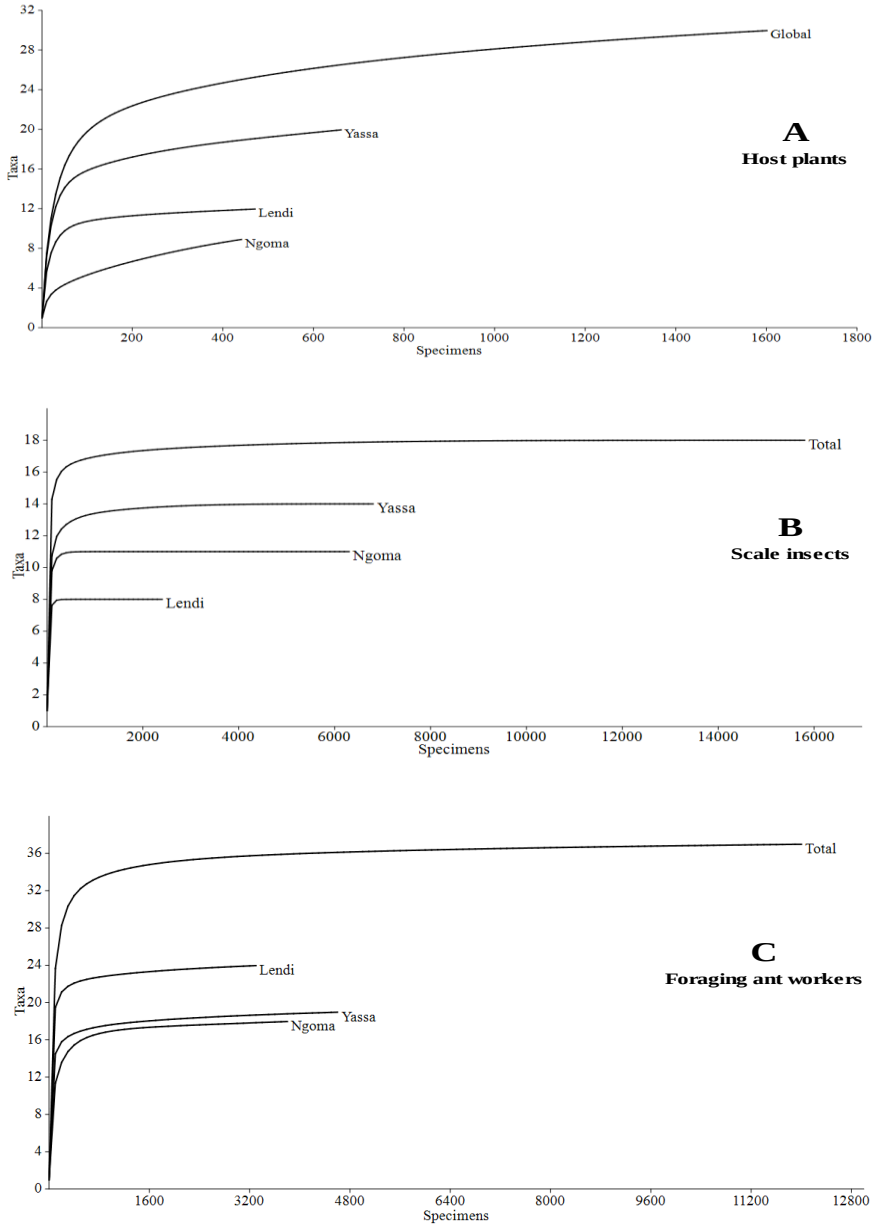

Fig. 3(A-C). Species rarefaction curve for the host plants, scale insects and foraging ant workers in the study sites

3.6 Dissimilarity between Sites and Species Abundance Distributions (SADs)

On the base of the species composition, although a few cosmopolitan species were sampled, a low level of dissimilarity was noted between assemblages of host plants from Lendi, Ngoma and Yassa localities, the Bray-Curtis dissimilarity indexes being in all cases inferior to the median value (Lendi vs. Ngoma: BC = 0.143; Lendi vs. Yassa: BC = 0.163; Ngoma vs. Yassa: BC = 0.065).

The same result was true for the scale insects' assemblages (Lendi vs. Ngoma: BC = 0.292; Lendi vs. Yassa: BC = 0.154; Ngoma vs. Yassa: BC = 0.109). Il was the same for the foraging ants' assemblages (Lendi vs. Ngoma: BC = 0.222; Lendi vs. Yassa: BC = 0.252; Ngoma vs. Yassa: BC = 0.192). Adjustment of the species abundance distributions (SADs) to the five commonly known theoretical models showed that in the case of host plants, the fit was of satisfactory quality in the global settlement's community (Pearson correlation: r = -0.975, 30 species, p<0.001) and of poor quality in Lendi (r = -0.933, 12 species, p<0.001), Ngoma (r = -0.937, 9 species, p<0.001) and Yassa (r = -0.924, 20 species, p<0.001).

In the case of the scale insects, the fit was of excellent quality in Ngoma (r = -0.994, 11 species, p<0.001), of satisfactory quality in Lendi (r = -0.983, 8 species, p<0.001) and of poor quality in Yassa (r = -0.928, 14 species, p<0.001) and in the global settlement (r = -0.920, 18 species, p<0.001). In the case of the foraging ant workers, the fit was of approximate quality in Ngoma (r = -0.952, 18 species, p<0.001) and of poor quality in Lendi (r = -0.886, 24 species, p<0.001), Yassa (r = -0.929, 19 species, p<0.001) and in the global settlement (r = -0.933, 37 species, p<0.001).

