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EPIDEMIOLOGY OF BOVINE FASCIOLIASIS: PREVALENCE AND HAEMATO-BIOCHEMICAL ALTERATIONS IN KATSINA ABATTOIR NORTH WESTERN NIGERIA

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ABSTRACT

Bovine fascioliasis, caused by liver flukes *Fasciola hepatica* and *Fasciola gigantica*, significantly affects cattle health and production globally. This study evaluated the prevalence and haemato-biochemical changes associated with bovine fascioliasis in 134 cattle at Katsina Central Abattoir. Using the sedimentation technique, faecal samples revealed a 3.73% infection rate, with females showing a higher prevalence (4.55%) than males (2.17%), though not statistically significant ($P > 0.05$). The age group 2-3 years had the highest prevalence (25.00%), with significant differences among age groups ($P < 0.05$). Among breeds, Wadara had the highest prevalence (20.00%) compared to White Fulani (4.93%), with a significant difference ($P < 0.05$). Medium-conditioned cattle showed the highest prevalence (6.67%) versus good-conditioned ones (1.37%) with significant difference ($P < 0.05$). Infected cattle exhibited significant reductions ($P < 0.05$) in packed cell volume (PCV), haemoglobin (Hb), and total erythrocyte count (RBC), as well as decreases in white blood cell count (WBC), mean cellular volume (MCV), and mean cellular haemoglobin concentration (MCHC). Biochemical analysis indicated elevated alanine transaminase (ALT), aspartate transaminase (AST), alkaline phosphatase (ALP), and total bilirubin (TB) levels ($P < 0.05$), with reduced albumin (ALB), total protein (TP), and conjugated bilirubin (CB) levels ($P < 0.05$). These results highlight the significant impact of bovine fascioliasis on cattle health in Katsina State, emphasizing the need for effective control strategies.

Keywords: Prevalence, Bovine, Fascioliasis, Haematology, Biochemical parameter

INTRODUCTION

Bovine fascioliasis is a parasitic disease that greatly affects the health and production of cattle globally. It is caused primarily by liver flukes namely;*Fasciola hepatica* and *Fasciola gigantica* (Hayward, *et al.,* 2021). Cattle are the ultimate host in the intricate life cycle of these trematodes, which also involve snail and mammalian hosts (Saijuntha, *et al.,* 2021). Geographically, the prevalence of bovine fascioliasis varies, but it is still a major concern in many areas, especially those where the intermediate host, freshwater snails, have favourable environmental circumstances (Siles-Lucas, *et al.,* 2021).

Infected cattle with this parasite infection experience a variety of haematological and biochemical changes that contribute to both subclinical and clinical symptoms (Villa, *et al.,* 2021). Haematology is the study of the numbers and morphology of the blood's cellular components, such as the red blood cells (erythrocytes), white blood cells (leucocytes), and platelets (thrombocytes), and it makes use of the findings to diagnose and track disease (Wajihah, *et al.,* 2023).According to Chikhaoui, *et al*., (2023) biochemical changes include variations in different blood components and serum parameters, whereas haematological changes relate to changes in the makeup of the blood. Comprehending these alterations is crucial for the prompt identification and handling of bovine fascioliasis, in addition to evaluating the general well-being of impacted animals (Caravedo, and Cabada, 2020).

According to Abdullah (2023), the life cycle of *Fasciola* entails the discharge of infectious larvae (metacercariae) onto vegetation, which are then consumed by cattle when they graze. After being consumed, the parasites move through the gastrointestinal tract, arrive in the liver, and settle in the bile ducts (Peters, *et al.,* 2021). The liver parenchyma and bile ducts are harmed by the liver flukes' feeding on blood and tissue (Kahl, *et al.,* 2021). Haematological and biochemical studies can identify a series of physiological alterations brought on by the host's immune system's reaction to the parasites as well as the direct harm the flukes inflict (Lalor, *et al.,* 2021).

