# INTRODUCTION

Ticks are among the most significant ectoparasites affecting livestock worldwide, serving as vectors for diseases that challenge traditional livestock farming. Tick infestations cause discomfort, irritation, and physical damage to hosts, leading to weight loss, reduced productivity, and increased susceptibility to secondary infections (Rechav et al., 1980; Rajput et al., 2006; Randolph, 2008). Additionally, ticks transmit critical diseases such as anaplasmosis, babesiosis, cowdriosis, theileriosis, and rickettsiosis, severely impacting livestock health and economic productivity (Manzano-Román et al., 2012). In West Africa, *Amblyomma variegatum* and the invasive *Rhipicephalus microplus* are the most prevalent tick species, contributing significantly to the transmission of diseases like heartwater caused by *Ehrlichia ruminantium* (Barré & Uilenberg, 2010; Some *et al*., 2023a, Some *et al.*, 2024b). As these ticks cause spread diseases and direct harm to livestock, the severity of their effects varies across their developmental stages, sexes, and feeding capacities.

Tick life stages cause similar but varying levels of impact on their hosts, as transmission potential differs by stage. Adult ticks are generally bigger than nymphs, and have a larger capacity for consuming blood, causing greater discomfort to their hosts (Karbowiak et al., 2015). Male and female ticks also differ in their effects on hosts. Females induce significant damage such as irritation, inflammation, and secondary infections (Kamaraj et al., 2022; Randolph, 2008; Nasirian, 2022). They are also more likely to intensify future infestations and disease transmission due to their reproductive capacity. Additionally, female and male ticks sometimes harbour different microbiota, contributing to differences in the diseases they transmit (Van Treuren et al., 2015; Desta, 2016; Nasirian, 2022).

There is growing evidence for tick species-level preferences for certain predilection sites on livestock hosts. For example, *A. variegatum* has in many studies shown notable preference for targeting the mammary breast area of livestock in some studies (Stachurski, 2006; Addo 2024; Kabore, 1998; Opara and Ezeh, 2011). This has been associated with significantly reduced milk production, and severe wounds (Stachurski, 2000). These preferences are influenced by factors such as the ability to attach to the host skin, host species, hair density, body temperature, blood vessel proximity, species-specific evolutionary traits, and environmental and microclimatic conditions (Nyangiwe et al., 2018; Biguezoton et al., 2016; Dantas-Torres & Otranto, 2013; Desta, 2016). While this is so, it may imply that certain taxa or sex or life stages of ticks would show special preference for part of the tick body. This would also change the community dynamics, since certain taxa may tend to be favourably found in one predilection area and not another.

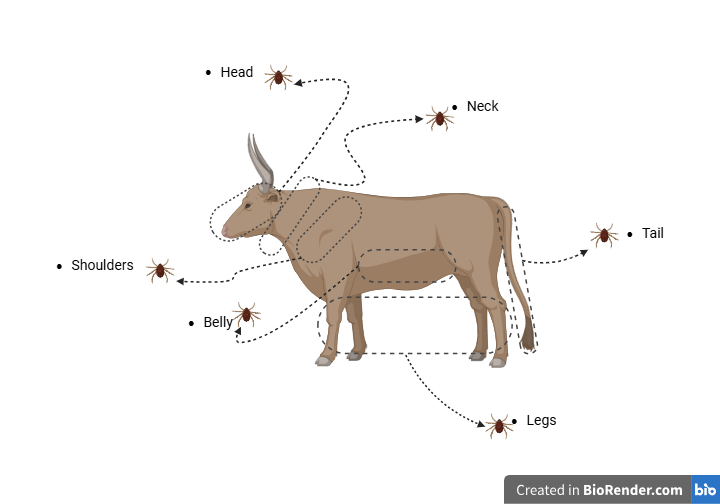
Livestock farming, particularly cattle trading, plays a crucial economic and cultural role in Nigeria, contributing 12.7% to the agricultural GDP (CBN, 1999; Kubkomawa, 2017). The livestock industry generates significant employment and fosters inter-ethnic relations, with Hausa traders dominating the market (Adamu et al., 2005). In southwestern Nigeria, most cattle originate from the northern states, where they are bred before being traced to southern regions (Swallow & Jabbar, 1994). They are a rich source of meat, hides, and milk and hold significant cultural and economic value in Nigeria and much of West Africa (Adamu et al., 2005; Kubkomawa, 2017; Santoze & Gicheha, 2019). Livestock farming in rural areas is crucial for sustaining livelihoods and supporting income generation (Adamu et al., 2005; Mafimisebi et al., 2013). However, tick infestations on cattle result in substantial economic losses for farmers due to prolonged attachment periods and their role as vectors of veterinary pathogens. Despite the burden of tick infestations, Fulani pastoralists of the north, who dominate cattle rearing in the region, seldom use acaricides and still adopt the traditional farming system (Awogbade, 1979; Bayer & Maina, 1984).

The diversity and abundance of ticks of cattle in Nigeria remain poorly studied. While some studies have examined tick prevalence at predilection sites, no research has evaluated species-specific preferences for these sites. Furthermore, many threatening tick vectors are not well monitored. For example, the invasive Brazilian tick, *Rh. microplus*, was first reported in high numbers in Edo State, Nigeria, by Adane et al. (2019). However, no follow-up studies have investigated its spread. This is an indication of scarcity of data which would be needed for tick control, especially for livestock that is of great economic importance to Nigeria.

Most studies on ticks in Nigeria have been done at the population level with limited insights into co-infestation patterns or community-level structures. Comprehensive studies using multivariate community-level approaches are needed to address these gaps. Understanding tick distribution and community structure can inform control measures, enhance disease management strategies, and assist pest regulatory agencies in mitigating tick-borne diseases (Farahi et al., 2016; Smith & Parker, 2010). In this study, we aim to address the knowledge gaps surrounding tick infestations in Edo State, Nigeria. Specifically, we would [1] estimate ixodic tick diversity and abundance on a cattle ranch in Edo State, [2] examine the community-level structure of these ticks across different predilection sites on cattle, and [3] investigate whether certain tick species, life stages, or sexes exhibit preferences for specific predilection areas.

# MATERIALS AND METHOD

2.3. Sampling and data collection



**Figure \_:** Schematic representation of the cattle predilection site where ticks were sampled

## 2.4. Statistical analysis

For this study, we used the R software (Version 4.4.0) and Paleontological Statistics (PAST) Version 4.03 software (Hammer & Harper, 2024) to analyse the tick data we collected. All data aggregation and manipulation was done in R.

Overall, species richness was estimated using the Chao 2 and Jacknife 2 estimators. In addition, a species accumulation curve (SAC) was used to visually show how much sampling effort influences the observed species richness. All species richness estimations were calculated in PAST Software. We calculated the tick prevalence (%) by calculating the percentage of infested cattle from the total number of cattle examined.

Margalef indices at each predilection site for individual cattle were calculated using PAST software as a measure of the species richness of each tick community.

Margalef index: *D = (S - 1) / ln(N)*

Where: D is the Margalef Index; S is the total number of species; N is the total number of individuals; ln is the natural logarithm.

