

# Diversity of Tick Species (Ixodidae) Parasitizing Livestock at the Niamey Slaughterhouse and Major Livestock Markets in Niamey, Niger

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## Abstract

The diversity of ticks in livestock is extensive, with major genera like *Rhipicephalus*, *Amblyomma*, and *Hyalomma* identified worldwide, each containing multiple species. This study was conducted between October and November 2024 across three major livestock markets and the slaughterhouse in Niamey, Niger. The objective was to identify the various tick species (*Ixodidae*) in livestock and to assess their abundance and the variability of infestation levels according to host species, tick genus, and tick species. Ticks were collected using manual removal from conveniently selected animals and preserved in 70% ethanol. A total of 160 animals were examined, 40 animals per site. In total, 330 ticks were collected from the examined animals. The majority of ticks were females, 68% (225/330). Morphological identification revealed 19 tick species belonging to five genera: *Amblyomma*, *Haemaphysalis*, *Hyalomma*, *Rhipicephalus* (*Boophilus*), and *Rhipicephalus*. *Rhipicephalus* was the most prevalent genus. Among the identified species, *Amblyomma variegatum* was the most dominant at 33.0% (109/330), followed by *Rhipicephalus sanguineus* at 13.3% (44/330), while *Hyalomma anatolicum* and *Hyalomma truncatum* were the least represented, each accounting for 0.3% (2/330) of the tick population. The Shannon-Weaver diversity indices calculated across the different study sites indicated that the environments were species-rich and ecologically

favorable. The Pielou's Evenness Index ( $E$ ) value was 0.5. This study highlights the diversity of tick species infesting livestock in Niamey. It establishes base-line data on tick infestation in the Niamey Region and highlights the critical need for further research to identify associated pathogens.

## Keywords

Ixodidae, Arthropods, Abundance, Domestic Animals, Niger Republic

## 1. Introduction

Ticks are a group of hematophagous arthropods of both ecological and medical importance. Within the subclass of *Acari*, ticks are classified in the order *Ixodida* [1]. Ticks are characterized by their ability to parasitize a wide range of vertebrate hosts, including mammals, birds, reptiles, and, in some cases, amphibians [2].

Approximately 900 tick species have been identified worldwide, classified into three major families: *Argasidae* (soft ticks, 190 species), *Ixodidae* (hard ticks, 700 species), and *Nuttalliellidae* [3] [4]. The latter family is represented by a single genus and species, *Nuttalliella namaqua*. In Africa, 223 tick species have been recorded: 180 belonging to the *Ixodidae* and 43 to the *Argasidae* families [5] [6]. Consequently, the *Ixodidae* family is the most abundant and diverse, largely due to its capacity to infest a broad spectrum of vertebrate hosts [3].

In West Africa, the genera *Amblyomma*, *Hyalomma*, and *Rhipicephalus* have been the most extensively studied in relation to livestock infestation [7]-[10]. Among the most abundant species in these regions are *Rhipicephalus (Boophilus) microplus* and *Amblyomma variegatum*, which primarily parasitize cattle [11].

Other tick species may also be present in this part of Africa, particularly those belonging to the subgenus *Boophilus*, which are monoxenous ticks that complete their parasitic life cycle on a single host individual. Rodents serve as hosts for ticks with two- or three-host life cycles [12].

This diversity holds particular significance for both public and animal health. Ticks are vectors of numerous pathogens and, after mosquitoes, represent the second most important group of disease vectors worldwide [13] [14]. They transmit a wide range of infectious agents including *bacteria*, *protozoa*, and *viruses* responsible for diseases such as Lyme disease, rickettsioses, tularemia, bartonellosis, canine piroplasmiasis, bovine babesiosis, and anaplasmosis [15]-[19], as well as viral infections such as tick-borne encephalitis and Crimean-Congo hemorrhagic fever [6] [16] [17] [20].

Several of these diseases have already been reported in both cattle and humans in West Africa [21]. In Mali, Crimean-Congo hemorrhagic fever (CCHF) has been identified in tick populations and human cases [22]. In Benin, babesiosis and theileriosis are significant tick-borne diseases affecting cattle [23]. Nigeria has also reported tick-borne diseases such as heartwater (Cowdriose fever) [24]. In Niger, a study conducted in the Dosso region (Boboye Department) revealed a seroprev-

alence of 9.1% for CCHF, with collected ticks belonging to the genera *Hyalomma* (91.7%), *Amblyomma* (5.7%), and *Rhipicephalus* (subgenus *Boophilus*) (2.6%) [25]. However, no current data are available regarding the tick species circulating among livestock in Niger.