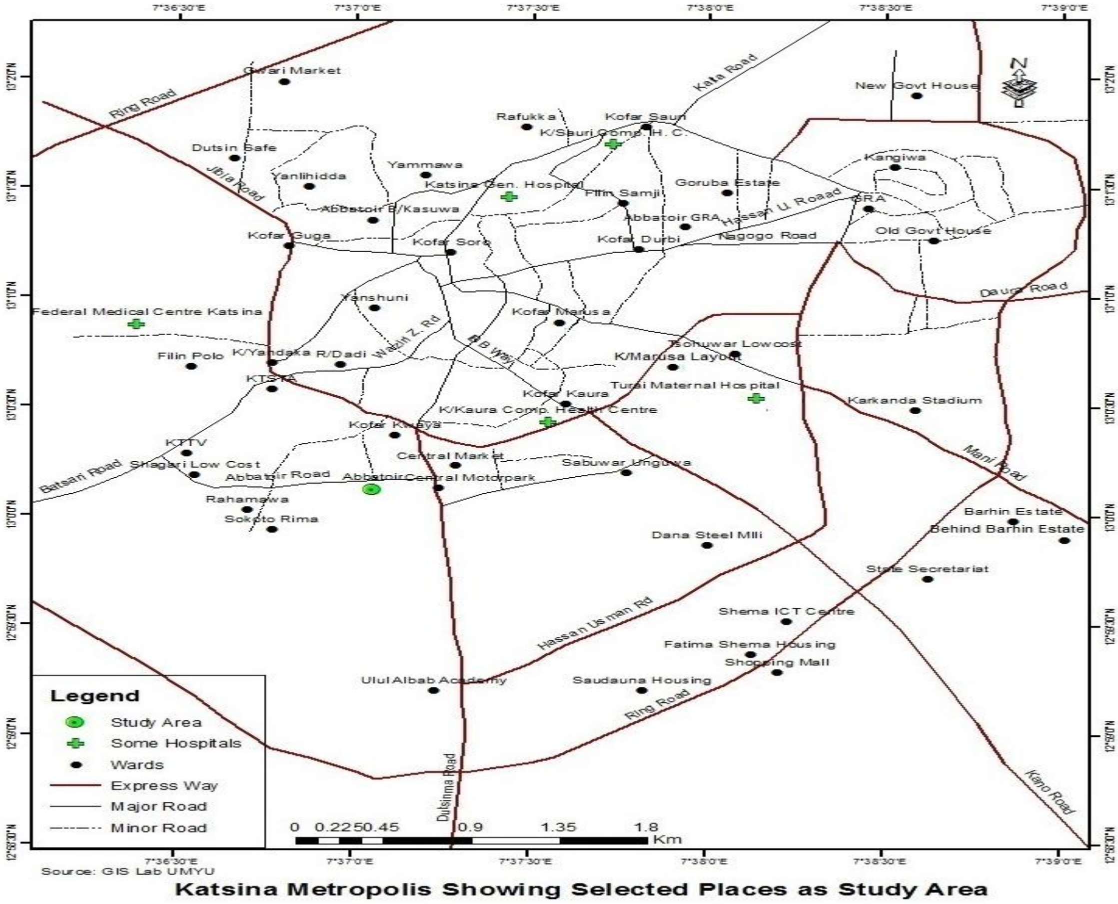
It has been discovered that the livestock industries have suffered significant financial losses as a result of animal deaths, weight loss from the carcass, decreased milk yield, liver damage, decreased production, subpar performances, and animal exposure to other diseases because of secondary complications, and high treatment costs (Mequaninit, and Mengesha, 2021). Few studies have been documented on the prevalence, haematological and biochemical alterations due to naturally acquired bovine fascioliasis in Nigeria. Therefore, this research aims to explore and elucidate the prevalence, haematological and biochemical alterations associated with bovine fascioliasis. The findings from this research will further pave way for veterinarians, researchers, and livestock managers to enhance their ability to diagnose and manage this parasitic infection effectively. Moreover, the insights gained from studying the haematological and biochemical aspects of bovine fascioliasis will contribute to the broader understanding of host-parasite interactions and provide a foundation for developing strategies to control and prevent the spread of this economically significant disease.