A negative binomial model compared ticks' mean abundance and species richness across all cattle predilection sites. This was computed using the ‘glm.nb()’ function of the “MASS” package in R (Venables & Ripley, 2002). As a post hoc to assess significant differences in abundance and across each predilection site, Tukey tests (α = 0.05) for multiple comparisons were computed using the ‘glht()’ function from the "multcomp" package (Hothorn et al., 2008), given the existence of five distinct habitat levels. Also, a Kruskal-walis test was computed on the calculated Margalef index to compare its difference across all predilection sites, using the ‘kruskal.test()’ function in the “dunn.test” package.

Non-metric Multidimensional Scaling (NMDS) was used to analyze and visualize the overall dissimilarity of the tick community at the cattle predilection sites, using the Bray-Curtis coefficient to create similarity matrices. Two dimensions adequately captured the pattern in the data. We employed Permutative Analysis of Variance (PERMANOVA) to check for significant changes in the tick community compositions for Sex, life stage and predilection sites, determined through 9999 permutations using the ‘adonis2()’ function from the “Vegan” package in R. As a post hoc, we used the ‘pairwise.adonis()’ function to check for significant differences (α = 0.05) between communities. Also, we tested for homogeneity of multivariate dispersion, which is a good way to represent the tick community variance between the predilection sites of the cattle. This was done using the ‘betadisper()’ function of the “Vegan” package.

To ordinate the preference of ticks by taxon, sex, developmental stage, and predilection site, we used a Factor Analysis of Mixed Data (FAMD). The data included qualitative variables (sex, predilection site, and tick life stage) and quantitative variables (abundance of each tick species). FAMD reduces the dimensionality of complex multi-dimensional datasets by projecting them into a principal component (PC) subspace, which can be visualized as a point cloud. In this space, the proximity of two points indicates their overall similarity based on the selected PCs. The FAMD was performed using the "FactoMineR" package (Kassambara & Mundt, 2020).

# RESULTS

**3.1. Prevalence, abundance and relative abundance of ticks**

In this survey, 75 of the 95 sampled cattle were infected with at least one tick species, revealing an overall tick prevalence of 78.95%. Each tick-infested cattle had a median of 3 distinct species of ticks. Overall, 1930 ticks consisting of 1679 females and 251 males were collected in the surveys. From this, 1689 were adults while 241 were nymphal stage ticks. Ticks were collected from all 6 predilection sites: belly (432), head (356), leg (417), Neck (282), shoulder (99) and tail (344). Four (4) genera of ixodic ticks were identified (*Amblyomma, Boophilus, Rhipicephalus and Haemaphysalis)*, consisting of fifteen (15) species of ticks as shown in Table 1. The most prevalent tick species were *B. annulatus, B. decoloratus* and *B. geigyi* with prevalence level of 65.26%, 72.63% and 66.32%, respectively (Figure 1)*.* Similarly, thesetickswere the most abundant ticks sampled*,* with relative abundance of42.38%, 29.38% and 20.93% for *B. annulatus*, *B. decoloratus*, and *B. geigyi,* respectively. These three species of ticks made up over 92% of ticks collected from all tick-positive cattle.

Relatively rare species, including *R. quilhoni*, *H. laechi*, and an unidentified species from the *Boophilus* genus, were observed. Each of these tick species was found on a single cattle, with a prevalence of 1.05% for each.

**Table 1:** Tick species relative abundance in all cattle predilection site investigated.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Species** | **Belly** | **Head** | **Leg** | **Neck** | **Shoulder** | **Tail** | **Overall** |
| ***A. coharenses*** | 0.23 | 0.56 | 0.48 | 0.71 | 0 | 0.58 | 0.47 |
| ***A. variegatum*** | 1.62 | 1.69 | 3.6 | 1.42 | 0 | 4.36 | 2.44 |
| ***B. annulatus*** | 49.31 | 37.36 | 41.97 | 41.84 | 21.21 | 45.93 | 42.38 |
| ***B. decoloratus*** | 30.32 | 28.09 | 33.57 | 25.89 | 44.44 | 22.97 | 29.38 |
| ***B. geigyi*** | 17.36 | 20.79 | 19.18 | 27.3 | 28.28 | 20.35 | 20.93 |
| ***Boophilus* sp*.*** | 0 | 0 | 0 | 0 | 0 | 0.87 | 0.16 |
| ***H. laechi*** | 0 | 0.28 | 0 | 0 | 0 | 0.58 | 0.16 |
| ***R. gulhoni*** | 0 | 3.09 | 0 | 1.06 | 2.02 | 0.87 | 0.98 |
| ***R. lunulatus*** | 0.46 | 2.53 | 0.96 | 0 | 4.04 | 2.03 | 1.35 |
| ***R. muhsame*** | 0.23 | 1.4 | 0.24 | 0.35 | 0 | 0.58 | 0.52 |
| ***R. quilhoni*** | 0 | 0.28 | 0 | 0 | 0 | 0.29 | 0.1 |
| ***R. sanguineus*** | 0 | 3.09 | 0 | 1.06 | 0 | 0 | 0.73 |
| ***R. senegalensis*** | 0.23 | 0.56 | 0 | 0.35 | 0 | 0.58 | 0.31 |
| ***R. fanguineus*** | 0.23 | 0 | 0 | 0 | 0 | 0 | 0.05 |
| ***R. gemma*** | 0 | 0.28 | 0 | 0 | 0 | 0 | 0.05 |

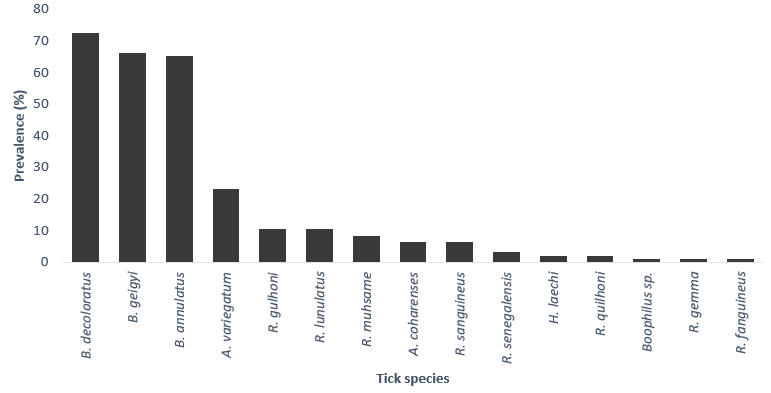


Figure 1: Tick species infestation prevalence (%) across all 95 cattle sampled.

**3.2. Tick community composition at the predilection areas**

The tick community composition of ticks at the predilection sites is represented in the NMDS plot (Figure 2). Visually, the plot shows that the six predilection areas have a high overlap in composition and level of dispersion of the ticks. In alliance with the NMDS plot, the PERMANOVA test revealed no significant difference (P> 0.05) in the overall community structure of ticks at the predilection areas. Nonetheless, there were non-significant differences between the tick’s community in all predilection areas, as shown in Table 2. Furthermore, the test for homogeneity of dispersion showed no significant difference (P> 0.05) amongst the predilection sites.