On the base of the AIC values (Table 5) and the SADs (Fig. 2), the broken-stick (BS) model (McArthur) best fitted the assemblage of foraging ant workers in Yassa (Table 5C) (S = 19 species, n = 4,760 workers, model parameter or the observed mean abundance: x = 251 ± 61 ant workers) and the theoretical model was n_i = (251)*sum(1/i) where n_i is the theoretical absolute abundance of the ith species ranged in decreasing order of the observed abundance and i = 1, 2, …, S. The log-linear (LL) model best fitted the scale insect assemblage in Ngoma (Table 5B) [slope of the log-linear regression: a = -0.168, Motomura environmental constant: m = 0.679, regression equation: Log(n_i) = (-0.168 ± 0.006)i + (3.50 ± 0.04), S = 11 species, determination coefficient: r^2 = 0.988, regression ANOVA: F(1; 9) = 742.23, p<0.001)].

The lognormal (LN) model best fitted the community structure of host plants in Lendi, Yassa and the global settlement (Table 5A). It also best fitted the global assemblage of scale insect (Table 5B). Moreover, it best fitted the arboreal foraging ant assemblage in Lendi and the global ant assemblage (Table 5C). In the case of the host plant assemblage in Lendi, parameters of the LN model were determined [maximum abundance: n_1 = 149 individuals; sample size: n = 488 individuals; species richness: S = 12 species; number of species in the modal octave: S_0 = 5 species; maximum octave: R_{max} = -4; LN model parameter a = 0.317; mean logarithm of S(R): mean S(R) = 0.201; then LN model was S(R) = $5e^{(-0.201)²R²}$ where S(R) represented the number of species in the R^{th} octave from the mode; standard deviation of the lognormal distribution: deviance: 17.37; σ = 0.634; Preston's constant: m' = 1/σ = 1.576; number of species theoretically available for observation: S* = 28 species; 16 rare species have therefore escaped our captures]. In the case of host plants in Yassa, we recorded the associated parameters [n_1 = 164 individuals; n = 672 individuals; S = 20 species; S_0 = 7 species; R_{max} = -4; a = 0.349; mean S(R) = 0.243; LN model: S(R) = $7e^{(-0.349)²R²}$; deviance: 53.87; σ = 0.697; m' = 1.434; S* = 36 species; 16 rare species have escaped our captures]. In the global assemblage of host plants, parameters were n_1 = 382 individuals; n = 1,616 individuals; S = 30 species; S_0 = 6 species; R_{max} = -4; a = 0.159; mean S(R) = 0.535; LN model: S(R) = $6e^{(-0.159)²R²}$; deviance: 511.92; σ = 0.318; m' = 3.141; S* = 67 species; then 37 rare species escaped our captures. In the case of the global assemblage of the scale insects, parameters were n_1 = 4,277 individuals; n = 15,935 individuals; S = 18 species; S_0 = 4 species; R_{max} = -7; a = 0.168; mean S(R) = 0.137; LN model: S(R) = $4e^{(-0.168)²R²}$; deviance: 511.92; σ = 0.336; m' = 2.973; S* = 42 species; 24 rare species escaped our captures. For the ant workers assemblage recorded in Lendi, the LN parameters were n_1 = 761 individuals; n = 3,426 individuals; S = 24 species; S_0 = 10 species; R_{max} = -6; a = 0.253; mean S(R) = 0.512; LN model: S(R) = $10e^{(-0.253)²R²}$; deviance: 146.48; σ = 0.506;

m' = 1.977; S* = 70 species; 46 rare species escaped our captures. For the global assemblage of the foraging ants, LN parameters were n_1 = 3,999 individuals; n = 12,126 individuals; S = 37 species; S_0 = 8 species; R_{max} = -6; a = 0.240; mean S(R) = 0.548; LN model: $S(R) = 8e^{(-0.240)^2R^2}$; deviance: 955.84; σ = 0.481; m' = 2.080; S* = 59 species; 22 rare species escaped our captures.

In contrast Z model fitted the host plant's SAD recorded in Ngoma (Table 5A) [n1 = 355 individuals; normalization constant: Q = 456 individuals; deviance: 10.71; 9 species; decay coefficient or the average probability of occurrence of a species: γ = 2.917; the model was formulated as $n_i = 456(i)^{-2.917}$]. A similar result was true for the scale insect assemblage in Yassa (Table 5B) [n_1 = 4,277 individuals; Q = 6,939 individuals; deviance: 370.97; 14 species; γ = 1.954; Z model: $n_i = 6939(i)^{-1.954}$]. In Ngoma, the foraging ants showed a similar result (Table 5C) and the Z parameters were n_1 = 2,644 individuals; Q = 3,940 individuals; deviance: 337.71; 18 species; γ = 2.05; Z model: $n_i = 3940(i)^{-2.05}$. The ZM model fitted the scale insect settlement recorded in Lendi (Table 5B) [deviance: 16.59, Q = 4,617, n_1 = 2,588 individuals, S = 8 species; starting point: $x_0 = (1; 1)^T$; tolerance of the functional value: ε = 0.001; damping factor: λ_0 = 100; β = 0.297; γ = 1.045; model: $n_i = 4{,}617(i+0.297)^{-1.045}$ with an average fractal dimension of the distribution of individuals among species (1/γ = 0.957)].

3.7 Interspecies Associations and Correlations

On the base of the presence/absence data on 1,616 sample units, overall the negative net association was suggested between the 82 recorded species (30 plant species, 36.6%; 15 species of scale insects, 18.3% and 37 species of foraging ants, 45.1%) (Schluter's variance ratio V = 0.028, W statistic: 44.66, df = 81, p <0.001).