MATERIALS AND METHODS

Study area

This study was carried out in the central abattoir of Katsina town, Katsina State, Nigeria. Katsina town, is the capital city of Katsina state as well as Headquarters of Local government

Area, Katsina state, Nigeria.Katsina town is approximately located on latitude 12^o N and longitude 7^o E. (Saheed, *et al*., 2019). The city is well known as a centre for Agriculture, producing both food and cash crops comprising groundnut, cotton, hides, millet, maize and guinea corn. The city is largely inhabited by the Haausa/Fulani ethnic groups (Saheed, *et al*., 2019). The climate of the area comprises the Sudan savanna vegetation which is characterized by scattered trees, seasonal rainfall which lasts for about five months annually (June to October) and distinct harmattan season which spans from November to February each year, with reduced temperatures, haze and low humidity (Thor West *et al.,* 2020).



Source: GIS Lab UMYU

Katsina Metropolis Showing Selected Places as Study Area

Figure 1: Map of Katsina Metropolis showing the study Area

Collection and examination of faecal samples

The samples were collected from the rectum or from the fresh stoolof the sampled cattle on the ground, in plastic carved sample containers for qualitative and quantitative microscopic examination of *Fasciola*eggs. Faecal samples were processed using faecal sedimentation method as described by (Rizwan, *et al.,* 2021). Samples that are not processed within 24 hours from collection were stored in a refrigerator at 4^0 C. During every faecal sampling, information on sex, breed, approximate age and body condition of the individual animals were recorded (Rizwan, *et al.,* 2021).

Collection of Blood sample

Samples were collected over a period of 12 weeks. During slaughtering, 134 blood samples were collected from Katsina central slaughter house into evacuated EDTA container for haematological analysis and stored at 4°C and into serum separating tubes for biochemical analysis. Sera were frozen in plastic tubes at −20°C. Samples were analyzed within 12 hours. The samples were transported to Haematology Laboratory at general hospital Daura Katsina State for haematological analysis and postgraduate research laboratory at Umaru Musa Yar'adua University Katsina for Biochemical analysis (Brahmbhatt,*et al.,* 2021).

Haemato-biochemical studies

Blood and serum samples were collected from the*Fasciola* infected and non infected animals for routine haematological and serum biochemical analysis. A total of four (5) blood and serum samples from *Fasciola* infected and one hundred and thirty (130) samples from healthy animals were collected during the study and analyzed. Haematological analysis of the blood samples was done by using Sysmex particle counter (Model 210) and biochemical analysis of the serum samples were done by withcommercial kit (Randox, UK) respectively (Brahmbhatt,*et al.,* 2021).

Data Analysis

The data obtained were analyzed using SPSS version 16. The Chi-square test was used to assess the significance of risk factors such as sex, age, body condition score, and breed, while a Student's t-test was employed to analyze the haematological and biochemical parameters of *Fasciola*-infected and non-infected samples. Values of $P \leq 0.05$ were considered significant. Results were expressed as means ± SD.

RESULTS AND DISCUSSION

The results of coprology showed that, out of the One Hundred and thirty four(134)cattle examined, 5 were infected, representing a prevalence of 3.73 percent, while One hundred and twenty nine (129) were not infected, with a prevalence of 96.3 percent (Table 1). Coprology's low prevalence of 3.73% is in line with findings from some previous researches by Akpabio (2014) and Okonkwo *et al.*(2023), who found low prevalence rates of 1.7% and 13.5% respectively. It is not, however, consistent with the results of Njoku-Tony (2011), Adedokun *et al.* (2008) and Abraham and Jude (2014), who found higher incidences ranging from 23.3% to 75% in the southern region of the Nigeria. The high prevalence in the southern part of Nigeria may be related to variations in the climate and dense vegetation, which would favor the growth of the snail vector and raise the infection rate. However, the results of researches conducted by Soba *et al.*(2023) and Njobdi *et al.*(2023), although done in Northern Nigeria, reported higher prevalences in Gombe (74.3%) and Benue (48.2%) states respectively, which are at odds with the low prevalence rate reported in this study. The variances in sample size, livestock abundance and climate in various areas could all be contributing factors to the discrepancies in prevalence.