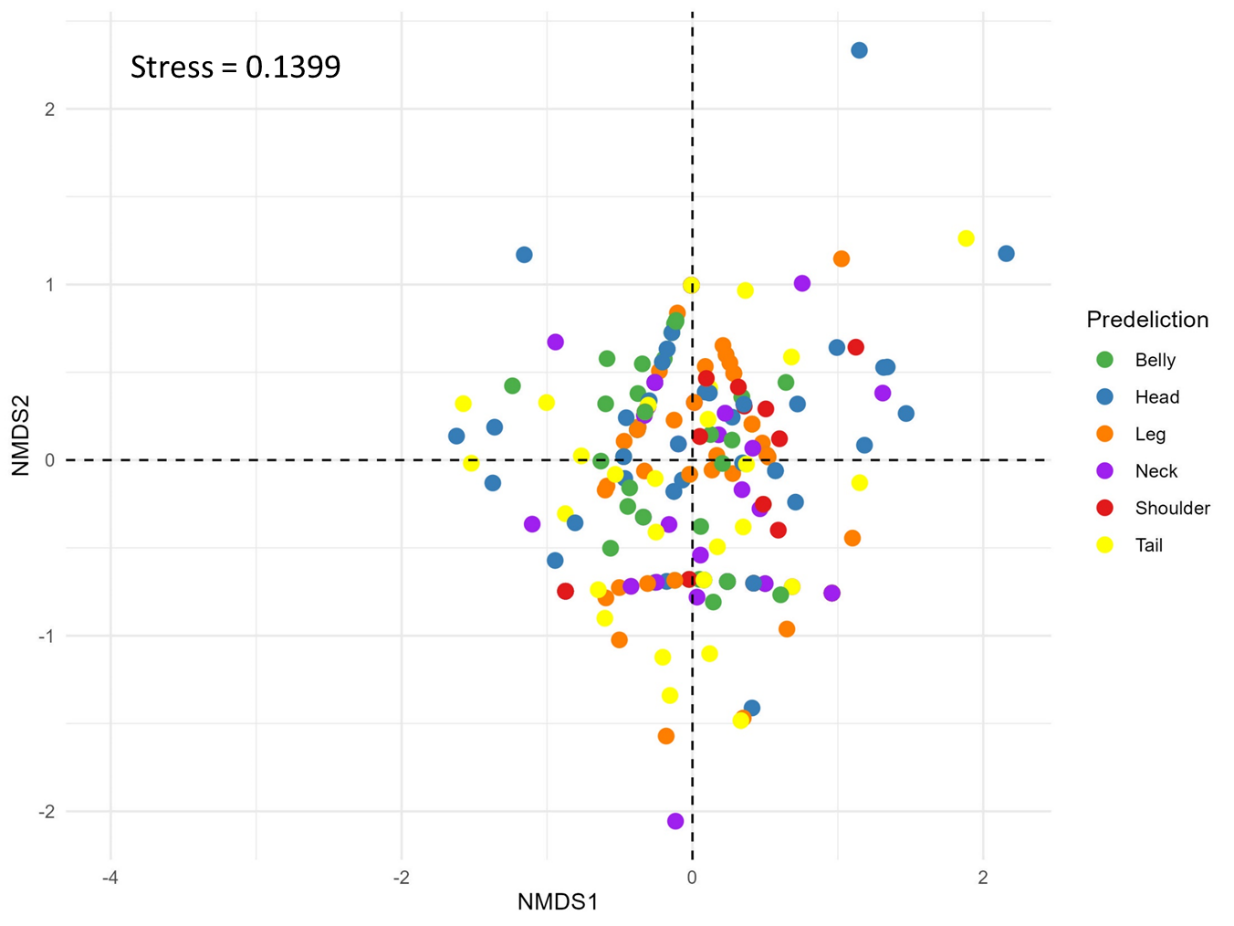


Figure 2: Non-metric multidimensional scale (NMDS) plot showing points representing the tick community in predilection sites. Points are coloured according to predilection sites.

Table 2: PERMANOVA test comparing the community structure of ticks at the predilection sites.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Predilection pairs** | F-Model | R2 | P-value | Adjusted P-value |
| **Belly vs Head** | 1.899 | 0.016 | 0.082 | 1 |
| **Belly vs Leg** | 0.711 | 0.005 | 0.553 | 1 |
| **Belly vs Tail** | 0.329 | 0.003 | 0.832 | 1 |
| **Belly vs Neck** | 0.686 | 0.006 | 0.592 | 1 |
| **Belly vs Shoulder** | 3.321 | 0.039 | 0.011 | 0.165 |
| **Head vs Leg** | 0.774 | 0.006 | 0.547 | 1 |
| **Head vs Tail** | 0.941 | 0.008 | 0.442 | 1 |
| **Head vs Neck** | 0.936 | 0.009 | 0.427 | 1 |
| **Head vs Shoulder** | 1.054 | 0.013 | 0.404 | 1 |
| **Leg vs Tail** | 0.700 | 0.006 | 0.592 | 1 |
| **Leg vs Neck** | 0.741 | 0.006 | 0.544 | 1 |
| **Leg vs Shoulder** | 0.955 | 0.011 | 0.424 | 1 |
| **Tail vs Neck** | 0.414 | 0.004 | 0.817 | 1 |
| **Tail vs Shoulder** | 2.536 | 0.034 | 0.035 | 0.525 |
| **Neck vs Shoulder** | 2.249 | 0.032 | 0.072 | 1 |

**3.3. Male and Female Tick community composition.**

Based on Sex, the tick community structure is represented in the NMDS plot (Figure 3). Visually, the plot shows that the male ticks have higher dispersion and heterogeneity compared to the female ticks which looked relatively homogenous. PERMANOVA test revealed a significant difference (P< 0.001) in the community structure of male and female ticks. Similarly, the test for homogeneity of dispersion showed significant differences (P< 0.001) amongst both sexes.