Moreover, several authors have emphasized that increased animal movement, climate change, and the degradation of natural habitats are contributing factors to shifts in the distribution and abundance of ticks, with significant epidemiological implications [26] [27]. A thorough investigation of tick species diversity is therefore essential to understand their ecology, transmission dynamics, and to support the implementation of effective surveillance and control strategies for vector-borne diseases.

The objective of this study is to conduct an inventory of tick genera and species infesting livestock in Niamey, specifically at three major livestock markets and the animal slaughter facility (Niamey Refrigerated Slaughterhouse). This work aims to assess the diversity of circulating tick species, their abundance, and the infestation levels of hosts in the targeted locations.

## 2. Materials and Methods

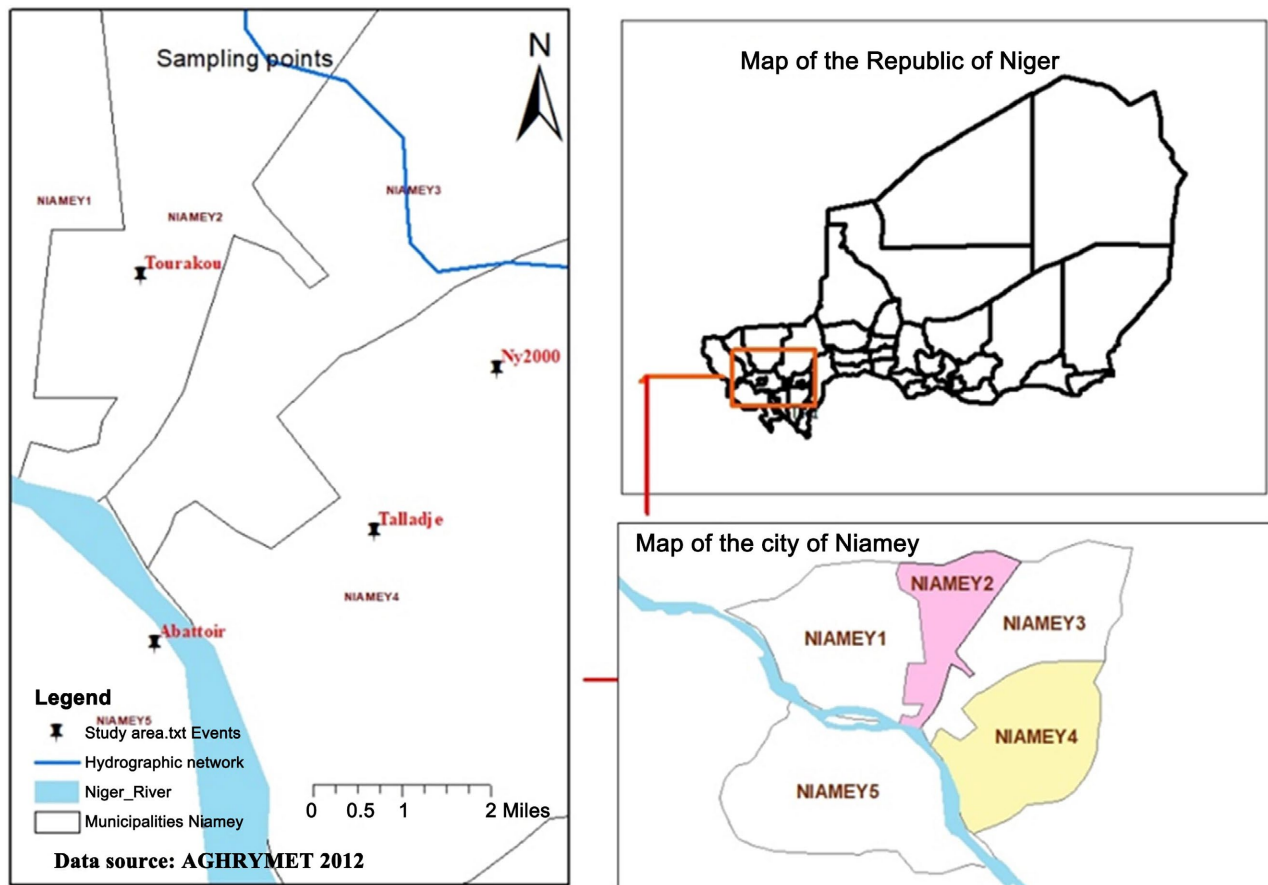
### 2.1. Study Site

This cross-sectional study was conducted at four locations within the Urban Municipality of Niamey (CUN), the capital of Niger, over a two-month period from October to November 2024. Niamey is characterized by a Sahelian climate, representing a transitional zone both floristically and climatically between the Saharan domain to the north and the Sudanian savannas to the south, where rainfall is more substantial. The sampling sites Talladgé, Tourakou, Niamey 2000, and the Niamey Refrigerated Slaughterhouse are all located on the left bank of the Niger River [28].

Niamey is divided into five municipal districts, four of which are located on the left bank of the Niger River, with only District V situated on the right bank [29] [30]. The sampling sites Talladgé, Tourakou, Niamey 2000, and the Niamey Refrigerated Slaughterhouse (AFN) are all located on the left bank of the Niger River (**Figure 1**). The animals sampled at these sites were primarily intended for slaughter or livestock trade. Due to repeated resale and the reluctance of some owners to disclose information, it was difficult to determine the precise geographic origin of the animals presented at the sampling sites.

### 2.2. Samples Collection

Ticks were collected over a two-month period (October to November), following the end of the rainy season. Collection was carried out manually on cattle, sheep, goats, and camels by two operators, who removed the ticks by simple pulling after the animals had been restrained by the herders. To ensure effective sampling, each animal was controlled and kept either standing or lying on the ground, in order to limit movements that could hinder inspection and rapid tick removal.



**Figure 1.** Map showing the location of the study area.

Ticks were extracted mechanically using forceps, without the application of any chemical substances, in order to preserve the integrity of the rostrum and capitulum two key anatomical features required for species identification.