The results of sex-specific distribution of the infection showed that females had a higher prevalence, representing 4.55 percent, compared to their male counterparts with a prevalence of 2.17 percent (Table 2). The sex distribution analysis results showed that the prevalence was higher in female cattle than in male cattle. The increased susceptibility of females to the illness could be the reason for this. This conclusion is consistent with other research findings (Njok-Tony, 2011; Ardo *et al.,* 2013; Uwalaka *et al.,* 2019; Shima *et al.,* 2015; Banwo *et al.,* 2023; Okolugbo *et al.,* 2023; Sabo *et al.,* 2023). It does, however, conflict with the results of some other researchers, like Oladele-Bukola and Odetokun (2014), Adangs *et al.,* (2015), Aliyu *et al.,* (2014) and Ikenna-Ezeh *et al.,* (2019), who found higher prevalences in males.This discrepancy could be explained by the custom of keeping a higher female-to-male ratio—particularly when it comes to the ratio of cows to oxen—and by keeping female animals around for the purpose of breeding and milk production.

The results of age-specific distribution of the infection revealed that the age group 2-3 years old, had the highest prevalence, representing 25 percent, followed by 3-4 years with 6.89 percent. The least prevalence was recorded in the age group 5 years and above with 1.74 percent. No prevalence was recorded in the age groups 0-1 year and 4-5 years, respectively (Table 3).Additionally, the study found a greater frequency in the age range of 2-3 years, which is in line with the findings of Uwalake *et al.*(2019) and Aliyu *et al.*(2014), who also found that young calves had a higher prevalence than adult cattle. This goes against the results of some other studies (Ardo *et al.*, 2013; Adang *et al.,* 2015) that showed a higher prevalence in adults than in young animals. Young cattle may be more susceptible to the high incidence because of their exposure to contaminated pasture, particularly when the pasture is chopped and fed to them.

The results of breed-specific distribution of the infection showed that Wadara had the highest prevalence, representing 20 percent, and the least prevalence was recorded in White Fulani (4.93%). Zero prevalence was recorded in Red Bororo and Azwak, respectively (Table 4). In addition, the research revealed that the Wadara and White Fulani breeds had a significant prevalence rate of infection, whereas the Red Bororo and Azwak breeds showed no infection. This implies that some breeds are more prone to contracting the fascioliaisis than others, which may be related to how frequently these types are slaughtered at the slaughterhouse. This vulnerability may also be linked to variations in extrinsic (environment and management techniques) and intrinsic (genetic, physiological and immune) host variables.This result is in conflict with the findings of Soba *et al.* (2023) and Banwo, *et al.* (2023), who showed high prevalence in Sokoto Gudali and Red Bororo, but it is consistent with the findings of a study conducted by Ikenna-Ezeh *et al.*(2019), who observed no infection in Red Bororo and a high prevalence in White Fulani.

The results of body condition score from this study, showed that those with medium condition revealed a high prevalence representing 6.67 percent, followed by those with poor condition(6.45%) and the least prevalence was recorded in those with good body condition (1.37%). The result was shown on (Table 5).Our findings are in line with the findings of Meharenet and Shitu (2021), who found that the medium conditioned animals were more infected in Ethiopia. However, our findings were in contrast to that of Uwalaka *et al.*(2019), who reported a higher prevalence among poor conditioned animals in Abia state, Nigeria. The lowest prevalence of infection is consistently recorded among good physical conditioned animals. This suggested that the prevalence of fascioliasis is closely related to body condition, with the medium and poor conditioned being more prone to infection than the good.

The results of the haematological indices determined for *Fasciola*-infected and non-infected cattle indicated that PCV, Hb, and RBC were lower in the infected cattle than in the non-infected ones. On the other hand, WBC, MCV, MCH, and MCHC were higher in the infected cattle compared to the uninfected animals. Statistical analysis revealed highly significant differences between the PCV, Hb, and RBC of the infected and non-infected cattle (p<0.05), and significant differences between the WBC, MCV, and MCH of both groups (p<0.05). However, no significant differences were observed between the MCHC of the infected cattle and the uninfected ones (Table 6).In comparison to the uninfected cattle, the haematological changes among the infected cattle, resulted in a substantial drop in the mean values of WBC, RBC, HGB, HCT, and MCH and a significant increase in the mean values of MCV and MCHC. The present discovery aligns with multiple other studies that have documented a decline in the same parameters' (Wyk *et al.*, 2012; Egbu *et al.,*2013 and Brahmbhatt *et al.,* 2021). But the lower values of RBC, WBC, HGB, and HCT in infected cows may be the result of an adult fluke's blood-sucking behavior as well as blood loss from hemorrhages brought on by the immature parasite's extensive migration through the bile duct and liver parenchyma as earlier suggested (Etim *et al.,* 2014 and Brahmbhatt *et al.,* 2021).The present study's findings regarding the significant increase in MCHC in infected cattle are consistent with those of Brahmbhatt *et al.* (2021).