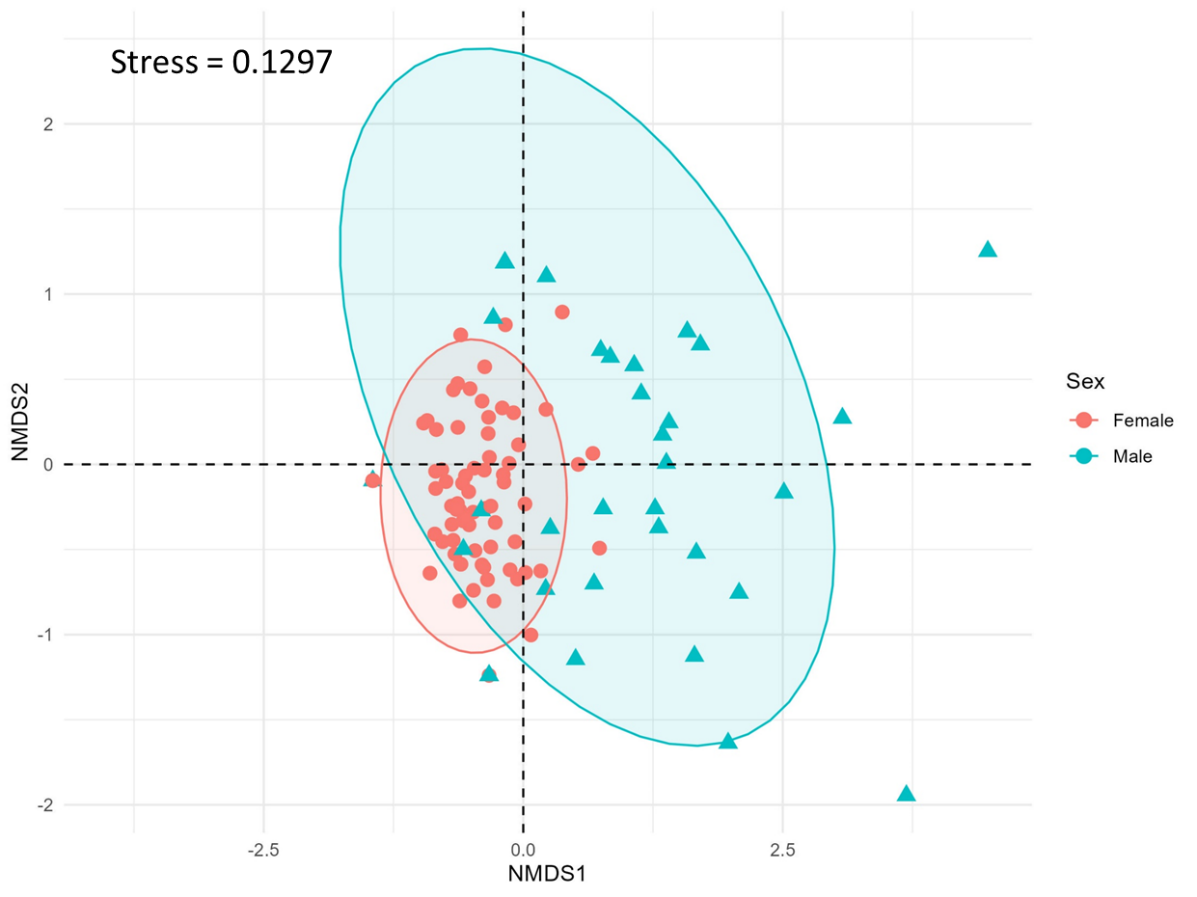


Figure 3: Non-metric multidimensional scale (NMDS) plot showing points representing the tick community in predilection sites. Points are coloured according to tick sex.

**3.4. Tick stage and community composition.**

Two tick stages were identified: nymph and adult. The NMDS plot in Figure 4 shows the community structure of both stages. PERMANOVA test shows a significant difference (p<0.001) in the community composition of both tick stages. However, the test of multivariate dispersion did not reveal any significant difference (p>0.05) for both tick stages.

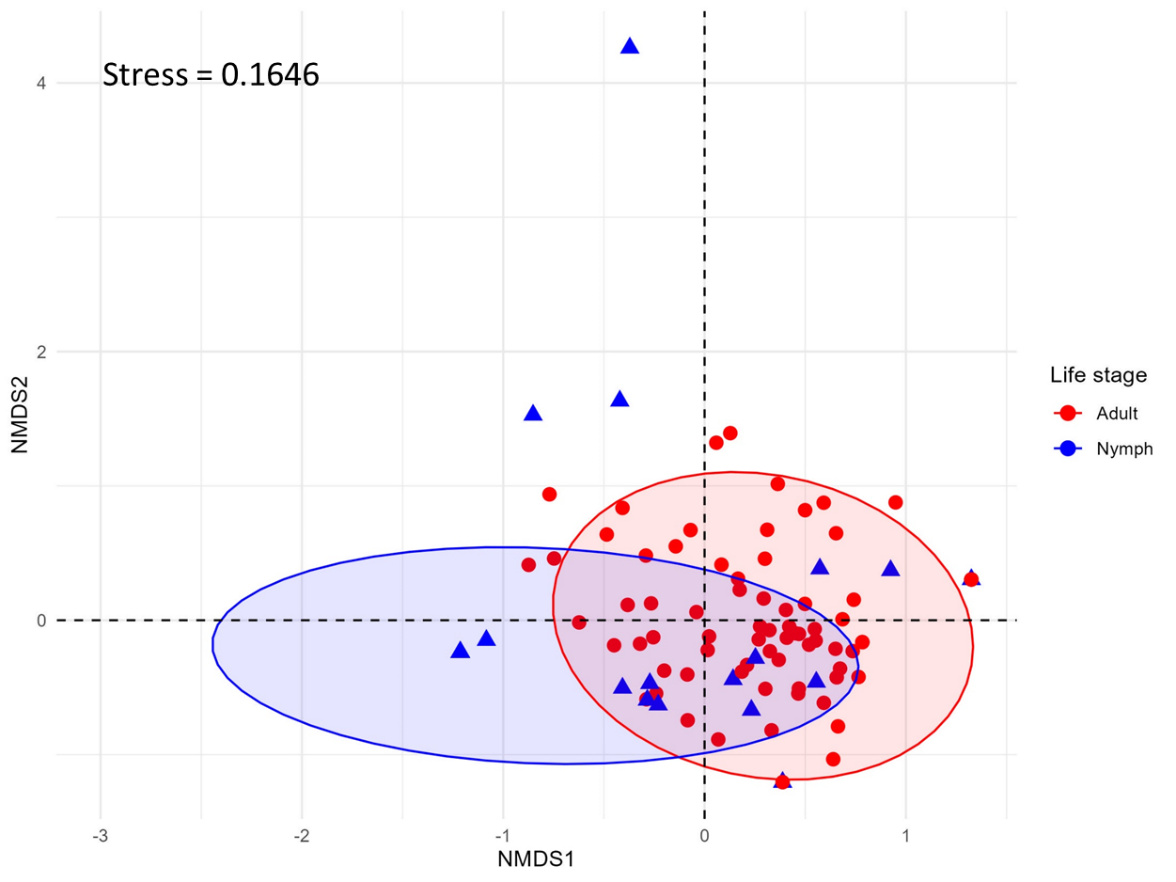
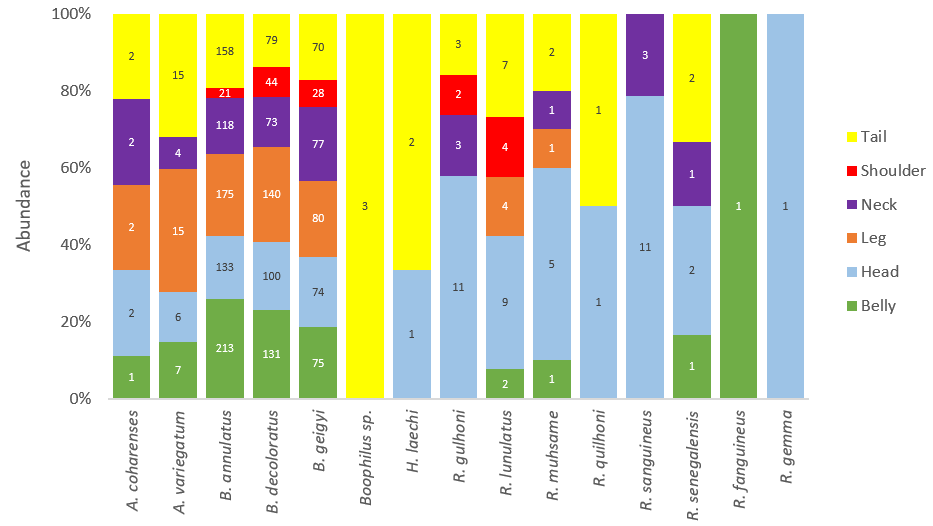


Figure 4: non-metric multidimensional scale (NMDS) plot showing points representing the tick community in predilection sites. Points are coloured according to tick life stage.



