Application of Body Condition Scorings to Effective Detection of African Trypanosomiasis in Camels and Cattle

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***Abstract*— Trypanosomiasis is a parasitic disease that is transmitted by tsetse flies. However, because of the limitation of conventional parasitological methods, conclusive epidemiological inferences on trypanosomiasis is challenging, leaving a high proportions of the disease to remain undetected which leads to difficulty in monitoring and strategic control. The present study therefore, employed the use of molecular methods to detect trypanosomes in trade camels and cattle, along line analysis of their body condition scores (BCS). Results of the study indicated that, all the infected camels and majority of the infected cattle had poor BCS. The average packed cell volume (PCV) of infected animals was lower than the average PCV of uninfected animals. Findings from this study revealed an infection rate of 48.75% with the most frequently encountered species being *Trypanosoma vivax* (18.75%), followed by *T. brucei* (12.50%), *T. congolense* (8.75%), *T. evansi* (6.25%) and mixed infection involving *T. brucei* and *T. congolense* (2.50%). Conclusively, animals with poor BCS are more susceptible suggesting that, the use of BCS may improve the quality of evaluation of trypanosomiasis in animals, especially for large scale epidemiological study.**

***Index Terms*— Body Conditions, Camels, Cattle, Trypanosomiasis.**

I. INTRODUCTION

African Trypanosomiasis is one of the major haemoparasitic diseases of domestic animals (Food and Agricultural Organization, FAO 2017). The tsetse-transmitted form of the disease is endemic throughout the tropical regions of Africa where the vector is prevalent (Akoda *et al*., 2009). According to the Pan African Tsetse and Trypanosomiasis Eradication Campaign, PATTEC progress report (2019), about 558,000 km^{2}areas of land in Nigeria are infested by tsetse flies, with only 52,100 km^{2}under control activities. The diseases is one of the biggest constraints to livestock productivity in sub – Saharan Africa, Nigeria inclusive, and since livestock marketers in Kano State usually travel from high – risk areas, there is likely of importing infected animals into the State. The present study therefore, employed molecular detection techniques, to detect the trypanosomes in cattle and camels, which will assist in providing the base line information on the current epidemiological status of Animal Trypanosomiasis in Kano State, for devising appropriate control measures to limit economic losses arising from the disease.

Trypanosomiasis has been a serious threat to livestock. However, a high proportion of the disease remains undetected because clinical signs are nonspecific and non – pathognomonic, diagnosis using parasitological approaches shows poor sensitivity, and serological methods lack specificity (Maigari and Dabo, 2018). Therefore, there is likelihood that impacts of the disease may be greatly underestimated. However, many studies have shown that technique based on the amplification and characterization of nucleic acid is very sensitive, specific and rapid (Gibson, 2007, 2009, Adams *et al*., 2006, 2008, Cox *et al*., 2005, Desquesnes *et al*., 2001). Hence, the need for molecular analysis to increase quality of diagnosis in epidemiological studies of Animal Trypanosomiasis becomes imperative.

II. MATERIALS AND METHODS

A. Sampling Techniques

The target population was identified to include cattle and camels of different ages, breeds, sexes and sources, brought to Kano State, Nigeria. Animals were selected by systematic sampling technique whereby every nth unit in the population is sampled (Suresh, 2011). The sampling interval was determined by the use of formula K = N/n (where N = total number of animals available and n = the number required in the sample). A random number (r) falling between 1 and K is then chosen by the use of card shuffling physical randomization technique according to World Organization for Animal Health (WOAH 2012).

B. Determination of Body Condition Scores (BCS) of Camels and Cattle

Cattle and camels were assessed at the point of slaughter using a 9 – point scale reference table according to Glenn (2016). United States of America (USA) scoring system was

DOI: http://doi.org/10.24086/biohs2022/paper.709

used to assign scores on all the important anatomical points, meticulously and systematically. To get the best estimated score, each animal was examined while standing and in mobility.

C. Blood Sample Collection and Preservation

Blood samples were collected from 800 camels and cattle, via the jugular vein, in which 100 µl of blood was subsequently applied directly onto DNA binding matrix (Flunders Technology Associates filter paper, FTA® cards, Whatman International Ltd., Abington, Cambridge, UK). These were air dried thoroughly, placed in containers with hygroscopic desiccant and then stored at room temperature before processing.

D. Genomic DNA Extraction

The genomic DNA extraction was performed according to manufacturer's instructions (AccuPrep®, Bioneer Corporation, Korea). Briefly, five individuals 3mm discs were excised from each card for each individual animal sampled using a Harris Micropunch© (Whatman, UK). To avoid cross contamination between samples, 5 discs were punched out from the blank filter cards after punching each sample. The FTA discs were washed twice for 15 minutes using 1ml of Whatman FTA purification reagent to remove haemoglobin, and to discard used reagent after each wash. The FTA cards were then washed twice for 15 minutes in TE buffer (10 mM Tris, 0.1 mM EDTA, pH 8.0) to remove the FTA purification reagents. The used buffer was then discarded after each wash. FTA discs were dried for 30 minutes in an oven at 37ºC. Chelex suspension (100µL of 5%) was added to the dry discs and incubated at 90 ^{0}C for 30 minutes to elute the DNA from the FTA discs. The recovered DNA pellets was thus suspended in 20µL triple distilled water and stored at – 20 ºC.