Data showed the negative correlation between *Ageratum conyzoides* (Asterales: Asteraceae) and *Amaranthus viridis* (Coryophyllales: Amaranthaceae) (Kendall's tau: τ = -1.0, p = $2.3x10^{-4}$), between *Ag. conyzoides* and *Pheidole megacephala* (Formicidae: Myrmicinae) (τ = -1.0, p = $2.4x10^{-40}$), and between *Ag. conyzoides* and *Pulvinaria* sp. (Hemiptera: Coccidae) (τ = -1.0, p = 2.4x10-40). The positive but not significant correlation was detected between *Ag. conyzoides* and *Coccus celatus* (Hemiptera: Coccidae) (τ = 0.165, p = 0.028), *Monomorium schultzei* (Formicidae: Myrmicinae) (τ = 0.045, p = 0.553), *Odontomachus troglodytes* (Formicidae: Formicinae) (τ = 0.123, p = 0.101) and *Tapinoma melanocephalum* (Formicidae: Dolichoderinae) (r = 0.036, p = 0.633). Am. viridis was negatively correlated with *Co. celatus* (τ = -0.165, p = 0.028) and *Ph. megacephala* (τ = -1.0; p = $2.4x10^{-40}$). A negative not significant correlation was detected between *Ag. conyzoides* and Mo. schultzei (τ = -0.045, p = 0.553), *O. troglodytes* (τ = -0.125, p = 0.101) and *Ta. melanocephalum* (τ = -0.036; p = 0.633) while it was positively correlated with *Pulveria* sp. (τ = 1.0, p = $2.4x10^{-40}$). A negative and not significant correlation was noted between Co. celatus and Mo. schultzei (τ = -0.098, p = 0.192), O. troglodytes (τ = -0.007, p = 0.925), *Ph. megacephala* (r = -0.165, p = 0.028), *Pulvinaria* sp. (τ = -0.165, p = 0.028) and positively correlated with *Ta. melanocephalum* (τ = 0.295; p = $9.0x10^{-5}$). *Mo. schultzei* was negatively correlated with *O. troglodytes* (τ = -0.445, p = $3.2x10^{-9}$). On the other hand, the negative correlation was not significant between *Mo. schultzer* and *Ph. megacephala* (τ = -0.045, p = 0.553), with *Pulvinaria* sp. (τ = -0.045, p = 0.553), and with *Ta. melanocephala* (τ = -0.130 , p = 0.084). *O. troglodytes* was negatively correlated with *Ta. melanocephalum* (τ = -0.358, p = $1.9x10^{-6}$). On the other hand, the negative correlation was not significant between *O. troglodytes* and *Ph. megacephala* (τ = -0.123, p = 0.101) and with *Pulvinaria* sp. (τ = -0.123, p = 0.101). *Ph. megacephala* was positively correlated with *Pulvinaria* sp. (τ = 1.0, p = $2.4x10^{-40}$) while a negative not significant correlation was detected between *Ph. megacephala* and *Ta. melanocephalum* (τ = -0.036, p = 0.633). The negative correlated detected between *Pulvinaria* sp. and *Ta. melanocephalum* was not significant (τ = -0.036, p = 0.633). In the case of the other combinations, data obtained were insufficient to determine the correlation.

Table 5. Values of the Akaike Information Criteria (AIC) for the adjustment of species abundance distributions (SADs) to theoretical models

	A. Host plants				B. Scale insects			
	Lendi	**Ngoma**	**Yassa**	**Total**	**Lendi**	**Ngoma**	**Yassa**	**Total**
BS	87.6	506.0	146.2	1100.2	372.3	398.8	4977.8	1100.2
LL	86.3	73.3	181.0	1027.4	144.4	**191.3***	2512.7	1027.4
LN	**80.6***	50.8	**151.1***	**655.9***	94.5	339.8	762.0	**655.9***
Z	103.0	**48.7 ***	204.0	1940.5	110.0	800.9	**470.1***	1940.5
ZM	85.4	49.3	184.5	1010.6	**78.5 ***	193.2	472.1	1010.6

	C. Ant workers			
	Lendi	**Ngoma**	**Yassa**	**Total**
BS	338.3	4510.3	**438.5***	4469.3
LL	505.8	2018.4	445.3	4016.3
LN	**298.2***	597.2	566.7	**1205.1***
Z	508.4	**443.7 ***	1144.0	1596.4
ZM	455.7	445.7	447.6	1598.4

*BS: Broken-Stick model (McArthur); LL: Log-linear nomocenosis model (Motomura); LN: Lognormal nomocenosis model (Preston); Z: Zipf model; ZM: Zipf-Mandelbrot model; * = the best fitted theoretical model (in bold)*