**Figure 5**: Abundance of tick species at each predilection site of cattle. Numbers embedded on the bars represent actual counts of the species.

The most abundant ticks were well represented in all predilection sites of the cattle (figure 4). This is especially in the highly abundant *B. annulatus, B. decoloratus*, and *B. geigyi*. Further to this, *A. coharenses* and *A. variegatum* were observed in all predilection areas except shoulders. All *R. gemma*, *R. fonguineus* and *Boophilus* sp. were found in just one predilection site each – Head, belly and tail, respectively. *H. laechi* and *R. sanguineus* were present only in the head and tail of the cattle.

**3.5. Species richness and taxonomic diversity of ticks**

Figure 6 is a SAC that estimates the species richness of ticks sampled at the cattle ranch. The observed number of tick species was 15. However, the SAC shows a mildly upward trend, which suggests that more sampling (of ticks) from more cattle in the ranch/market would have revealed additional tick species. Furthermore, the Jackknife 2 and Chao 2 species richness estimates also support this trend. That is, in line with the prediction by the SAC curve, Chao 2 estimates a tick species richness of 16 species, while Jackknife 2 predicts that 19 species are in the area.

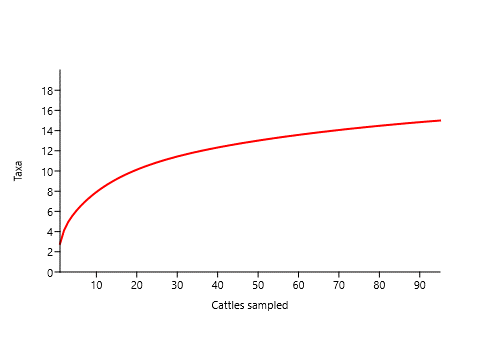


Figure 6: Species accumulation curve (SAC) of ticks sampled from 95 cattle in the ranch.

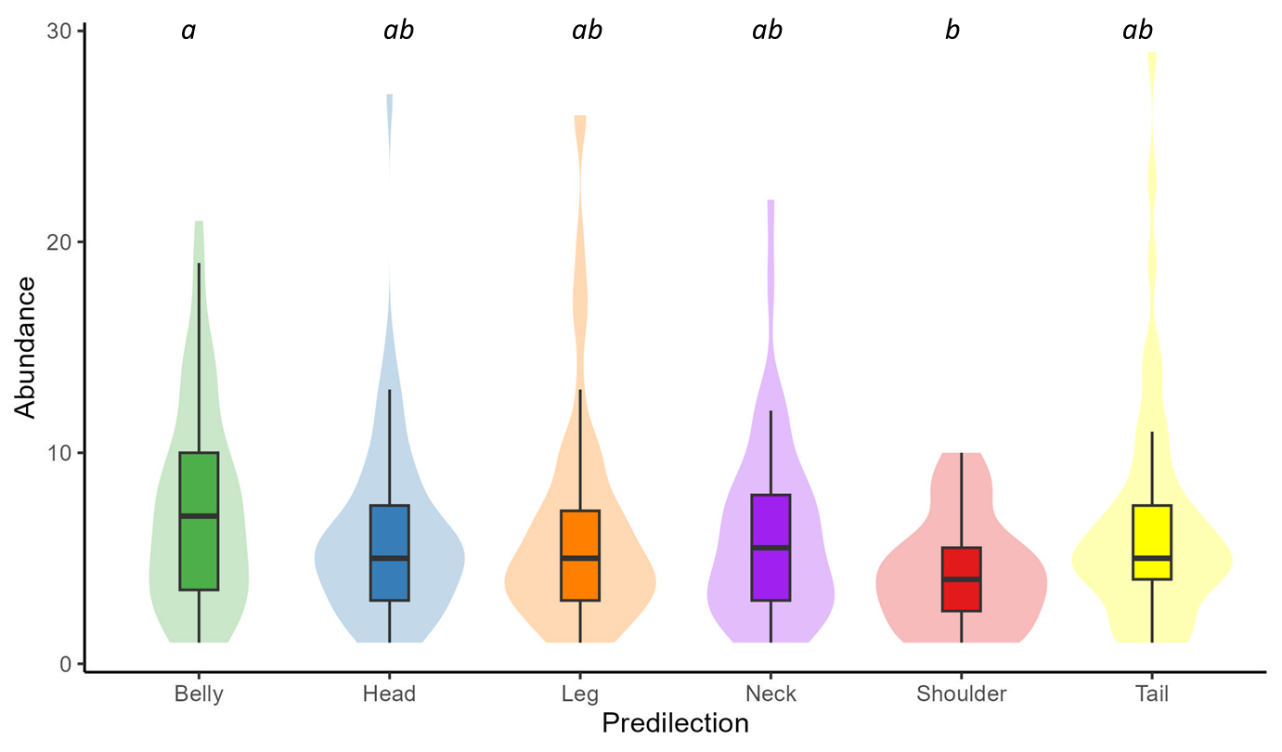


Figure 7: Abundance of ticks at the predilection areas in cattle sampled. different letters show significant differences between predilections.

The overall abundance of ticks for each predilection area is represented in the figure 7. The tick community in the belly had the highest mean abundance (7.32±0.62), followed by the tail, leg, neck and head, which had a mean abundance of 5.49+0.77, 6.51+0.68, 6.13+0.64 and 6.03+0.55. Particularly, the Shoulder had the lowest number of ticks with mean abundance of 4.30+0.55. The negative binomial model showed that the abundance of ticks at the shoulders were significantly (P<0.05) lower than those in the belly.