Collected ticks were stored in 70% ethanol for preservation and subsequent identification [3]. Each vial was labeled with the following information: location, date of collection, geographic coordinates, host type, sampling date, site, and sex of the animal. Samples were transported on dry ice to the Medical Entomology Laboratory at the Medical and Health Research Center (CERMES) for identification.

### 2.3. Tick Identification

The collected ticks were transported to the laboratory for identification. To minimize contamination from microorganisms present on work surfaces, the ticks were immersed in 70% ethanol. Initially, specimens were sorted by developmental stage into larvae, nymphs, and adults. Subsequently, males and females were differentiated by examining the dorsal surface of the ticks [16] [31].

Using a stereomicroscope (LEICA EZ 4), genus-level identification was performed based on direct morphological observations, including the presence of chitin on the tick's body, the position of the anal groove relative to the anal open-

ing, the length and shape of the rostrum, the structure of the capitulum base, the presence or absence of posterior festoons, and the presence or absence of anal plates [32].

Species-level identification was based on observable morphological characteristics such as scutum punctation, leg coloration, the presence of marbling, the shape of the spiracles (comma-shaped or round), groove patterns, festoon structure, eye shape, the number and dimensions of pore areas, and the shape of the adanal plates [33].

## 2.4. Data Analysis

The number of ticks collected was recorded by species, physiological stage, host animal, and sex of the host. To determine whether tick distribution is independent of host type, a chi-square test of independence will be applied to the contingency matrix of tick species versus host categories.

The software Jamovi (version 0.9.5.12) was used to calculate ecological indices such as Total Species Richness ( $S$ ) and Relative Abundance (RA). Species richness refers to the total number of species present in a given community within an ecosystem (Blondel, 1979). Relative abundance is the percentage of individuals of a given species ( $N_i$ ) relative to the total number of individuals ( $N$ ) across all species [34].

The formula used is as follows:

$$F(\%) = N_i/N \times 100$$

- $N_i$ : Number of individuals of the species under consideration
- $N$ : Total number of individuals across all species

The software PAST (*PA*laeontological *S*Tatistics) version 4.03 was used to calculate diversity indices. Specifically, the Shannon-Weaver diversity index and the evenness index were computed. The Shannon-Weaver index reflects the diversity of species within a given community.