4. DISCUSSION

4.1 Species Richness, Abundance and Dominance

The present study is the first step in evaluating the functioning of the three-component complex made up of plants, mealybugs and arboreal foraging ants in the suburb's areas of Douala (Littoral-Cameroon). A total of 29,640 specimens were collected on 1,616 sample units (mean ± se: 18 ± 0 specimens) in three localities (1,947 plant specimens, 7.9% of the total collection, mean ± se: 1 ± 0 plants; 11,961 arboreal foraging ants, 48.5% of the total collection, 7 ± 0 ant workers; 15,732 scale insects, 63.8% of the total collection, 10 ± 0 individuals). These specimens belonged to 23 families [30 plants (87.0%), two scale insects (8.7%) and one foraging ants (4.3%)], 54 genera [26 host plants (48.1%), 12 scale insects (22.2%) and 16 arboreal foraging ants (29.6%)] and 85 species [20 host plants (35.3%), 16 species of scale insects (18.8%) and two mealybug morphospecies (2.4%) and 37 species of the arboreal foraging ants (43.5%)]. The urban and suburbs studied presented a low level of species richness compared to the situation in other perturbed environments. As example, recent report in Cameroon point out a total of five ant subfamilies, 14 genera of ants and 28 ant species in Douala urban quarters [31], in vegetable crops, 13 families and 22 species were reported associated with eggplants [34], 18 families and 23 species were reported associated with the potato plants [35]. The absence of certain taxa of scale insects and foraging ants could be the result of the sampling success influence by biotic factors (diet behaviour of each species and interspecies interactions) as well as abiotic factors (time periods, seasons, the weather, the duration of observations) and the location of sampling sites. For example, field investigations were done daily, excluding nocturnal ants. Ants are known for their mutualistic relationship (trophobiosis) with scale insects and they protect pests from their natural enemies [36,37]. The number of Hemiptera was quite high in Ngoma, with regard to cassava monoculture, but low in Yassa and Lendi. The number of ants observed was however low, particularly in Yassa and Lendi, this would be due to the low infestation of the plants by scale insects and consequently the low production of honeydew [38]. It is obvious that despite the low abundance of scale insects and honeydew collecting ants, they damage cultivated vegetables, as it is the case elsewhere where they transmit viruses responsible of plant diseases and the yield looses. Anthropized environments are known to present low abundances and low numbers of species, compared with the situation in natural environments all over the world and anthropogenic disturbance plays a key role in shaping species diversity and community structures [39-43]. According to the reports of these authors, the strongly anthropized sites are clearly less diverse than the sites undergoing regeneration process represented by the old fallows.

The low diversity is associated with low abundance in several native ants, resulting in the weak exploitation of resources. Moreover, the

exploitation of both food and nest sites was mostly achieved by *Pa. longicornis, Ph. megaphala* and *So. geminata*. The low species diversity of scale insects and arboreal foraging ants reflects either the low level of maturity of the communities, or the degradation of the environmental quality or the negative effect of the presence of both native and invasive species (*Pa. longicornis, Ph. megacephala*, *So. geminata* and *Ta. melanocephalum*). The high abundance level of the invasive alien species *So. geminata* in its introduced range is well known [44]. The striking result is the high occurrence of *Pa. longicornis* and *Ph. megacephala* in their native range, in the presence of the non-native species. *Pa. longicornis, Ph. megacephala* and *So. geminata* are tramp species considered as among the most ecologically destructive in human residences and cultivated areas where they have been introduced [44-46].

Since in undisturbed areas, ant species are organized in structured communities and as long as there is no disturbance, potential pests are regulated by competition or predation and can not reach high population densities, our investigations confirm that in the Littoral-zone of Cameroon, ant community is perturbed by non-native ant species. Ant species such as *Ph. megacephala* and *So. geminata* are known to be associated with several scale insects, showing their strong involvement in trophobiosis [3,44 47,48].

Ants promote the proliferation of honeydew-producing insects, protecting them from predators [3]. Invasive scale insect species and associated foraging ants are able to destroy crops of agricultural importance. They belong mostly to the category of rare species. Their populations could increase in the near future as a result of intense anthropogenic activities (land use, city extension, urbanization leading to the deforestation) which eliminates native competitive species.

Pseudococcidae and Coccidae are worldwide distributed but more common in subtropical and tropical regions. They feed on the plant's sap, sucking it up by inserting their stylets into the epidermis of aeral plan and during food intake, they inject a toxic substance into the plant, which induces necrosis, deformation, premature fall of the attaked organ and the death of the plant in extreme cases. Sap feeding can cause the accumulation of honeydew (sugar enriched faeces) loved by nectarivorous insects (ants, wasps and bees).

Frequently the development of sooty mold is reported on attacked plants, making it difficult to sell infested fruits or causing quarantine releases [15]. Mealybugs are difficult to manage. Members are polyphagous, pests (vectors of plant viruses) of a wide variety of crops in tropical, subtropical, and temperate regions [49,50]. Their small size and cryptic habits allow them to easily escape phytosanitary chemicals [49,51]. They have poor dispersal abilities and therefore, long distance movements can be easily achieved through human activities [29,52,53]. *Pseudococcus viburni* and *Ps. longispinus* are cosmopolitan pests of many types of plants, commonly found together on the same plants [54-58].

4.2 Community Structure and Functioning

Quantification of the richness and diversity is important when comparing sites, these variables being influenced by local and regional factors [59]. On the base of the AIC values, foraging ants in Yassa functioned like the broken-stick (BS) model which describes the continuous and non overlapping process of niche partitioning, the weakest competitors being the most tolerant of poor conditions in order to survive [32,60-62]. It is well known that geographic variation in niche-assemblage mechanisms contributes to differences in species diversity among temperate and tropical ecosystems [63].

The geometric model (GM) fitted the scale insect assemblage in Ngoma with a high environmental constant exceeded the median value (m = 0.679). This model is suitable for communities in which interspecies relations are elementary, competition being essentially limited to the level of the resource (physical space). The low value of GM parameter "m" low values suggestes that the assemblage is organized with few predominant species (lowly diverse communities) [32,59,64-66]. The GM niche partitioning model is reported fitting SADs of several insect communities including the dung beetles in mountain grasslands of the Southern Alps [64,65], Carabidae and Heteroptera inhabiting road verges and meadow-pasture pairs in managed grasslands in Central Finland [67], grasshopper in the Littoral zone of Cameroon [68], insects associated with eggplants and potato in Balessing (Cameroon) [34,35]. This model characterizes open forests and disturbed environments with strong competition between pioneer species.