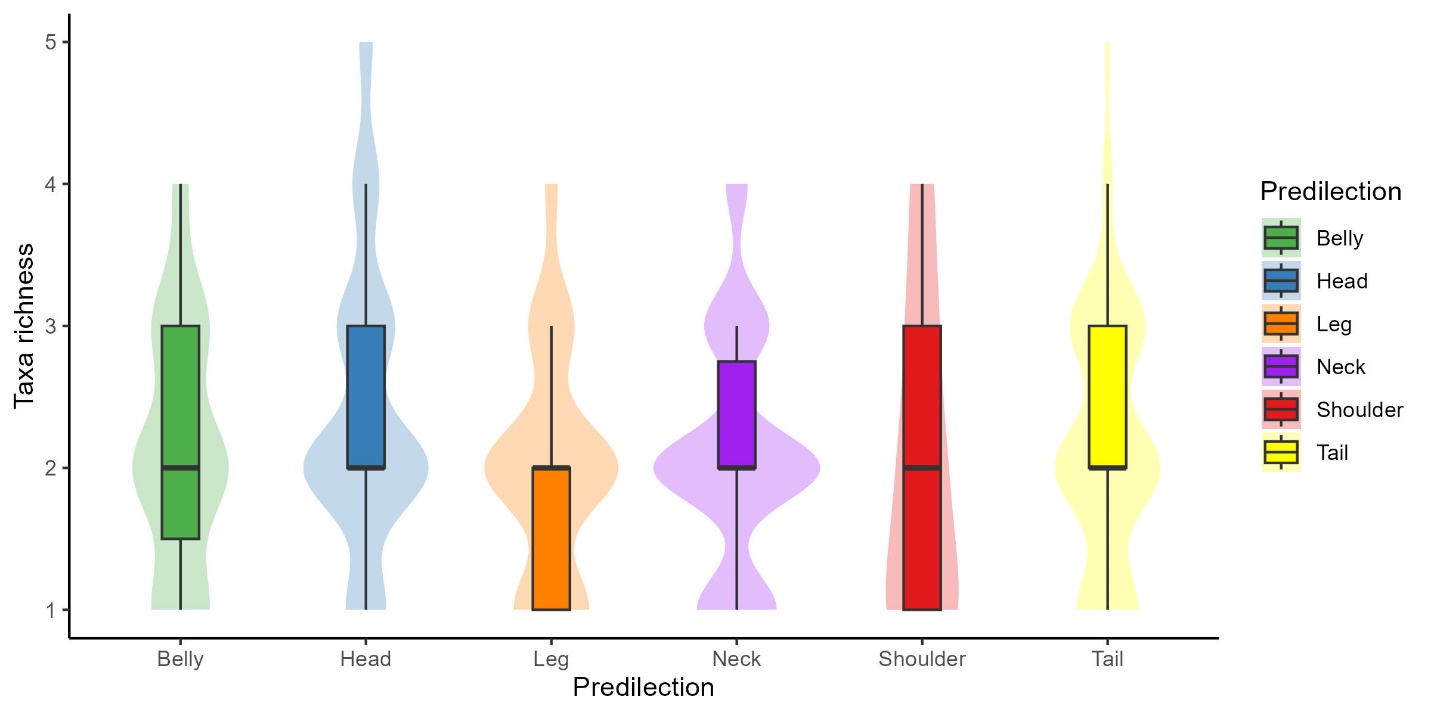


Figure 8: Species richness of ticks at the predilection areas in cattle sampled.

The median species richness was two (2) across all predilection sites Figure 8. However, non-significant variation in tick richness persisted. For example, the cattle’s head had the highest mean tick-species richness of 2.42+0.55, followed by tail, belly and neck which had a richness of 2.19+0.77, 2.13+0.62 and 2.09+0.64, with the lowest observed in legs (1.98+0.68). While most cattle had two species of ticks at median, a few had up to 5 distinct tick species infestations in the head and tail.

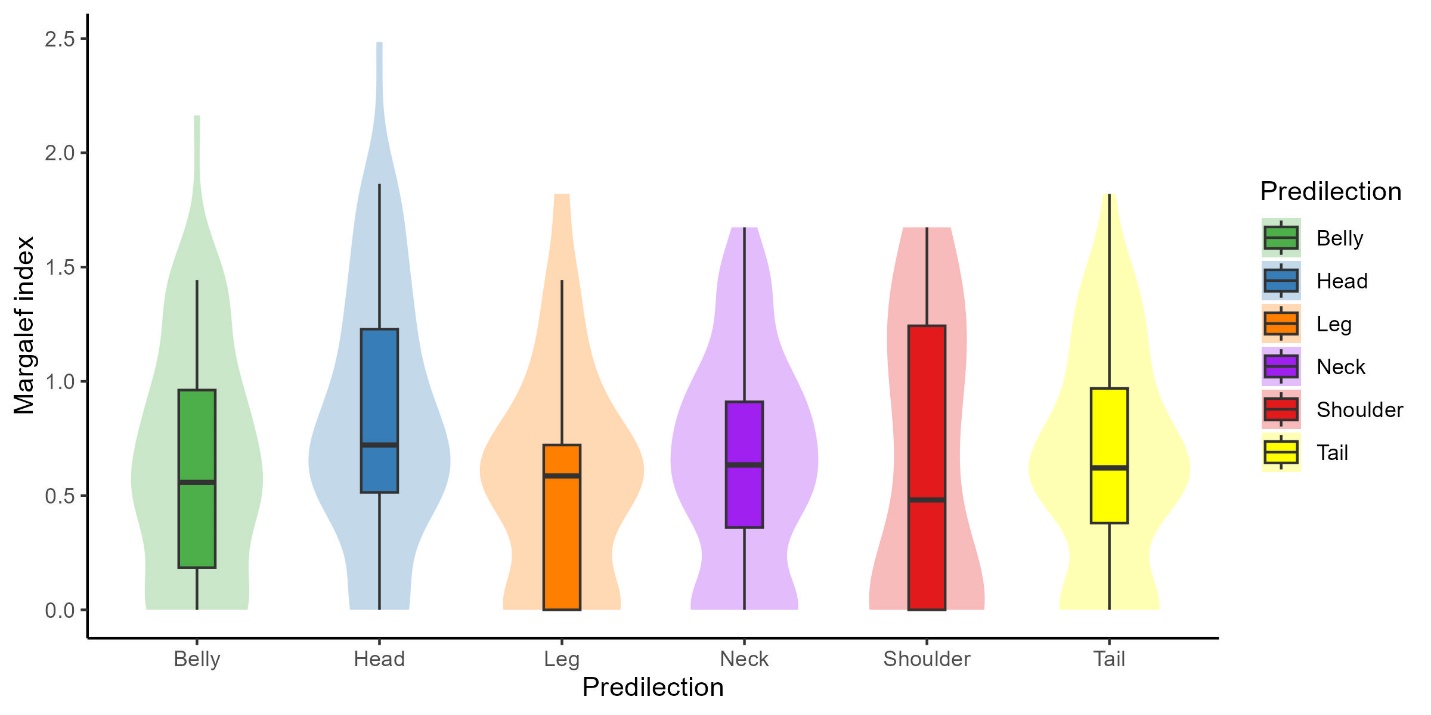
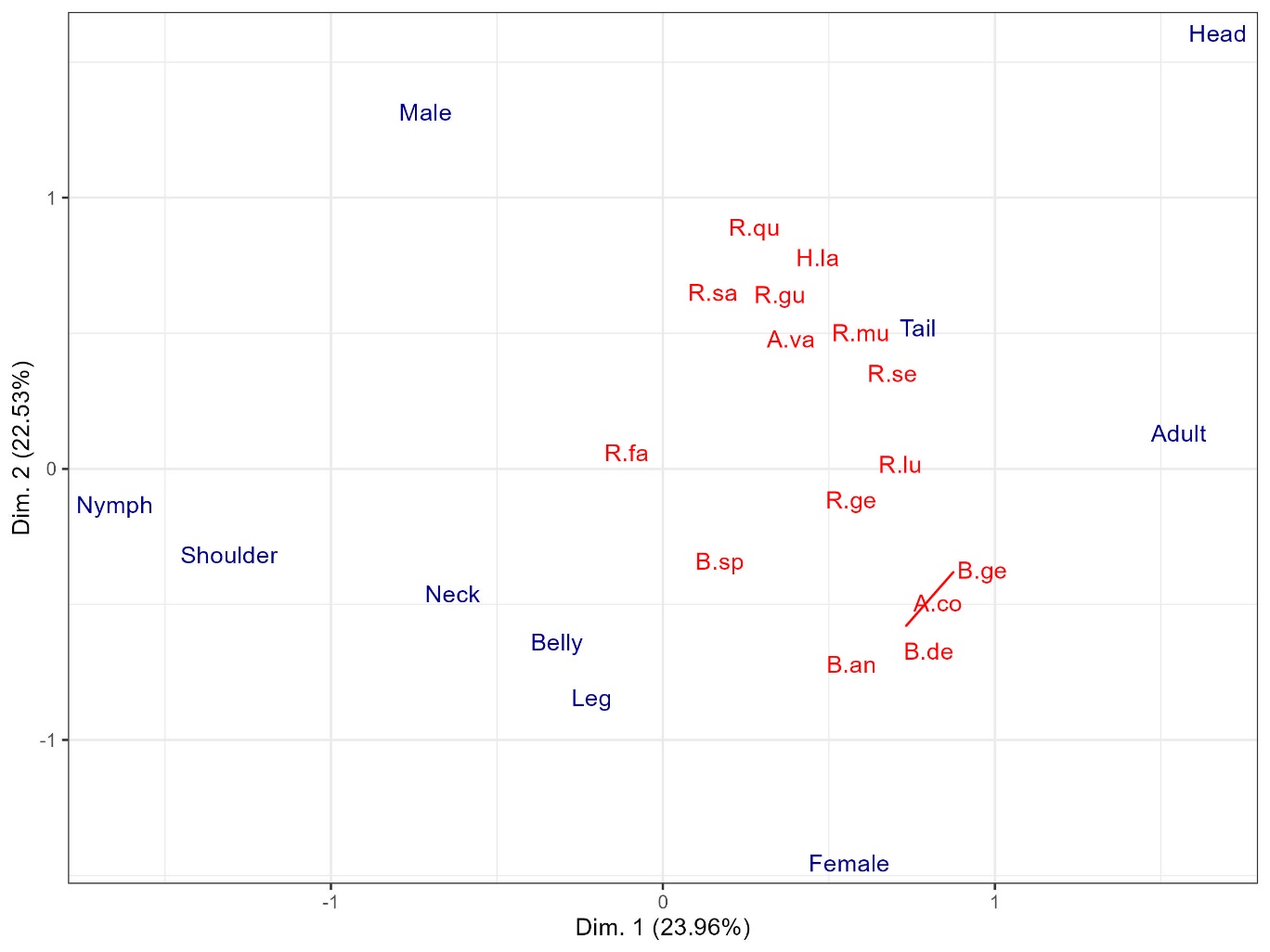