The formula used is as follows:

$$H' = -\sum q_i * \log_2(q_i)$$

$H'$ : Shannon-Weaver diversity index, expressed in bits,

$q_i$ : Relative frequency of species  $i$  in relation to the total population,

$n_i$ : Number of individuals of species  $i$  in the sample,

$N$ : Total number of individuals across all species,

Log<sub>2</sub>: Logarithm base 2.

This index provides insight into the species diversity of each sampled environment. A low value (close to 0 or 1) indicates low species richness or an unfavorable habitat, whereas a higher value (greater than 2) suggests high species richness and a favorable environment. The diversity index varies according to both the number of species present and the abundance of each species [35].

### Evenness Index ( $E$ )

The evenness index (Pielou's Evenness Index) was calculated using the follow-

ing formula:

$$H'_{\max} = \log 2 * S$$

- $S$ : Total species richness,
- $H'_{\max}$  : Maximum possible diversity, expressed in bits,
- $E = H'/H'_{\max}$ .

This index represents the ratio of observed diversity  $H'$  to the maximum theoretical diversity  $H'_{\max}$  (Blondel, 1979). Values of  $E$  range from 0 to 1. When  $E$  approaches 0, it indicates an imbalance among species, with dominance by one or a few species. Conversely, values approaching 1 suggest that individuals are evenly distributed among species, reflecting ecological equilibrium [35].

### 3. Results

#### 3.1. Relative Abundance of Collected Ticks by Gender

A total of 330 tick specimens were collected, with a predominance of females at 68% (225/330) compared to males (Figure 2).

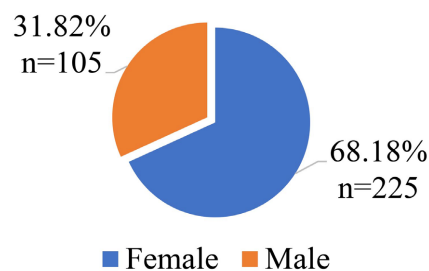


Figure 2. Relative abundance of male and female ticks.

#### 3.2. Relative Abundance of Identified Tick Genera

All collected ticks were classified into five genera, the Chi2 test of adjustment carried out between their abundances varies significantly (Figure 3,  $p = 0.001$ ). The most abundant genera were *Rhipicephalus* (35%) and *Amblyomma* (33.0%), followed by *Hyalomma* (21.0%), *Rhipicephalus (Boophilus)* (9.0%), and *Haemaphysalis*, which was observed at a low frequency (2.0%).

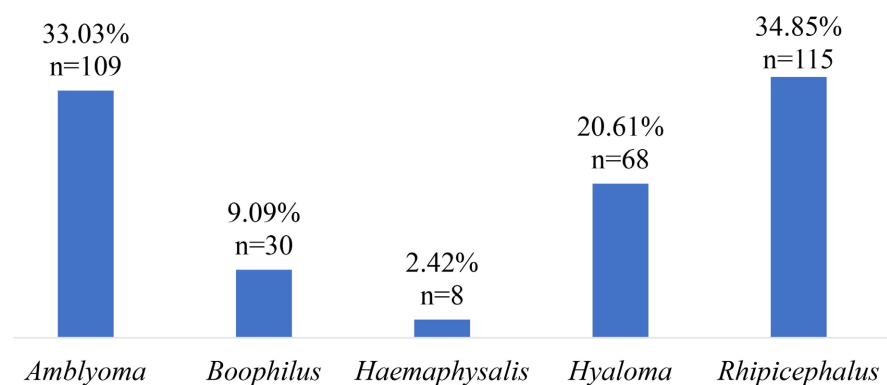


Figure 3. Distribution of tick genera identified.

### 3.3. During the Study Relative Abundance of Identified Tick Species

A total of nineteen tick species were identified. The most prevalent species was *Amblyomma variegatum* (33.0%), it was followed by *Rhipicephalus sanguineus* (13.3%). The Chi2 test of adjustment carried out between the frequencies of the species varies significantly (Table 1,  $p = 0.001$ ).