The lognormal (LN) model fitted assemblage of host plants in Lendi (m' = 1.576), in Yassa (m' = 1.434) and the global settlement (m' = 3.141), global assemblage of scale insects (m' = 2.973), ant workers in Lendi (m' = 1.971) and the global settlement of ants (m' = 2.080), with environmental constants m' greater than 1. According to the log-normal model, the increase in the environmental constraint may be the consequence of the reduction in the species evenness, the high number of common and rare species and the change of the overall shaping of the SADs, as it is the case along seasonality gradient in Brazilian savannas [69]. A similar situation may occur in host plants in Lendi. The LN model characterizes open or less disturbed environments with strong competition between species.

Zipf (Z) model fitted SADs of the host plants in Ngoma, the scale insects in Yassa, and the foraging ants in Ngoma, with high values of the average probability of occurrence of a species (γ = 2.917, γ = 1.954 and γ = 2.05 respectively) compared to the litterature [70]. Scale insects in Lendi fitted the Zipf-Mandelbrot model (evolved ecosystems where the multi-species networked structure corresponds to an optimal structure for the circulation of information carried out on spatio-temporal scale) [70]. Human activities resulting in urbanization, growing cities, extensive deforestation and the extension of cultivated areas have been reported to modify land cover, to reduce the area of natural habitats, to affect ecosystem functioning and contribute to the loss of biodiversity [71].

5. CONCLUSION

As background information useful to the scientific community (entomologist) and to crop pest management programs, a total of 24,640 specimens were collected [1,616 host plants, 15,935 scale insects and 12,126 arboreal foraging ants] belonging 17 orders [15 (88.2%) for plants, one (5.9%) for scale insects and foraging ants respectively] to 23 families [20 (87.0%) for plants, two (8.7%) for scale insects and one (4.3%) for ants], five subfamilies of ants, 54 genera [26 (48.1%) for plants, 12 (22.2%) for scale insects and 16 (29.6%) for ants] and 85 species [30 (35.3%) for plants, 18 (21.2%) for scale insects and 37 (43.5%) for ants]. Abundance distributions suggested the existence of a few codominant. Pooled data showed low richness, diversity and dominance by a few species. Foraging ants in Yassa functioned according to broken-stick (BS) model (pioneer species in highly perturbed environments). Mealybugs in Ngoma functioned according to loglinear model (open forests and disturbed environments with strong competition between pioneer species). Host plants in Lendi and Yassa and the global host plant assemblage, the global scale insects, the foraging ants in Lendi and the global one, functioned according to lognormal model (less disturbed environments with strong competition between species). Host plants in Ngoma, mealybugs in Yassa, and Zipf model adjusted the foraging ant assemblage in Ngoma.

Zipf-Mandelbrot model (for evolved ecosystems) fitted the scale insect settlement in Lendi, suggesting that the locality had developed a complex network of information close to the natural environments and presented a fairly significant regeneration force.

ACKNOWLEDGEMENTS

The Cameroonian Ministry of Higher Education provided funds through the research support program. Authors are grateful to the members of the Biological Control Unit (University of Douala), for the field technical support. We are grateful to Professor Jacques Hubert Charles Delabie, Danièle Matile-Ferrero and Barry Bolton for the identification of the Hemipterans and ants, respectively during the past project CORUS program (research agreement 02 412 062) and therefore duplicates of the identified specimens were kept in our laboratory. We would like to thank the inhabitants of Douala town and suburbs for having warmly welcome us in their respective homes and/or in their respective plantations.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Clouvel P, Brevault T, Amadji G, Assogba-Komlan F, Bordat D, Diallo MD, et al. Le projet scientifique de DIVECOSYS : « Diversité des systèmes de production et gestion agro-écologique des bio-agresseurs en Afrique de l'Ouest ». CIRAD, Montpellier, France; 2013. French