E. Polymerase Chain Reaction (PCR)

Nested PCR was carried out to amplify ITS – 1region for the identification of the different trypanosome species using generic primers (Cox *et al*., 2005). Briefly, the amplification was conducted in a total volume of 50 µl containing 5 µl of PCR buffer 10× (10 mM Tris-HCl (pH 9.0), 50 mM KCl), 3 µl $MgCl_2$ (1.5 mM), 3 µl of forward primer (1.5 mM), 3 µl of reverse primer (1.5 mM), 3 µl of deoxynucleotide-triphosphate (dNTP), 1µl of Taq DNA polymerase, 30 µl of sterile water and 2 µl DNA template. Thermal cycling was carried out using Peltier Thermal Cycler (MyGene ™ Series Peltier Thermal Cycler, Model MG96 G, Long Gene Scientific Instruments Co., Ltd.) which involves pre – denaturation at 98˚C for 10 seconds, followed by 35 cycles of denaturation at 98˚C for 30 seconds, hybridization of primers at 65˚C for 30 seconds, elongation at 72˚C for 30 seconds, and then final extension at 72˚C for 10 min.

List of primers:

Nested ITS generic primers for all Trypanosomes (Adams *et al*., 2006)
ITS1 outer forward (5′GATTACGTCCCTGCCATTTG3′)
ITS2 outer reverse (5′TTGTTCGCTATCGGTCTTCC3′)
ITS3 inner forward (5′GGAAGCAAAAGTCGTAACAAGG3′)
ITS4 inner reverse (5′TGTTTTCTTTTCCTCCGCTG3′)

F. Agarose gel electrophoresis

All the PCR products were resolved on 2% w/v agarose gel. Briefly, 2g agarose gel was weighed and dissolved in 100 ml of 1X TAE buffer. Complete dissolution was aided by heating in a microwave oven for 2 minutes with intermittent shaking. After allowing the solution to cool down, 3 µl of loading die was added (EZ visions IN – GEL Solution 10, 10, 000χ). Combs were placed into secured gel caster and the solution was gently poured-in. The gel polymerized after 25 minutes, and then the combs were removed and the gel caster re-positioned in the tank (Bio – Rad, Power Pac_{HC}, 250v/ 3.0A/ 300w). The PCR products (10 µl) were carefully loaded into each well, while 10 µl of DNA ladder (Quick – Load ® 100bp marker, Purple 100 bp DNA ladder, Bio Labs Inc, New England) (Appendix II) were loaded into the first well. The tank was then covered and the electrodes connected to the power pack and run at 100V for 45 minutes. Thereafter, the gel was removed from the tank and the bands visualized under ultra – violet (UV) light. This was repeated several times until all the amplified samples were visualized.

G. Data Analyses

Data collected from each animal were coded into appropriate variables and entered in MS excel worksheets. Biostatistical analysis was performed using MaxStat (Version 3.0). Categorical data such as the difference between the infection rates of the studied animals were analyzed by using chi – square test of independence while Kruskal – Wallis test was used for pairwise comparisons to determine significant differences between the PCV values of infected and uninfected animals. In all the analyses, a value of $p < 0.05$ was considered as significant.

III. RESULTS AND DISCUSSION

The BCS of camels and cattle in relation to their breeds, sex, age and sources is presented in Table 1. Of the 240 camels screened, 148(18.50%) had good BCS and 92(11.50%) had poor BCS. On the basis of sex, majority of male camels, bulls and cows had good BCS, 61(7.63%), 305(38.13%) and 105(13.13%), respectively. A high proportion of younger camels (camels >1≤3 years), had good BCS while majority of camels greater than three years, 80(33.33%), had poor BCS. Mai Adua had the highest number of camels with good BCS, 63(26.25%) followed by Agadas, 30(12.50%), and Maigatari, 27(11.25%). Similarly, Dambatta had the highest number of cattle with good BCS, 129(23.03%) followed by cattle screened from Mai Adua, 112(20.00%) and Maigatari, 84(15.00%).

The PCV of camels and cattle in relation to their breeds, sex, age and sources is presented in Table 2. The mean PCV±STD of *C. dromedarius* was found to be 26±0.8, *Adamawa Gudali* had 34±3.32, *Red Bororo* had 33±2.70, *Sokoto Gudali* had 33±4.35 while *White Fulani* had 34±1.2. On the basis of sex, the mean PCV±STD of male and female camels was 24±0.06 and 28±0.05, respectively. The mean PCV±STD

DOI: http://doi.org/10.24086/biohs2022/paper.709

of bulls was 30±0.55 while that of cows was 34±0.08. The mean PCV±STD of camels from Agadas, Azare, Gaidam, Garin Alkali, Gingime, Hadejia, Mai Adua and Maigatari were 31±0.05, 29±0.05, 30±0.00, 23±0.06, 26±0.04, 22±0.00, 26±0.05 and 28±0.05, respectively. Similarly, the mean PCV±STD of cattle from Dambatta, Gaidam, Garko, Getso, Kafin Hausa, Mai Adua, Maigatari and Wudil, were 33±0.06, 30±0.05, 36±0.05, 30±0.00, 26±0.09, 36±0.08, 36±0.06 and 30±0.07, respectively. On conducting the analysis of the variables, it was found that the differences observed in the mean PCV of the study animals was statistically not significant among the breeds (p=0.0573), sexes (p=1.7958) and sources (p=2.2009) of the animals. Similarly, in all the variables, the t – values obtained (t<5.0) were lower than the t – critical (t=5.0) indicating a non – significant difference with respect to the mean PCV values between camels and cattle.

The frequency of the 9 – points BCS and distribution of trypanosomes in camels from January to December, 2017 is presented in Table 3. Of the 4 emaciated (BCS I) camels screened, 1 (0.4%) was found to be infected. Out of 21 very thin camels (BCS II), 2 (0.8%) were found to be infected. Out of 40 underweight camels (BCS IV), 2 (0.8%) were found to be infected. However, all the 18 thin camels (BCS III), 44 moderate camels (BCS V), 49 good camels (BCS VI), 49 very good (BCS VII), 12 obese camels (BCS VIII) and 3 camels that were very obese (BCS IX) were found to be uninfected. On analyzing these findings using chi – square test of independence, the $\chi 2$ value was found to be 8.607 at 8 degrees of freedom, which was higher than the chi – critical (3.84), indicating a significant difference between the infected camels with BCS 1, II and IV. The p – value obtained was also lower (0.003) than the threshold p – value (0.05), confirming further that the infection rate of camels with BCS 1, II and IV varied significantly.