**Table 1.** Distribution of tick species collected in the study area: absolute frequencies.

Species	Count	Percent (%)
<i>A. variegatum</i>	109	33.03
<i>R. sanguineus</i>	44	13.33
<i>B. decoratus</i>	30	9.09
<i>H. dromedarii</i>	24	7.27
<i>R. camicasi</i>	18	5.45
<i>R. guilhoni</i>	15	4.55
<i>H. rufipes</i>	15	4.55
<i>H. impeltatum</i>	13	3.94
<i>R. lunulatus</i>	12	3.64
<i>H. impressum</i>	9	2.73
<i>R. muhsamae</i>	8	2.42
<i>Hae. Leachi</i>	8	2.42
<i>R. senegalensis</i>	8	2.42
<i>R. praetextatus</i>	7	2.12
<i>H. scupense</i>	3	0.91
<i>R. turanicus</i>	3	0.91
<i>H. excavacum</i>	2	0.61
<i>H. anatolicum</i>	1	0.30
<i>H. truncatum</i>	1	0.30
<b>Total</b>	<b>330</b>	<b>100.00</b>

### 3.4. Relative Abundance of Ticks by Host Type

Among the hosts examined, *Amblyomma variegatum* was the predominant species on camels (62.5%) and cows (42.0%), whereas *Rhipicephalus sanguineus* was the most frequent species on goats (33.3%) and sheep (29.1%). There is significant association between tick species and host (Table 2,  $p = 2.67 \times 10^{-32}$ ).

### 3.5. Type Relative Abundance of Ticks by Site

Overall, *Amblyomma variegatum* was the dominant tick species at Abattoir (36.6%), Ny2000 (33.3%) and Tourakou (28.0%), whereas *Hyalomma rufipes* predominated at Talladjé (37.5%). The association between tick species and sampling site is statistically significant (Table 3,  $p = 7.4 \times 10^{-21}$ ).

**Table 2.** Distribution of tick species according to host.

Species	Hosts							
	Camel		Cow		Goat		Sheep	
	Count	Percent (%)	Count	Percent (%)	Count	Percent (%)	Count	Percent (%)
<i>A. variegatum</i>	55	62.5	47	41.96	0	0.00	7	6.80
<i>B. decoratus</i>	2	2.27	24	21.43	0	0.00	4	3.88
<i>H. anatolicum</i>	0	0.00	1	0.89	0	0.00	0	0.00
<i>H. dromedarii</i>	12	13.64	10	8.93	1	3.70	1	0.97
<i>H. excavacum</i>	0	0.00	1	0.89	0	0.00	1	0.97
<i>H. impeltatum</i>	7	7.95	3	2.68	0	0.00	3	2.91
<i>H. impressum</i>	3	3.41	5	4.46	0	0.00	1	0.97
<i>H. rufipes</i>	6	6.82	8	7.14	0	0.00	1	0.97
<i>H. scupense</i>	0	0.00	1	0.89	1	3.70	1	0.97
<i>H. truncatum</i>	0	0.00	1	0.89	0	0.00	0	0.00
<i>Hae. leachi</i>	3	3.41	2	1.79	3	11.11	0	0.00
<i>R. camicasi</i>	0	0.00	0	0.00	2	7.41	16	15.53
<i>R. guilhoni</i>	0	0.00	2	1.79	3	11.11	10	9.71
<i>R. lunulatus</i>	0	0.00	1	0.89	1	3.70	10	9.71
<i>R. muhsamae</i>	0	0.00	1	0.89	3	11.11	4	3.88
<i>R. praetextatus</i>	0	0.00	0	0.00	2	7.41	5	4.85
<i>R. sanguineus</i>	0	0.00	5	4.46	9	33.33	30	29.13
<i>R. senegalensis</i>	0	0.00	0	0.00	1	3.70	7	6.80
<i>R. turanicus</i>	0	0.00	0	0.00	1	3.70	2	1.94
<b>Total</b>	<b>88</b>	<b>100.00</b>	<b>112</b>	<b>100.00</b>	<b>27</b>	<b>100.00</b>	<b>103</b>	<b>100.00</b>