Figure 9: Margalef index of ticks at the predilection areas in cattle sampled.

Margalef diversity estimates of ticks at the predilection sites are shown in Figure 9. While this index statistically did not vary significantly (P>0.05), slight differences were observed. The Tick head had the highest mean Margalef index (0.83+0.07), followed by the tail (0.65+0.07), neck (0.64+0.07), belly (0.63+0.07) and shoulder (0.62+0.13). The legs had the lowest Margalef index (0.57+0.06) amongst all predilection sites.

**3.6. Predilection preference of ticks**

The FAMD explains 46.5% of the variance in the tick data using the two dimensions only, with the first and second explaining 23.96% and 22.53%, respectively (Figure 10). The FAMD has revealed notable differences in the qualitative variables (Tick life stages, Predilection area and Sex) of the ticks. The FAMD plot does not show notable species-specific preference for certain predilection areas. However, the adult and nymph stages of ticks would contain different tick species compositions as shown in their high disparity on the FAMD plot. Also, the neck, belly and leg of the cattle are qualitatively more similar.



***Figure 10:*** Factorial design of predilection site, life stage and species of ticks in the cattle ranch. *A.va, A. variegatum; A.co, A. coharenses; B.an, B. annulatus; B.de, B. decoloratus; B. ge, B. geigyi; H.la, H. laechi; R.gu, R. gulhoni; R.lu, R. lunulatus; R.mu, R. muhsame; R.sa, R. sanguineus; R.se, R. senegalensis; B.sp, Boophilus species; R.qu, R. quilhoni; R.ge, R. gemma; R.fa, R. fanguineus.*

# DISCUSSION

In this study, we were able to investigate—at a community level—the prevalence of ticks at predilection sites of cattle, after sampling ticks from 6 predilection areas of 95 cattle in a trade market in Edo State, Nigeria. Generally, our survey has shown that 78.95 % of cattle were infected with at least one tick species. This was far significantly higher than in Adane *et al*. (2019)’s study in a cattle trade market in Edo State, from which a prevalence of 21.5% was reported.

To the best of our knowledge, this study has shown the highest diversity of ticks from a single cattle market/ranch in Nigeria. The observed species richness is 15, and the Chao 2 and Jacknife2 estimates suggest that while a substantial number of tick species were recorded, further sampling is likely to reveal additional species in the cattle ranch.

Based on the records since Adene et al. (2019)’s study, we have seen significant changes in the species of ticks found. In our study, each cattle has a median of 3 distinct species of tick, and an overall of 15 species. This is much way higher than in Adane et al. (2019)’s report of 3 species of ticks (*A. variegatum*, *Rhipicephalus* sp., *R. microplus*) as the total in 209 out of 258 tick-infested cattle in the ranch. In this study, we find that *B. annulatus, B. decoloratus and B. geigyi were the most abundant ticks in the cattles sampled, constituting* 42.38%, 29.38% and 20.93% of the total ticks sampled from the cattles. However, Adene et al. (2019) had only *A. variegatum*, *R. microplus* and a *Rhiphicephalus* species. In this study, the exotic *R. microplus* was not present, but had a significantly high prevalence (21.5%) in Adene et al. (2019)’s survey. A study in Maiduguri, Northern Nigeria by Musa et al. (2014) showed *B. microplus*, *Am. variegatum*, *Hyalomma* spp., *Rh.* sanguineous and *Ornithodorus* spp. as the only ticks present in the area.