Of the 560 cattle examined, 21 were emaciated (BCS 1) with an infection rate of 0.2%, 67 were very thin (BCS II) with an infection rate of 1.4%, 131 were thin (BCS III) with an infection rate of 0.9%, 81 were underweight (BCS IV) with an infection rate of 0.7%, 75 were moderate (BCS V) with an infection rate of 0.5%, and, 95 were good (BCS VI) with an infection rate of 0.2%. However, all the 49 cattle with very good BCS (BCS VII), 34 obese cattle (BCS VIII) and 7 very obese cattle (BCS IX) were uninfected. *T. brucei*, *T. congolense* and *T. vivax* were the species encountered, with the most frequent species being *T. vivax*. Similarly, the chi – square value of infected cattle with BCS II was found to be significantly higher ($\chi 2 = 11.279$) than the chi – critical (3.84) at 8 degrees of freedom. Moreover, the p – value (0.0008) was lower than the threshold p – value (0.05), confirming the significant differences of the infection rate with respect to their BCS scores.

The mean PCV of parasitaemic and aparasitaemic camels and cattle is presented in Table 4. The mean PCV of the parasitaemic camels ranges between 14% and 21%, whereas the mean PCV of the aparasitaemic camels ranges between 22% and 31%. However, the mean PCV of parasitaemic cattle ranges between 17% and 23%, whereas the mean PCV of aparasitaemic cattle ranges between 26% and 36%. On analysing the result using Kruskal – Wallis test, which is analogous to a one – way ANOVA that can even specify the pairwise comparisons as post – hoc tests, the values obtained showed that the average PCV values of parasitaemic camels and cattle were significantly lower (P<0.05) compared to the aparasitaemic camels and cattle.

The gel image of amplified ITS – 1 was presented in Plates I to X. In all the plates, lane M is indicating a 100 bp DNA ladder. Lanes Ct 1 and Ct 5 had 500 bp (*T. brucei*), lanes Ct 6, 7 and 8 had 620 bp (*T. congolense*), lane Ct 9 is a mixed infection of *T. brucei* and *T. congolense*, lane 2, 3 and 4 showed negative results (Plate I). Lanes Ct 10 had 480 bp (*T. brucei*), lanes 12, 13 and 14 had 300 bp (*T. vivax*), lanes 15 and 16 showed negative results (Plate II). Lanes Ct 18, 19 and 21 had 500 bp (*T. brucei*), lane Ct 23 had700 bp (*T. congolense*), lanes Ct 17, 20, 22, 24 and 25 showed negative results (Plate III). Lanes Ct 28 and 32 had 300 bp (*T. vivax*), lane 29 had 280 bp (*T. vivax*), lane 30 had 250 bp (*T. vivax*), lanes Ct 26, 27 and 31 showed negative results (Plate IV). Lanes Ct 35, 38 and 39 had 480 bp (*T. brucei*), lanes Ct 36 had 250 bp (*T. vivax*), lane 37 had 280 bp (*T. vivax*), lanes Ct 33, 34, 40 and 41 showed negative results (Plate V). Lane Ct 42 had 300 bp (*T. vivax*), lanes 43, 44, 45, 46, 47 and 48 were the negative results (Plate VI).

Lane Ct 50 is a mixed infection of *T. brucei* and *T. congolense*, lanes Ct 54 and Cm 57 had 250 bp (*T. vivax*), lanes Ct55 had 700 bp (*T. congolense*), lane Ct 56 had 620 bp (*T. congolense*), lanes Ct49, 51, 52 and 53 showed negative results (Plate VII). Lane Cm 59 shows band at 480 bp (*T. brucei*), lane Cm 60 shows band at 250 bp (*T. vivax*), lane Cm 61shows band at 700 bp (*T. congolense*), lane Cm 63 shows band size of 400 bp. (*T. evansi*), lanes Cm 58, 60, 63 and 64 showed negative results(Plate VIII). Lanes Cm 67, 70 and 71 showed bands at 400 bp (*T. evansi*), lanes Cm 68 and 69 showed bands at 250 bp (*T. vivax*), lanes Cm 65, 66, 72 and 73 showed negative results (Plate IX). Lane Cm 74 shows band at 400 bp, suggesting the presence of *T. evansi*, while lane labelled as M is a DNA ladder (Plate X).

Overall, the results revealed an overall infection rate of 48.75%. The most prevalent species detected by PCR was *T. vivax* (18.75%), followed by *T. brucei* (12.50%) and *T. congolense* (8.75%) while *T. evansi* (6.25%) was the least trypanosome detected. The PCR also detected mixed infection involving *T. brucei* with *T. congolense* (2.50%).

The findings from this study shows higher prevalence of trypanosomes in camels and cattle with poor BCS. This supports previous findings (Tehseen *et al.*, 2017) who reported a similar trend in which animals with poor BCS had significantly higher infection rates than those with good BCS, which reaffirms that under conditioned animal may be more vulnerable to infectious diseases because of their compromised immunity. In contrast, quality and plentiful pastures and water sources may contribute in making infected animal to look healthier and thus possess good BCS as evinced in this study by few infected animals. The detection of Trypanosomes in good conditioned animals suggests long endemicity in the sources of the animal and the possibility of a high numbers of chronic cases. These asymptomatic carriers may constitute a source of infection, not only to livestock but possibly also as zoonosis to humans (Takeet *et al*., 2017), and is of significance as it is often fatal if left untreated.