2. Gibernau M, Dejean A. Ant protection of a Heteropteran trophobiont against a parasitoid wasp. Oecologia. 2001;126:53-57.
3. Delabie JHC. Trophobiosis between formicidae and hemiptera (Sternorrhyncha and Auchenorrhyncha): An overview. Neotrop Entomol. 2001;30:501-516.
4. Ramage T, Ravary F. Les bio-indicateurs myrmécologiques: Synthèse bibliographique. OEIL, Nouvelle-Calédonie; 2015. French
5. Billy Annan I, Tingey WM, Schaefers GA, Tjallingii WF, Backus EA, Saxena KN. Stylet penetration activities by *Aphis craccivora* (Homoptera: Aphididae) on plants and excised plant parts of resistant and susceptible cultivars of cowpea (Leguminosae). Ann Entomol Soc Am. 2000;93(1):133-140.
DOI: 0013-8746/00/0133-0140$02.00/0
6. Climate-Data.org 2023. Douala Climate (Cameroon). Assessed 27 March 2023.
Available:https://en.climate-data.org/africa/cameroon/littoral/douala-890444/
7. Okafor JC. *Myrianthus arboreus* P. Beauv. In: Grubben GJH, Denton OA editors. PROTA (Plant Resources of Tropical Africa/Ressources végétales de l'Afrique tropicale), Wageningen, Netherlands; 2004. Accessed 2nd May 2022.
Available:http://www.prota4u.org/search.asp
8. Pinto AC de Q, Cordeiro MCR, de Andrade SRM, Ferreira FR, Filgueiras HA de C, Alves RE, et al. *Annona* species. International Centre for Underutilised Crops, University of Southampton, Southampton, SO17 1BJ, UK; 2005.
9. Apetorgbor MM. *Albizia zygia* (DC.) J. F. Macbr. In: Louppe D, Oteng-Amoako AA, Brink, M. editors. PROTA (Plant Resources of Tropical Africa / Ressources végétales de l'Afrique tropicale), Wageningen, Netherlands; 2007.
Accessed on 27th April 2022.
Available:https://uses.plantnet-project.org/fr/Albizia_zygia_(PROTA)
10. Beentje HJ, Mbago FM. A guide to the fig trees of western Tanzania with special emphasis on Gombe and Mahale National Parks. J East Afr Nat Hist. 2007;96(1):1-26.
11. Lemmens RHMJ. *Albizia adianthifolia* (Schumach.) W. Wight. In: Louppe D, Oteng-Amoako AA, Brink M editors.. PROTA (Plant Resources of Tropical Africa / Ressources végétales de l'Afrique tropicale), Wageningen, Netherlands; 2007.
Accessed on 27th April 2022
Available:https://uses.plantnetproject.org/en/*Albizia_adianthifolia*_(PROTA)
12. Maroyi A. *Syzygium guineense* (Willd.) DC. In: Louppe D, Oteng-Amoako AA, Brink M editors. PROTA4U Record Display. PROTA (Plant Resources of Tropical Africa/ Ressources végétales de l'Afrique tropicale), Wageningen, Netherlands; 2008.
Accessed on 2nd May 2022.
Available;https://www.prota4u.org/database/protav8.asp?g=psk&p=Syzygium%20guineense
13. Orwa C, Mutua A, Kindt R, Jamnadass R, Anthony S. Agroforestree Database: A tree reference and selection guide version 4.0; 2009.
Availablehttp://apps.worldagroforestry.org/treedb/AFTPDFS/Persea_americana.PDF
14. Todou G, Meikeu Kamdem MG.. *Musanga cecropioides* R. Br. ex Tedlie. In: Lemmens RHMJ, Louppe D, Oteng-Amoako AA editors. PROTA4U Record Display. PROTA (Plant Resources of Tropical Africa / Ressources végétales de l'Afrique tropicale), Wageningen, Netherlands; 2011. Accessed 2nd May 2022.
Available;http://www.prota4u.org/search.asp.
15. Abdalla WE, Guma'a AGN, El Ghazali GEB, Khalid HE. An updated species check-list for the genus *Cassia* L. sensu lato in the Sudan. J Nat Res Environ Studies. 2016;4(2):1-12.
16. MNHN & OFB. *Plumeria alba* L., 1753. National inventory of natural heritage/ Inventaire national du patrimoine naturel (INPN); 2022.
Accessed on 27th April 2022
Available:https://inpn.mnhn.fr.
https://inpn.mnhn.fr/espece/cd_nom/630456/tab/fiche
17. GBIF. *Alchornea cordifolia* (Schumach. & Thonn.) Müll. Arg. GBIF Backbone Taxonomy. Checklist dataset; 2021a.
Accessed via GBIF.org on 2th May 2022
Available:https://doi.org/10.15468/39omei accessed via GBIF.org
18. GBIF. *Bridelia micrantha* (Hochst.) Baill. GBIF Backbone Taxonomy. Checklist dataset; 2021b.
Accessed via GBIF.org 2th May 2022.

Available:https://doi.org/10.15468/39o:ei

19. GBIF. *Terminalia glaucescens* Planch. ex Benth. In: GBIF Secretariat (2021). GBIF Backbone Taxonomy. Checklist dataset; 2021c.
Accessed via GBIF.org on 2th May 2022.
Available:https://doi.org/10.15468/39omei
20. CABI. *Cecropia peltata* (trumpet tree). Invasive species compendium. Detailed coverage of invasive species threatening livelihoods and the environment worldwide; 2022. Accessed 2th May 2022.
Available:https://www.cabi.org/isc/datasheet/11955
21. Taylor B. The Ants of (sub-Saharan) Africa (Hymenoptera: Formicidae). Profusely illustrated with original drawings and photographs and Catalogue notes on all ant species described from sub-Saharan Africa. 12th edition (formerly Ants of West Africa); 2019. Accessed 29th March 2023
Available:https://www.antsofafrica.org/
22. Hita Garcia F, Wiesel E, Fischer G. The Ants of Kenya (Hymenoptera: Formicidae) - Faunal Overview, First Species Checklist, Bibliography, Accounts for All Genera, and Discussion on Taxonomy and Zoogeography. J East Afr nat hist. 2013; 101(2):127-222.
Available:https://doi.org/10.2982/028.101.0201
23. Hita Gacia F, Fisher BL. The ant genus *Tetramorium* Mayr (Hymenoptera: Formicidae) in the Malagasy region - Introduction, definition of species groups, and revision of the *T. bicarinatum, T. obesum, T. sericeiventre* and *T. tosii* species groups. Zootaxa, 2011;3039:1-72.
Available:https://doi.org/10.11646/zootaxa.3039.1.1
24. Hita Garcia F, Fischer G, Peters MK, Wägele JW. A preliminary checklist of the ants (Hymenoptera: Formicidae) of Kakamega Forest (Kenya). J East Afr nat hist. 2009;998:147-165.
Available:https://doi.org/10.2982/028.098.0201
25. Ward PS, Brady SG, Fisher BL, Schultz TR. The evolution of myrmicine ants: phylogeny and biogeography of a hyperdiverse ant clade (Hymenoptera: Formicidae). Syst Entomol. 2015;40: 61-81.
Available:https://doi.org/10.1111/syen.12090
26. Guerrero RJ. Taxonomic identity of the ghost ant, *Tapinoma melanocephalum* (Fabricius, 1793) (Formicidae: Dolichoderinae). Zootaxa. 2018;4410(3) :497–510.
Available:https://doi.org/10.11646/zootaxa.4410.3.4
27. Braet Y, Taylor B. Ants from the Pongara National Park, Gabon-an updated list (Hymenoptera: Formicidae). Bull Ann Soc R Belge Entomolog. 2018;154:154-164.
28. AntWeb. Family: Formicidae Latreille, 1809. Version 8.87. California Academy of Science; 2023. Accessed 29th March 2023.
Available:https://www.antweb.org
29. Kenne M, Djiéto-Lordon C, Orivel J, Mony R, Fabre A, Dejean A. Influence of insecticide treatments on ant-hemiptera associations in tropical plantations. J Econ Entomol. 2003;96:251-258.
30. Kenne M, Fénéron R, Djiéto-Lordon C, Malherbe M-C, Tindo M, Ngnegueu PR, Dejean A. Nesting and foraging habits in the arboreal ant *Atopomyrmex mocquerysi* André, 1889 (Hymenoptera: Formicidae: Myrmicinae). Myrmecol News. 2009; 12:109-115.
31. Biawa-Kagmegni M, Foguieng-Saha AD, Guetsop-Ngouadjie RP, Tsekane SJ, Fouelifack-Nintidem B., Moumite Mohamed B, et al. Ants community structure in the urban and the city suburbs areas of Douala (Littoral-Cameroon). J Insect Biodivers. 2021;025(2):033-059.
32. Wilson JB. Methods for fitting dominance/diversity curves. Journal of Vegetation Science. 1991;2(1):35-46.
Available:https://doi.org/10.2307/3235896
33. Ludwig JA, Reynolds JF. Statistical Ecology: A Primer on Methods and Computing. Wiley-Interscience Pub., New York; 1988.
34. Fouelifack-Nintidem B, Yetchom-Fondjo JA, Tsekane SJ, Ngamaleu-Siewe B, Kenne EL, Biawa-Kagmegni M et al. Diversity and Abundance of Pest Insects Associated with *Solanum aethiopicum* Linnaeus, 1756 (Solanaceae) in Balessing (West-Cameroon). Am J Entomol. 2021; 5(3):70-91.
DOI: 10.11648/j.aje.20210503.14