The high level of tick diversity and prevalence in the cattle trade area of Edo state, Nigeria calls for quick public animal health intervention. Most of the species of ticks that are highly prevalent in our survey are known to transmit multiple tick-borne diseases (TBDs). For example, *Boophilus* *decoloratus*, a common tick species in Africa, is an important vector of several tick-borne livestock diseases. It transmits *Ba. bigemina* and *An. marginale* to cattle, causing babesiosis and anaplasmosis respectively (Akinboade et al., 1981). Additionally, *B. annulatus*, the, is capable of transmitting *Anaplasma marginale* through transstadial transmission, leading to anaplasmosis (Samish et al., 1993). *B. geigyi* is recognized for its ability to transmit the protozoan parasite *Babesia bovis*, which can be detected in tick eggs, larvae, and hemolymph during various stages of infection (Akinboade & Dipeolu, 1981). *B. geigyi*, has been identified as a carrier of *Borrelia theileri*, the agent responsible for bovine borreliosis, in Mali (Mccoy et al., 2014). Also, *A. variegatum* has been collected in cattle from multiple regions in Nigeria such as in North-central Nigeria (Ogo et al. 2013), Borno (James-Rugu & Jidayi, 2004), Kano (Unsworth, 1952), Nigeria.

The female ticks in our study showed greater homogeneity in the overall community structure on all tick-infested cattle. This means that the female community of tick species was less diverse in structure compared to males with higher diversity. However, there were more counts of female than male ticks in our survey. Therefore, this means that just some tick species account for most of the female community structure of ticks. Many studies have shown that female ticks are typically the main carriers of TBD, as they feed for longer periods and consume more blood than males, making them more likely to acquire and transmit pathogens (Kamaraj et al., 2022; Nasirian, 2022).

A larger female tick population increases the risk of disease spread to both cattle and humans. Additionally, since female ticks can lay thousands of eggs, a higher number of females could lead to a larger overall tick population, heightening the chances of future infestations and the spread of TBD (Nasirian, 2022; Nabbout, 2023). While male ticks are less likely to transmit diseases due to shorter feeding times, their diverse population, as shown in this study, may still pose indirect risks by contributing to the ecological dynamics that support female ticks' survival and reproduction.

This study revealed that, at median, each tick-infested cattle was infested by approximately three distinct tick species. The presence of multiple tick species on a single host raises concerns about the potential for co-infections with tick-borne diseases (TBDs), as different species may serve as vectors for various pathogens. Adult ticks are often more involved in disease transmission due to their longer feeding duration and greater blood meal sizes compared to nymphs. The higher prevalence of adult ticks on cattle could elevate the risk of transmitting tick-borne diseases to both cattle and potentially humans.

The diversity of tick species, as measured by the Margalef index, did not significantly vary across the different predilection sites on the cattle. This suggests that the diversity of tick infestation is relatively uniform across the body (at least for the predilection areas we investigated), with no specific predilection site harbouring a significantly more diverse tick population. The non-significant difference in tick diversity between body regions also points to the fact that ticks may not exhibit strong site preferences when it comes to attaching to their hosts. Thus, each predilection site—whether head, tail, belly, or leg—had similar levels of tick diversity.

The absence of significant differences in tick diversity between predilection sites also implies that factors such as cattle movement, environmental exposure, and host immune responses are likely to play a more substantial role in determining tick attachment and diversity than the physical characteristics of the predilection sites themselves. For this cattle ranch study, we have shown that at a community and population level, there is no obvious attachment preference at the predilection sites. However, this, in many ways, contrasts with previous studies that suggested certain body areas, could be more favourable for tick attachment primarily due to easier access or proximity to blood vessels (Kabore, 1998).

While we have observed 15 species, some are however rare, we do not doubt that further sampling would have revealed more tick infestation in the cattle at the ranch. The SAC, Jackknife 2 and Chao 2 estimates also attest to this claim. We are limited on how many species of ticks are there. The cattle trade market is known to receive cattle from every part of Nigeria. This is of public health importance. This is a resounding call for country-wide monitoring of ticks. Cattle in Nigeria are mostly raised by the Hausa herdsmen, and these people are largely not formally educated (Adisa & Badmos, 2010; Arowolo et al., 2013).

Interestingly, we did not find the invasive species, *Rh. microplus* which was reported in Adane *et al*. (2019)’s study. Since our study site is a cattle market where cattle are brought from the North and other far places, there is a high tendency that this species has spread across many parts of Nigeria. Lorusso et al. (2013) also had no detection of this invasive species in their survey in central Nigeria. Our results are similar to Lorusso et al. (2013) who *had Rh. decoloratus, Rh. annulatus, Rh. guilhon* and *Rh. geigy* as their most abundant species. Similar to our results, too, Lorusso et al. (2013) reported a disproportionately higher ratio of females to males in these ticks, except for in *Rh. guilhoni* which had a higher number of males (2.3 male:1 female). However, it is no news that more ticks are females is the case (Kiffner et al., 2010; Rehman et al., 2017), but many studies have reported otherwise, especially with other taxa of ticks (Opara and Ezeh, 2011).(Golo et al., 2017; Isaac et al., 2016)

Since there is an overlap in species similarity between predilection sites, we can infer that ticks sampled from one predilection area would be a good estimator for what is available at another at the taxa level. This is supportive of the observations of low taxon preference for the sites. However, we cannot exactly say the same thing for the sex of ticks, as there seems to be higher taxonomic diversity in males than in females. Though we find that most ticks are females, the majority of them are from a small subset of tick species, while males have high species variation.

**Limitations and Future Studies**

We recognize that smaller or immature ticks might have been missed during field sampling, introducing potential bias. As a result, estimates of the ratio between mature and immature tick populations may not accurately reflect field conditions. Additionally, we are limited in our ability to comment on the phylogeny, age, or sex of the cattle. Furthermore, the results concerning tick abundance should be interpreted cautiously, as factors such as cattle size, age, breed, location, and the characteristics of the predilection area can influence the findings. These factors should be investigated in future studies to find possible phylogenetic relationships that may affect species preference.

**Conclusion**

This study highlights a high prevalence and diversity of tick species in cattle from a trade market in Edo State, Nigeria, with 15 species recorded and evidence suggesting the potential for additional species with further sampling. The findings demonstrate significant changes in the community composition of ticks compared to previous studies in the region, including the absence of the invasive *Rh. microplus* and the high prevalence of *B. annulatus*, *B. decoloratus*, and *B. geigyi* as dominant species. The presence of multiple tick species per host, combined with the predominance of female ticks—key vectors of tick-borne diseases (TBDs)—raises serious concerns about the health risks posed to cattle and potentially humans. We did not observe significant variation in tick diversity across predilection sites, indicating a uniform distribution of species throughout the sampled body areas. However, males exhibited greater species diversity than females, despite females being more numerous.

The findings underscore the need for a comprehensive, country-wide monitoring system to track tick prevalence and diversity in Nigeria, particularly given the significant role of cattle trade in spreading tick species across regions. Future research should prioritize more extensive and standardized sampling protocols to build a more complete understanding of tick-host dynamics in Nigeria.

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