The range of PCV of parasitaemic camels and cattle recorded in this study was found to be within the ranges reported by

DOI: http://doi.org/10.24086/biohs2022/paper.709

several authors such as Abdallah *et al*. (2015), Omer *et al*. (2006) and Majid *et al*. (2002). This shows that, the degree of anaemia, as estimated by measuring PCV, could be used as indicator of Trypanosomiasis in camels or cattle herds. Similarly, although anaemia is not in itself pathognomonic (Abdallah *et al.*, 2015), it still remains one of the useful indicators of animal Trypanosomiasis since the ability of trypanosome infected animal to control development of anaemia is considered as a criterion of Trypanotolerance (Abdallah *et al.*, 2015). Preventive measures may be taken the moment PCV value of an animal decline to 23% and below (Abdallah *et al.*, 2015; Maigari and Dabo, 2018). This is evinced in the present study considering the fact that, the range of PCV of infected camels was between 14% and 21%; and that of cattle was between 17% and 23%.PCV values of <21% to be used as yardstick for decision making on trypanocidal drug intervention even when the animal has not shown symptoms of parasitic infection (Abdallah *et al.*, 2015; Maigari and Dabo, 2018).The variation encountered in the level of PCV recorded in this study might be due to the fact that, several factors may act individually or synergistically in the outcome of anaemia. For example, anaemia may occur during pregnancy if the body of an animal cannot meet its increased need for red blood cells (RBCs). Similarly, certain autoimmune disorders and other conditions may cause animals' body to make proteins that destroy their RBCs, which can lead to anaemia. Heavy internal or external bleeding may lead to loss of blood and consequently causes anaemia.

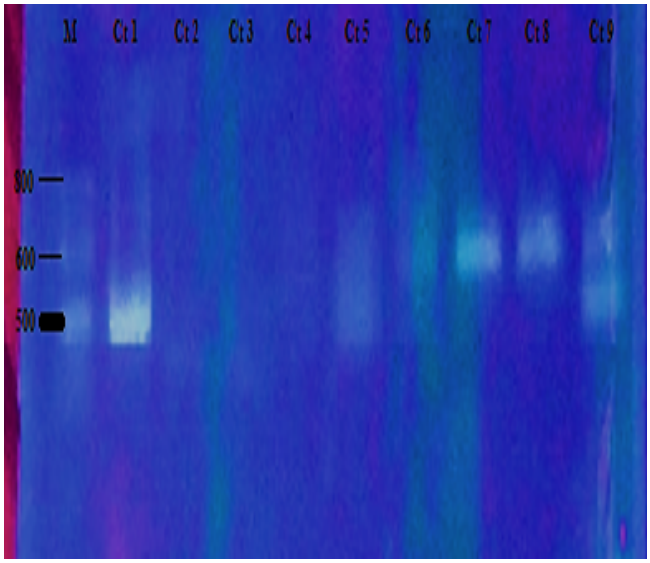

Plate I: Gel Image of Amplified ITS – 1 (Sample 1 to 9)
Lanes 1 and 5 had product size of 500 bp (suggestive of T. brucei), lanes 6, 7 and 8 had product size of 620bp (indicating T. congolense), Lane 9 is a mixed infection of T. brucei and T. congolense, Lane 2, 3 and 4 showed negative result while lane M is the DNA Ladder.

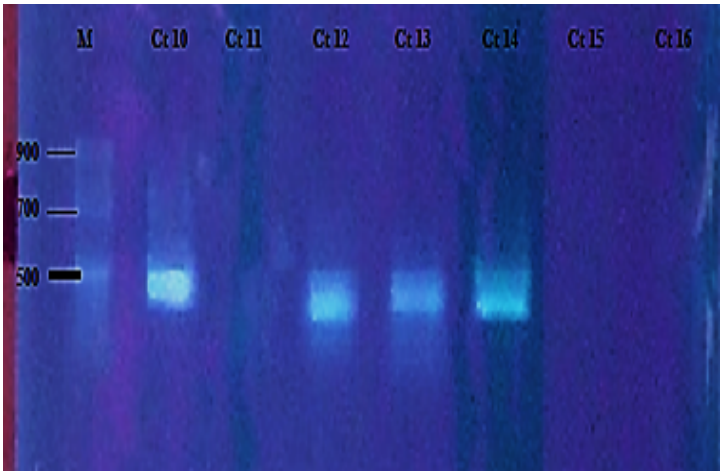

Plate II: Gel Image of Amplified ITS – 1 (Samples 10 to 16)
Lane 10had product sizes of 480 bp (T. brucei), lanes 12, 13 and 14 had product sizes of 300 bp (T. vivax), lanes 15 and 16 showed negative samples while the lane labelled as M is the 100 bp DNA ladder

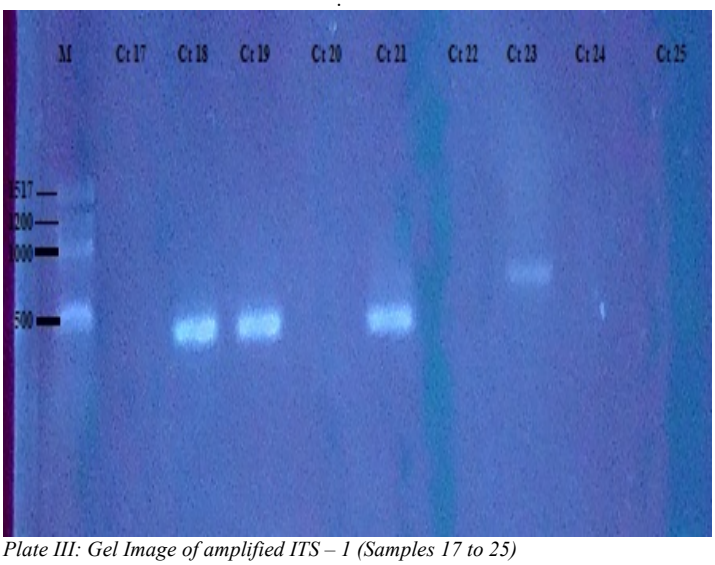

Plate III: Gel Image of amplified ITS – 1 (Samples 17 to 25)
Lanes 18, 19 and 21 had band sizes of 500 bp (T. brucei), lane 23 had a band size of 700 bp (T. congolense) lanes 17, 20, 22, 24 and 25 showed negative samples while DNA ladder is labelled as M