**Table 3.** Distribution of tick species according to site.

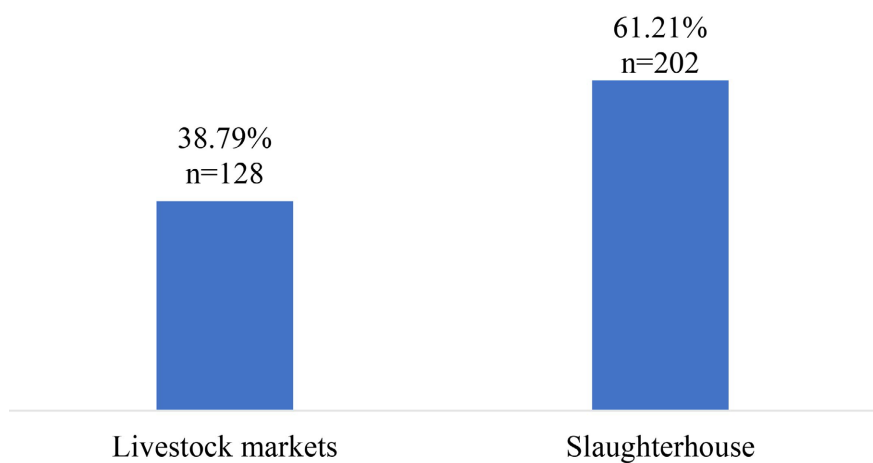
Species	Sites							
	Abattoir		Ny2000		Talladjé		Tourakou	
	Count	Percent (%)	Count	Percent (%)	Count	Percent (%)	Count	Percent (%)
<i>A. variegatum</i>	74	33.63	4	33.33	3	18.75	28	28.00
<i>B. decoratus</i>	27	13.37	2	16.67	1	6.25	0	0.00
<i>H. anatolicum</i>	0	0.00	0	0.00	0	0.00	1	1.00
<i>H. dromedarii</i>	10	4.95	0	0.00	1	6.25	13	13.00
<i>H. excavacum</i>	0	0.00	2	16.67	0	0.00	0	0.00
<i>H. impeltatum</i>	10	4.95	1	8.33	1	6.25	1	1.00
<i>H. impressum</i>	8	3.96	0	0.00	0	0.00	1	1.00

Continued

<i>H. rufipes</i>	8	3.96	0	0.00	6	37.50	1	1.00
<i>H. scupense</i>	0	0.00	1	8.33	2	12.50	0	0.00
<i>H. truncatum</i>	1	0.50	0	0.00	0	0.00	0	0.00
<i>Hae. leachi</i>	5	2.48	0	0.00	2	12.50	1	1.00
<i>R. camicasi</i>	9	4.46	1	8.33	0	0.00	8	8.00
<i>R. guilhoni</i>	8	3.96	0	0.00	0	0.00	7	7.00
<i>R. lunulatus</i>	6	2.97	1	8.33	0	0.00	5	5.00
<i>R. muhsamae</i>	2	0.99	0	0.00	0	0.00	6	6.00
<i>R. praetextatus</i>	0	0.00	0	0.00	0	0.00	7	7.00
<i>R. sanguineus</i>	25	12.38	0	0.00	0	0.00	19	19.00
<i>R. senegalensis</i>	8	3.96	0	0.00	0	0.00	0	0.00
<i>R. turanicus</i>	1	0.50	0	0.00	0	0.00	2	2.00
<b>Total</b>	<b>202</b>	<b>100.00</b>	<b>12</b>	<b>100.00</b>	<b>16</b>	<b>100.00</b>	<b>100</b>	<b>100.00</b>

### 3.6. Comparison of Relative Tick Abundance between the Slaughterhouse and Livestock Markets

The slaughterhouse (Gamkale) exhibited the highest relative abundance of collected ticks (61.21%), compared to the combined total from the livestock markets of Tourakou, Talladje, and Niamey 2000, which together accounted for 38.79% (Figure 4,  $p = 0.001$ ).



**Figure 4.** Comparative representation of tick species between the refrigerated slaughterhouse and the three livestock markets.

### 3.7. Total Species Richness of Ticks

Species richness per site ranged from 7 to 15 species. The Niamey refrigerated slaughterhouse exhibited the highest species richness, with 15 identified species, followed by Tourakou with 14 species. The sites of Niamey 2000 and Talladje showed the lowest species richness, with 7 species each (Table 4).