35. Ngamaleu-Siewe B, Fouelifack-Nintidem B, Yetchom-Fondjo JA, Moumite Mohamed B, Tsekane JS, Kenne EL et al. Diversity and Abundance of Pest Insects Associated with *Solanum tuberosum* L. 1753 (Solanaceae) in Balessing (West-Cameroon). Am J Entomol. 2021;5(3): 51-69.
DOI: 10.11648/j.aje.20210503.13

36. Stajić S, Cvjetićanin R, Čokeša V, Miletić Z, Novaković-Vuković M, Eremija S, Rakonjac LJ. Plant species richness and diversity in natural beech and oak dominated forests of Kosmaj protected area (Serbia). Appl Ecol Environ Res. 2021;19(4):2617-2628.
DOI: http://dx.doi.org/10.15666/aeer/1904_26172628

37. Stadler B. Mutualism ants and their insect partners. Cambridge university press. 2008;24-229.

38. Leblanc. Inventaire faunistique des ravageurs et auxiliaires des agrumes en Martinique : les bases d'une gestion « integree » du verger. 2000;5-16. French

39. Torchote P, Sitthicharoenchai D, Chaisuekul C. Ant Species Diversity and Community Composition in Three Different Habitats: Mixed Deciduous Forest, Teak Plantation and Fruit Orchard. Trop Nat Hist. 2010;10(1):37–51.

40. Uno S, Cotton J, Philpott SM. Diversity, abundance, and species composition of ants in urban green spaces. Urban Ecosyst. 2010;13:425-441.
Available:https://doi.org/10.1007/s11252-010-0136-5

41. Dias RKS, Kosgamage KRKA. Occurrence and Species diversity of ground-dwelling worker ants (Family: Formicidae) in selected lands in the dry zone of Sri Lanka. Journal of Science, University of Kelaniya, 2012;7:55-72.

42. Solar RRC, Barlow J, Andersen AN, Schoereder JH, Berenguer E, Ferreira JN, Gardner TA. Biodiversity consequences of land-use change and forest disturbance in the Amazon: A multi-scale assessment using ant communities. Biol Conserv. 2016;197:98–107.

43. Silva IA, Cianciaruso MV, Batalha MA. Abundance distribution of common and rare plant species of Brazilian savannas along a seasonality gradient. Acta Bot Bras. 2010;24(2):407-413.

44. Holway DA, Lach L, Suarez AV, Tsutsui ND, Case TJ. The causes and components of ant invasions. Annu Rev Ecol Evol Syst. 2002;33:181-233.

45. Lowe S, Browne M, Boudjelas S. 100 of the world's worst invasive alien species. Global Invasive Species Database (GISD), The Invasive Species Specialist Group (ISSG), Species Survival Commission (SSC), World Conservation Union (IUCN), Aliens; 2000.

46. Shea K, Chesson P. Community ecology theory as a framework for biological invasions. Trends Ecol Evol. 2002;17(4): 170-176.

47. Baloup S. Diversity of myrmecofauna in a monospecific plot of rubber trees. National Center for Scientific Research (CNRS); 2009.

48. Gibernau M, Dejean A. Ant protection of a Heteropteran trophobiont against a parasitoid wasp. Oecologia. 2001;126:53-57.

49. Correa MCG, Zaviezo T, Maguet JL, Herrbach E, Malausa T. Characterization of microsatellite DNA libraries from three mealybug species and development of microsatellite markers for Pseudococcus viburni (Hemiptera: Pseudococcidae). Bull Entomol Res. 2013;104:213-2020.

50. Geiger CA, Daane KM. Seasonal movement and distribution of the grape mealybug (Homoptera: Pseudococcidae): Developing a sampling program for San Joaquin Valley Vineyards. J Econ Entomol. 2001;94(1):291-301.