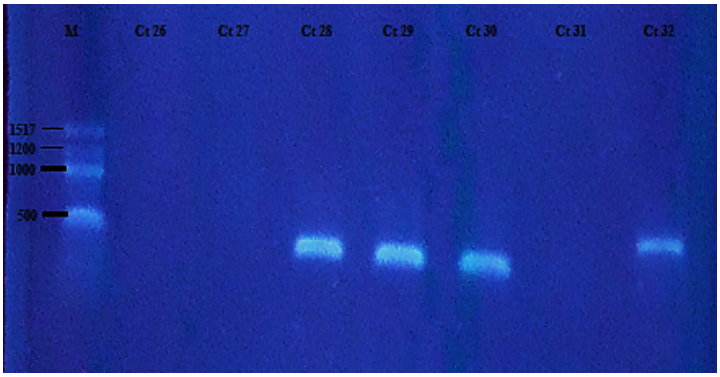

Plate IV:Gel Image of amplified ITS – 1 (Samples 26 to 32)
Lanes 28 and 32 had product sizes of 300 bp (suggestive of T. vivax), lane 29 had product size of 280 bp (T. vivax), lane 30 had 250 bp (suggestive of T. vivax), lanes 26, 27 and 31 showed negative samples while M is the 100 bp DNA ladder.

DOI: http://doi.org/10.24086/biohs2022/paper.709

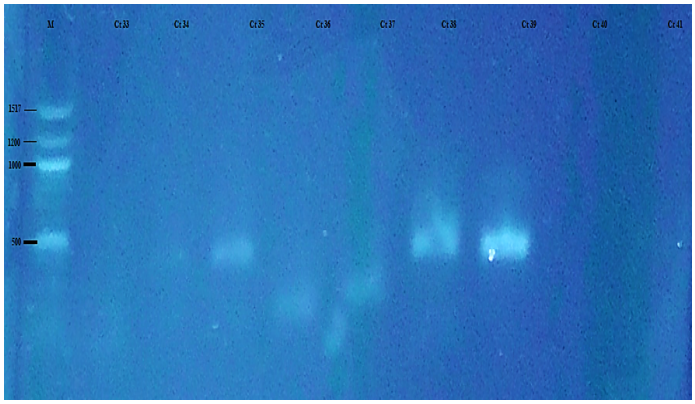

Plate V: Gel Image of amplified ITS – 1 (Samples 33 to 41)
Lanes 35, 38 and 39 had band sizes of 480 bp (T. brucei), lane 36 had product size of 250 bp (T. vivax), lane 37 had product size of 280 bp (suggestive of T. vivax), lanes 33, 34, 40 and 41 showed negative result while lane labelled as M indicates the 100 bp DNA ladder.

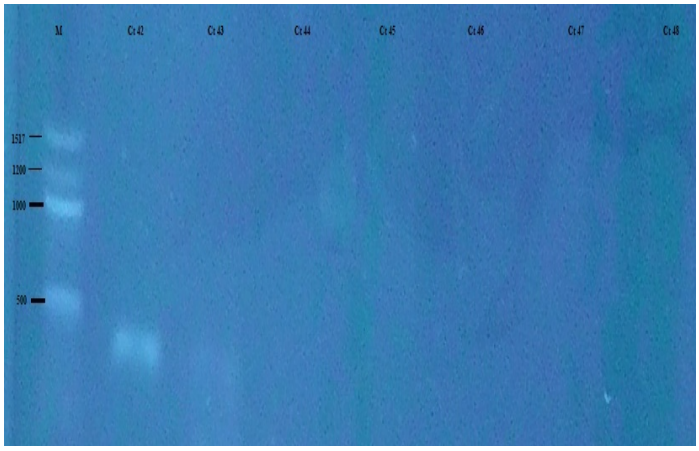

Plate VI: Gel Image of Amplified ITS – 1 (Samples 42 to 48)
Lane 42 had a band size of 300 bp (suggestive of T. vivax), lane 43, 44, 45, 46, 47 and 48 showed negative results, while M indicates a 100 bp DNA ladder.

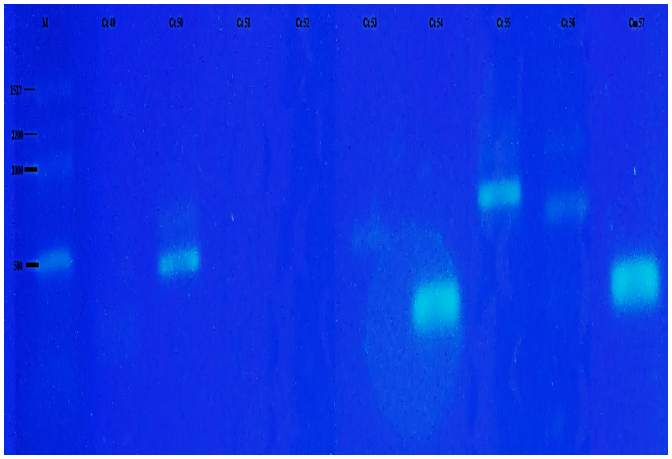

Plate VII: Gel Image of Amplified ITS – 1 (Samples 49 to 57)
Lane 50 is a mixed infection of T. brucei and T. congolense, lanes 54 and 57 had 300 bp (suggestive of T. vivax), lane 55 had band size of 700 bp (T. congolense), lane 56 had band size of 620 bp (suggestive of T. congolense), lanes 49, 51, 53 and 52 showed negative result while M indicates the 100 bp DNA ladder.