**Table 4.** Species richness of ticks collected by site.

	Site			
	Niamey 2000	Abattoir	Talladje	Tourakou
<b>Total Richness</b>	7	15	7	14

***Shannon-Weaver Diversity Index (H') and Evenness Index (E) by Site***

The values of the Shannon-Weaver diversity index ( $H'$ ) ranged from 1.72 to 2.13 bits, indicating moderate species diversity across all sites. The evenness index ( $E$ ) values were all above 0.5, suggesting a relatively balanced distribution of species abundances at each site (Table 5).

**Table 5.** Species richness of ticks collected by site.

Diversity index	Site			
	Ny2000	Tourakou	Talladje	Abattoir
<b>Shannon-Weaver Diversity <math>H'</math> (bits)</b>	2.13	1.79	1.72	2.13
<b>Equitability (E)</b>	0.78	0.92	0.88	0.81

**4. Discussion**

This cross-sectional study describes the diversity of ticks collected from major livestock markets and the Niamey refrigerated slaughterhouse in 2024. Females were more abundant than males. Female ticks pose several concerns for both human and veterinary health, not only due to their bites but also because of their capacity to transmit infectious agents. Studies by Dib *et al.*, (2002) in Algeria and Maïna *et al.*, (2020) in Niger support our findings, also reporting a predominance of females over males [25] [36].

Across the four study sites in Niamey, it was revealed that all collected species belonged to five genera: *Amblyomma*, *Hyalomma*, *Haemaphysalis*, and *Rhipicephalus* (including the subgenus *Boophilus*). Our results are consistent with those of several authors such as Barker and Murrell (2004), Biguezoton *et al.*, (2016), Kouassi *et al.*, (2016), and Diarra *et al.*, (2017), who have reported that these tick genera are commonly associated with livestock in West Africa [8]-[11]. According to other researchers (Farougou *et al.*, 2013; Yao *et al.*, 2016; Biguezoton *et al.*, 2016), these ticks are responsible not only for direct effects such as blood loss, weight reduction, decreased milk production, and skin lesions that facilitate secondary infections and teat loss but also for indirect effects as vectors of numerous pathogens [8] [27] [37]. These include agents responsible for diseases such as heartwater (cowdriosis), babesiosis, anaplasmosis, theileriosis, ehrlichiosis, and Crimean-Congo hemorrhagic fever (CCHF) virus [38].

In our study, the genera *Rhipicephalus* and *Amblyomma* were the most abundant. These findings are consistent with those of Yessinou *et al.*, (2018) in Benin, who previously identified *Rhipicephalus* and *Amblyomma* as among the most

common tick genera infesting livestock in West Africa. However, our results contrast with those of Alima *et al.*, (2020), who reported a predominance of the genus *Hyalomma*, representing 97% of the ticks collected [25] [39].

This discrepancy may be explained by the fact that their study focused exclusively on cattle, whereas ours included cattle and camelids in addition to small ruminants, thereby broadening the host range.

During this study, nineteen tick species were identified, with *Amblyomma variegatum* being the most abundant. A similar distribution was observed in Burkina Faso by Kaboré *et al.*, (1998), in Senegal by Guèye *et al.* (1990), by Awa (1997), and in Nigeria by Bayer and Maina (1984) [40]-[43].

In our study, this species was primarily found on cattle, goats, and camelids. According to McCoy and Boulanger (2015), *A. variegatum* is a major parasite of cattle, sheep, and goats [3]. Morel (1980) and Petney *et al.*, (1987) also reported that this species can infest a wide range of vertebrates, including reptiles, birds, and both small and large mammals [44] [45]. Several authors have emphasized that *A. variegatum* is an indigenous tick species responsible for significant economic losses [40] [41] [43] [46] [47].

Another species, *Rhipicephalus (Boophilus) decoratus*, showed a strong affinity for cattle in our study. Our findings align with those of Yao *et al.*, (2020), who reported this species exclusively on cattle in Burkina Faso [48]. Similarly, studies by Phalatsi *et al.*, (2004) in South Africa confirmed that *Boophilus decoloratus* has a strong preference for cattle, which are its primary hosts. It is commonly referred to as the “blue tick” of livestock [49].

In our study, certain species of the genus *Hyalomma*, such as *Hyalomma dromedarii* and *H. impeltatum*, exhibited clear host specificity for camels.