51. Correa MCG, Lombaert E, Malausa T, Crochard D, Alvear A, Zaviezo T, et al. Mealybug species from Chilean agricultural landscapes and main factors influencing the genetic structure of *Pseudococcus viburni*. Scientific Reports, 2015;5:16483.
DOI: 10.1038/srep1648

52. Meissner H, Lemay A, Bertone C, Schwartzburg K, Ferguson L, Newton L. Evaluation of pathways for exotic plant pest movement into and within the greater Caribbean Region. Caribbean Invasive Species Working Group (CISWG), Plant Epidemiology and Risk Analysis Laboratory (PERAL), Center for Plant Health Science and Technology (CPHST),

United States Department of Agriculture (USDA), USA; 2009.

53. Ekka PA, Kumari S, Rastogi N. Facultative associations of two sympatric lycaenid butterflies with *Camponotus compressus* field study and larval surface ultrastructure. Halteres. 2020;11:44-55.
DOI: 10.5281/zenodo.4043261

54. Abd-Rabou S, Shalaby H, Germain J-F, Ris N, Kreiter P, Malausa T. Identification of mealybug pest species (Hemiptera: Pseudococcidae) in Egypt and France, using a DNA barcoding approach. Bull Entomol Res. 2012;102:515-523.

55. Daane KM, Almeida RPP, Bell VA, Walker JTS, Botton M, Fallahzadeh M, et al. Biology and Management of Mealybugs in Vineyards,. In: Bostanian NJ, Vincent C, Isaacs R editors. Arthropod Management in Vineyards: Pests, Approaches, and Future Directions. Springer Science and Business Media B.V., Dordrecht; New York. 2012;271-307.

56. Mani M, Shivaraju C. Mealybugs and their Management in Agricultural and Horticultural Crops. Springer, New Delhi, India; 2016.

57. Koo H-N, Kim S, Lee JS, Kang WJ, Cho WS, Kyung Y, Seo JW, Kim HK, Kim GH, Cho S. *Pseudococcus orchidicola* (Hemiptera: Pseudococcidae), a newly found mealybug pest, confused with *P. longispinus* in Korea. J Entomol Res. 2017;47:185-193.

58. Meyer JB, Kasdorf GGF, Nel LH, Pietersen G. Transmission of Activated-Episomal Banana streak OL (Badna) Virus (BSOLV) to CV. Williams Banana (Musa sp.) by Three Mealybug Species. Plant Dis. 2008;92:1158-1163.

59. Errouissi F, Labidi I, Jay-Robert P, Nouïra S, Lumaret J-P. Dung beetle assemblages organization in two contrasted areas of the Mediterranean region: affinities and divergences. Ann Soc Entomol Fr (n.s.). 2011;47(3–4):402-417

60. Tokeshi M. Species Coexistence: ecological and evolutionary perspective. London: Blackwell Science Ltd; 1999.

61. Wishieu IC. How organisms partition habitats: Different types of community organization can produce identical patterns. Oikos. 1998;83:246-258.

62. Gordon CE. The coexistence of species. Rev Chil Hist Nat. 2000;73:175-198.

63. Diaz DMV, Spasojevic MJ, Dalling J, McMahon SM, Turner BL, LaMana JA, et al. MacArthur's niche hypotheses revisited: the role of niche space, niche breadth and niche overlap in explaining global patterns of species diversity. Symposium of Association for Tropical Biology and Conservation. Conference: Annual Meeting of the Association for Tropical Biology and Conservation. Le Corum, Montpellier, France; 2016

64. Errouissi F, Haloti S, Jay-Robert P, Janati-Idrissi A, Lumaret J-P. Effects of the attractiveness for dung beetles of dung pat origin and size along a climatic gradient. Environ Entomol. 2004a;33:45-53.

65. Errouissi F, Jay-Robert P, Lumaret JP, Piau O. Composition and structure of dung beetle (Coleoptera: Aphodiidae, Geotrupidae, Scarabaeidae) assemblages in mountain grasslands of the Southern Alps. Ann Entomol Soc Am. 2004b;97:701-709

66. Ferreira FC, Petrere-Jr M. Comments about some species abundance patterns: clazssic, neutral, and niche partitioning models. Braz J Biol. 2008;68(4, Suppl.):1003-1012.

67. Komonen A., Elo M. Ecological response hides behind the species abundance distribution: Community response to low-intensity disturbance in managed grasslands. Ecol Evol. 2017;7:8558-8566.

68. Yetchom-Fondjo JA, Kekeunou S, Kenne M, Missoup AD, Sheng-Quan X. Diversity, abundance and distribution of grasshopper species (Orthoptera: Acrididea) in three different types of vegetation with different levels of anthropogenic disturbances in the Littoral Region of Cameroon. J Insect Biodivers. 2020;14(1):16-33.

69. Silva LF, Souza RM, Solar RRC; Neves FS. Ant diversity in Brazilian tropical dry forests across multiple vegetation domains. Environ Res Lett. 2017;12:035002.

70. Li W.. Zipf's Law Everywhere. Glottometrics, 2002;5:14-21.

71. McDonald RI, Marcotullio PJ, Güneralp B. Urbanization and Global Trends in Biodiversity and Ecosystem Services. In: Elmqvist T, Fragkias M, Goodness J, Güneralp B, Marcotullio PJ, McDonald RI, Parnell S, Schewenius M, Sendstad M, Seto KC, Wilkinson C editors. Urbanization, Biodiversity and Ecosystem

Services: Challenges and Opportunities. A Global Assessment. A Part of the Cities and Biodiversity Outlook Project. The Netherlands: Springer Open, Springer, Dordrecht, Heidelberg, New York, London. 2013;31-52.

Peer-review history:
The peer review history for this paper can be accessed here:
https://www.sdiarticle5.com/review-history/100223