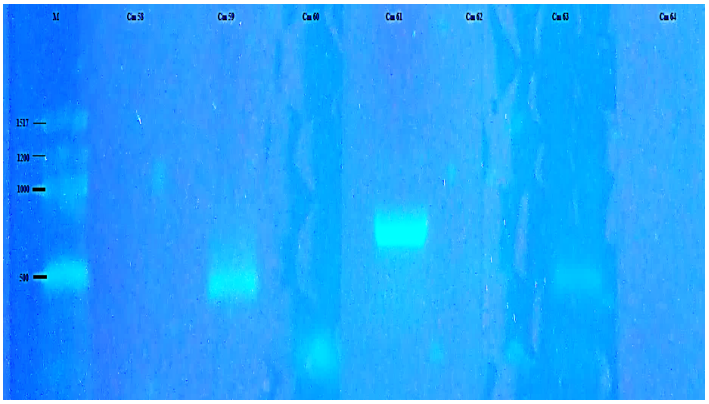

Plate VIII: Gel Image of Amplified ITS – 1 (Samples 58 to 64)
Lane 59 shows band at 480 bp (T. brucei), lane 60 shows band at 250 bp (suggestive of T. vivax), lane 61shows band at 700 bp (T. congolense), lane 63 shows band size of 400 bp. (suggestive of T. evansi), lanes 58, 60, 63 and 64 showed negative results while M is a 100 bp DNA ladder.

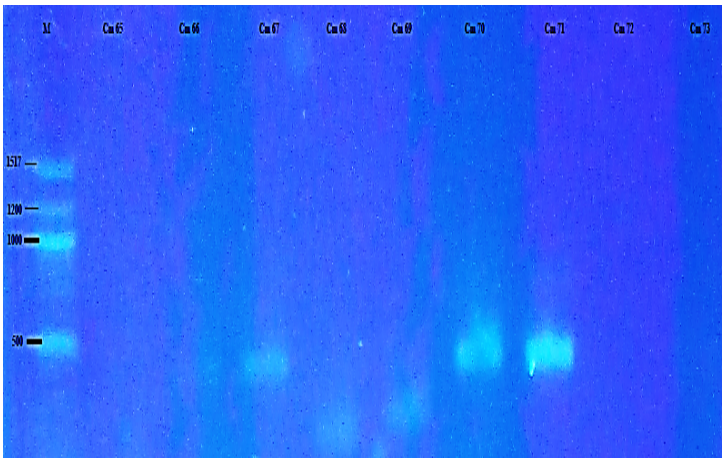

Plate IX: Gel Image of Amplified ITS – 1 (Samples 65 to 73)
Lanes 67, 70 and 71 showed bands at 400 bp (suggestive of T.evansi), lanes 68 and 69 showed bands at 250 bp (T. vivax), lanes 65, 66, 72 and 73 showed negative results while the lane labelled as M is the DNA ladder.

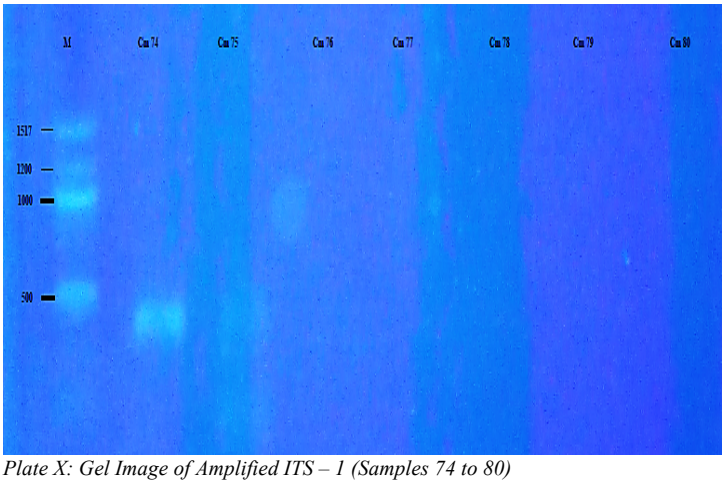

Plate X: Gel Image of Amplified ITS – 1 (Samples 74 to 80)
Lane 74 shows band at 400 bp, suggesting the presence of T. evansi, while lane labelled as M is 100 bp Molecular marker.

CONCLUSION

This study revealed infection rates of 48.75% of at least one of *T. brucei*, *T. congolense*, *T. evansi*, *T. vivax*, and mixed

DOI: http://doi.org/10.24086/biohs2022/paper.709

infection of *T. brucei* and *T. congolense*. Infected animals had poor BCS and that, majority were found to be anaemic. The present study therefore, underscores the relevance of using BCS to increase the quality of diagnosis in the evaluation of trypanosomiasis especially for large scale epidemiological study of animal Trypanosomiasis.