Our findings are consistent with those of Bouhous *et al.* (2008) in Algeria, who reported this species as predominant (79.31%) on camels [50]. Similar results have been documented regarding the preference of this species for dromedaries by Van Straten and Jongejan (1993) in Egypt (95.6%), Idris *et al.*, (2000) in Oman (89.55%), and Antoine-Moussiaux *et al.*, (2005) in the Agadez region of Niger (100%) [51]-[53].

According to these authors, this specificity may be linked to the species' selective affinity for dromedaries or its concentration in desert regions [33].

Another species, *Rhipicephalus sanguineus*, was observed in a relatively balanced distribution among goats, sheep, and cattle, suggesting lower host selectivity. According to Karen *et al.* (2015), this species, found across various biogeographic zones, primarily parasitizes dogs but can also be found on humans and certain domestic herbivores (cattle, sheep) via the surrounding canine population [16]. It is therefore often considered a secondary species, dependent on the presence of a dense canine population in the environment [16] [54].

In our study, species richness varied across sites, with some locations being more diverse than others. The slaughterhouse exhibited the highest species richness, in contrast to the livestock markets. Notably, species such as *Hyalomma*

*scupense*, *Rhipicephalus turanicus*, *Hyalomma excavatum*, *Hyalomma anatolicum*, and *Hyalomma truncatum* were identified. The simultaneous presence of multiple tick species from the same family has previously been reported by Boka *et al.*, (2004) and Tuo *et al.*, (2020) [55] [56]. This may result from shared grazing areas among regional herds. Indeed, the risk of cattle infestation by similar tick species is often linked to communal pastures and the intermingling of herds [27].

During our sampling, the slaughterhouse showed the highest relative abundance of all collected ticks, compared to the livestock markets. The lower number of tick species observed in the markets may be explained by prophylactic measures taken against mites, as well as cleaning practices implemented upon the arrival of animals from villages before the massive proliferation of these vectors. These measures likely reduce the ease of tick dispersion at these sites. Another contributing factor could be the condition of the animal enclosures.

Finally, the Shannon-Weaver diversity index ( $H'$ ) values ranged from 1.72 to 2.13 bits, indicating moderate species diversity across all sites. The evenness index (E) values were all above 0.5. The Shannon-Weaver indices recorded at all sites exceeded 1.5 bits, suggesting that these environments are species-rich and ecologically favorable. Our results align with those of Amrouche Fadila and Ouachek Yasmine (2016) in Algeria [57]. The evenness values across the four sites being above 0.5 indicate that species abundances are evenly distributed and that these communities are balanced. Similar findings were reported by Bia Lycia (2017) and Bouizegarene *et al.*, (2014) in Algeria [58] [59].

The main limitations of this study are the short sampling period, limited study duration, restricted geographic scope (Niamey), and seasonal timing, which may have constrained the depth of the findings. Additionally, the study did not employ PCR or MALDI-TOF techniques, which are rapid and effective methods for species identification and pathogen detection in ticks.

## 5. Conclusion

This study identified five tick genera and nineteen species in Niamey. The relative abundances of tick species across sites ranged from 0.3% to 33.0%, with *Amblyomma variegatum* being the most frequent species. A high species richness and balanced distribution were found. Further studies are needed in other regions and over extended timeframes to better understand the seasonal dynamics of tick populations. Molecular and epidemiological research should be deepened to monitor the evolution of tick-borne diseases. Advancing fundamental knowledge will enhance control strategies against these formidable vectors. Entomological surveys will contribute to a better understanding of tick-borne hemorrhagic fevers and help highlight the epidemiological aspects of emerging and re-emerging diseases.

## Authors' Contributions

Ibrahim M. L., Moustapha M. L., and Rabi O. C. conceived the study. Iro M. S. and Jafarou C. A. conducted the study and drafted the first version of the manu-

script. Diallo O. D. and Kader S. H. analyzed the data. Moustapha M. L., Rabi O. C., and Ibrahim M. L. read and revised the manuscript; all authors read and approved the final version of the manuscript.

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### AI Use Statement

The authors acknowledge the use of ChatGPT-5 for language refinement and structural organization of this manuscript. All conceptual and analytical content originates from the authors.

### Conflicts of Interest

The authors declare that they have no conflict of interest regarding the publication of this article.

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