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DOI: http://doi.org/10.24086/biohs2022/paper.709

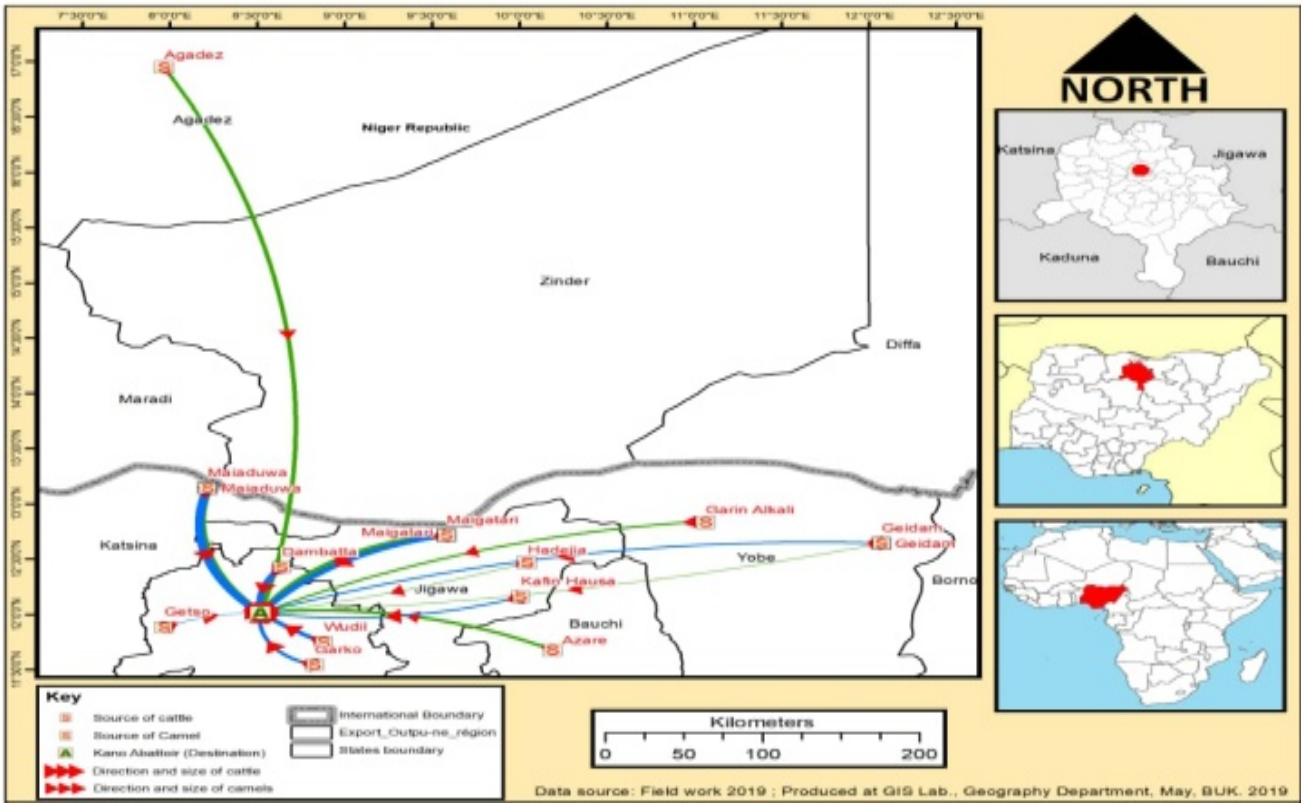

Figure 1: Map Indicating the Sources, Movement and Direction of Camels and Cattle Brought to Kano Abattoir from January to December, 2017 (Source: GIS Lab., Geography Department, BUK, 2019)

DOI: http://doi.org/10.24086/biohs2022/paper.709

Table 1: BCS of Camels and Cattle in Relation to their Breeds, Sex, Age and Sources

Variables	Subjects	No. with good BCS (%)	No. with poor BCS (%)	Total (%)
Breeds	*C. dromedaries*	148(18.50)	92(11.50)	240(30.00)
	*Red Bororo*Cattle	245(30.63)	90(11.25)	335(41.88)
	Sokoto Gudali Cattle	50(6.25)	10(1.25)	60(7.50)
	White Fulani Cattle	115(14.37)	50(6.25)	165(20.63)
	Total	**558(69.75)**	**242(30.25)**	**800(100.00)**
Sex	Male Camels	57(7.13)	61(7.63)	118(14.75)
	Female Camels	91(11.38)	31(3.88)	122(15.25)
	Bulls	305(38.13)	133(16.63)	438(54.75)
	Cows	105(13.13)	17(2.13)	122(15.25)
	Total	**558(69.75)**	**242(30.25)**	**800(100)**
Age	Camels			
	≤1	0(0.00)	0(0.00)	0(0.00)
	>1≤2	27(11.25)	2(0.83)	29(12.08)
	>2≤3	62(25.83)	10(4.17)	72(30.00)
	>3	59(24.58)	80(33.33)	139(57.92)
	Total	**148(61.67)**	**92(38.33)**	**240(100.00)**
	Cattle			
	≤1	7(1.25)	0(0.00)	7(1.25)
	>1≤2	33(5.89)	0(0.00)	33(5.89)
	>2≤3	51(9.11)	50(8.93)	101(18.04)
	>3	319(56.96)	100(17.86)	419(74.82)
	Total	**410(73.21)**	**150(26.79)**	**560(100.00)**
Sources	Agadas	30(12.50)	0(0.00)	30(12.50)
	Azare	15(6.25)	10(4.17)	25(10.42)
	Gaidam	1(0.42)	0(0.00)	01(0.42)
	Garin Alkali	9(3.75)	4(1.67)	13(5.42)
	Gingime	2(0.83)	1(0.42)	03(1.25)
	Hadejia	1(0.42)	0(0.00)	01(0.42)
	Mai Adua	63(26.25)	60(25.00)	123(51.25)
	Total	**148(61.67)**	**92(38.33)**	**240(100.00)**
	Dambatta	129(23.03)	10(1.78)	139(24.82)
	Gaidam	0(0.00)	3(0.53)	03(0.54)
	Garko	7(1.25)	1(0.18)	08(1.43)
	Getso	1(0.18)	0(0.00)	01(0.18)
	Kafin Hausa	3(0.53)	0(0.00)	03(0.54)
	Mai Adua	112(20.00)	65(11.61)	177(31.61)
	Maigatari	84(15.00)	60(10.71)	144(25.71)
	Wudil	74(13.21)	11(1.96)	85(15.18)
	Total	**410(73.21)**	**150(26.79)**	**560(100.00)**

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Table 2: Mean PCV of Camels and Cattle in Relation to their Breeds, Sex, Ages and Sources

Variables	Subjects	No. Examined (%)	Mean PCV±STD	P-value	t – Stat
Breeds	*C. dromedaries*	240(30.00)	26±0.81	0.0573*	3.0295
	Adamawa Gudali	25(3.13)	34±3.32		
	Red Bororo	310(38.75)	33±2.70		
	Sokoto Gudali	60(7.50)	33±4.35		
	White Fulani	165(20.63)	34±1.20		
Sex	Male Camels	118(14.75)	24±0.06	1.7958*	3.0300***
	Female Camels	122(15.25)	28±0.05		
	Bulls	438(54.75)	30±0.55		
	Cows	122(15.25)	34±0.08		
Age	Camels			0.0115**	3.0300***
	≤1	0(0.00)	0.00		
	>1≤2	29	29±0.8		
	>2≤3	72	25±0.8		
	Cattle				
	≤1	07	30±0.5		
	>1≤2	33	28±0.5		
	>2≤3	101	33±0.4		
	>3	419	30±0.8		
Sources	**Camels**			2.2009*	3.0294***
	Agadas	30	31±0.05		
	Azare	25	29±0.05		
	Gaidam	01	30±0.00		
	Garin Alkali	13	23±0.06		
	Gingime	03	26±0.04		
	Hadejia	01	22±0.00		
	Mai Adua	123	26±0.05		
	Maigatari	44	28±0.05		
	Cattle				
	Dambatta	139	33±0.06		
	Gaidam	03	30±0.05		
	Garko	08	36±0.05		
	Getso	01	30±0.00		
	Kafin Hausa	03	26±0.09		
	Mai Adua	177	36±0.08		
	Maigatari	144	36±0.06		
	Wudil	85	30±0.07		

*Mean PCV values along the rows of breeds, sexes and sources of the animals are not statistically different at $p<0.05$

**Mean PCV values of different age groups in both cattle and camels are statistically different at $p<0.05$.

***t-values are lower than t-critical (t=5.00) indicating that, the mean PCV values of camels and cattle in all the observed variables are not statistically different.

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Table 3: Frequency of the 9 – points BCS and Distribution of Trypanosomes in Camels and Cattle (Jan. – Dec., 2017)

Animals	BCS	No. Examined	Infection rates (%)	Species
Camels	I – Emaciated	4	1(0. 42)[a]	*T. evansi*
	II – Very Thin	21	2 (0.83)[b]	*T. evansi*
	III – Thin	18	0	0
	IV – Underweight	40	2(0. 83)[c]	*T. evansi*
	V – Moderate	44	0	0
	VI – Good	49	0	0
	VII - Very Good	49	0	0
	VIII – Obese	12	0	0
	IX - Very Obese	03	0	0
	Total	**240**	**5(2.08)**	***T. evansi***
Cattle	I – Emaciated	21	1(0.18)[d]	*T. vivax*
	II – Very Thin	67	8(1.43)[e]	*T. brucei, T. congolense, T. vivax*
	III – Thin	131	5 (0.89)[f]	*T. congolense, T. vivax*
	IV – Underweight	81	4 (0.71)[g]	*T. congolense, T. vivax*
	V – Moderate	75	3 (0. 54)[h]	*T. vivax*
	VI – Good	95	1 (0.18)[i]	*T. vivax*
	VII - Very Good	49	0	0
	VIII – Obese	34	0	0
	IX - Very Obese	07	0	0
	Total	**560**	**22(3.93)**	***T. brucei, T. congolense, T. vivax***

[a, b, c] Values with different superscript along the rows are significantly different ($\chi 2 = 8.607$, df = 8, p – value = 0.003).
[d, e, f, g, h, i] Values with different superscript along the rows are significantly different ($\chi 2 = 11.279$, df = 8, p – value = 0.0008).

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Table 4: Mean Packed Cell Volume (PCV) and Trypanosome Infection in Study Animals by their Sources

Animals	Sources	No. Examined	Infected (%)	Mean PCV of Infected ± STD	Uninfected (%)	Mean PCV of Uninfected ± STD	P - value
Camels	Agadas	30	0	0	30 (12.5)	31 ± 0.05	
	Azare	25	3 (1.3)	18^{a} ± 0.03	22 (9.2)	22^{b} ± 0.05	0.002
	G/ Alkali	13	1 (0.4)	14^{c}± 0.00	12 (5.0)	24^{d}± 0.06	0.001
	Gaidam	1	0	0	1 (0.4)	30 ± 0.0	
	Gingime	3	0	0	3 (1.3)	26 ± 0.04	
	Hadejia	1	0	0	1 (0.4)	22 ± 0.00	
	Mai Adua	123	1 (0.4)	23^{e}± 0.00	122 (50.8)	24^{f}± 0.05	0.028
	Maigatari	44	0	0	44 (18.3)	25 ± 0.05	
Cattle	Dambatta	139	6 (1.1)	23^{g}± 0.05	133 (23.7)	35^{h}± 0.06	<0.001
	Gaidam	3	0	0	3	30 ± 0.05	
	Garko	8	0	0	8	36 ± 0.05	
	Getso	1	0	0	1	30 ± 0.00	
	Kafin Hausa	3	0	0	3	26 ± 0.09	
	Mai Adua	144	3 (0.5)	26^{i} ± 0.09	174 (31.1)	33^{j}± 0.08	0.0020
	Maigatari	177	8 (1.4)	21^{k}± 0.09	136 (24.3)	34^{l}± 0.07	<0.001
	Wudil	85	5 (0.9)	22^{m}± 0.11	80 (14.3)	34^{n}± 0.07	<0.001

Data in columns represent matched observation where, in each parameter of variables, superscript with different letters indicate significant difference between values, at $p < 0.05$.

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