The differential counts of Fasciola-infected cattle and the uninfected ones revealed a perceptible increase in the neutrophils of the infected cattle and a clear decrease in the levels of eosinophils, monocytes, lymphocytes, and basophils in the infected cattle. The differences in the neutrophils, eosinophils, monocytes, and lymphocytes of both groups were highly significant at $P \leq 0.05$.According to the current findings; peripheral blood from infected animals had higher neutrophil counts than from uninfected animals, suggesting that neutropilia developed during the *Fasciola* infection of cows. A substantial rise in monocytes, basophils, and eosinophils is indicative of a parasite infection. This is consistent with a research finding by Brahmbhatt *et al.* (2021), which reported that between infected and non-infected Gir cattle, there were low levels of eosonophils, monocytes, and basophils and high levels of neutrophils. However, these results conflict with those of Egbu, (2013) and Matanovic *et al.*(2007), who found that the infected group had significantly higher neutrophil and eosinophil counts compared to the uninfected, and that the infected group had significantly, lower levels of monocytes and lymphocytes.The variations in the differential counts could be the result of a toxin-mediated lesion of the bone marrow or a body defence mechanism against the obstructive effects of *Fasciola*as earlier suggested (Egbu *et al.,* 2013).

The results of the biochemical changes indicated that the means and standard deviations of ALT, AST, ALP, and TB were higher in the infected cattle than the uninfected ones, while ALB, TP, and CB were higher in uninfected cattle than their infected counterparts (Table 8).An additional sign of internal organ injury is observed from the results of biochemical analysis. ALB, TP (total protein), and CB levels considerably decreased among the infecrted cattle ($p<0.05$) in the current study, while ALT, AST, ALP, and total bilirubin levels increased also among the infected ($p<0.05$). These discoveries agreed with the results from other researches (Brahmbhatt *et al.*, 2021; Ellah *et al.*, 2014; Kitila Megersa, 2014). Higher AST and ALT activity is typically seen in cases of *Fasciola* infection because the parasite damages the liver through migratory activity, which in turn triggers the activation of inflammatory cells that produce fibrosis and necrosis and increases AST and ALT activity.The cause of the hypoproteinemia is a severe liver infection that destroyed the liver parenchyma and drastically changed the protein value. Reduced albumin production brought on by liver injury could be the cause of the hypoalbuminemia. Biliary blockage, values, and cholangitis are caused by fasciolosis infections. Reduced albumin production brought on by liver injury could be the cause of the hypoalbuminemia. Cholangitis, biliary obstruction, fibrosis and loss of hepatic tissue, and anemia are all caused by fascilococcal infections as earlier reported (Brahmbhatt, 2021).

CONCLUSION

The study reveals that bovine fascioliasis poses a significant health and productivity challenge for cattle in Katsina state, evidenced by a 3.73% prevalence rate and notable haemato-biochemical alterations in infected cattle. The higher infection rates observed in females, younger age groups, Wadara breed, and medium-conditioned cattle suggest specific vulnerabilities within these subgroups. Hematological impacts, including reduced PCV, Hb, RBC, WBC count, MCV, and MCHC, alongside altered leukocyte profiles, indicate compromised blood health in infected cattle. Additionally, the biochemical changes elevated ALT, AST, ALP, and TB levels, and reduced ALB, TP, and CB levels highlight liver function disruption in infected animals. These findings underscore the urgent need for targeted control and management strategies to mitigate the adverse effects of bovine fascioliasis.

Table 1: Prevalence of Fasciolisis in Katsina Abattoir

Cattle	No. Examined	Prevalence (%)
No. Positive	05	3.73
No. Negative	129	96.27
Total	134	3.73

Table 2: Sex Specific Distribution of Fascioliasis in Katsina Abattoir

Sex	No. Examined	No. Infected	Prevalence (%)	P value
Male	46	01	2.17	0.49
Female	88	04	4.55	
TOTAL	134	05	3.73	

($P<0.05$)

Table 3: Age Specific Distribution of Fascioliasis in Katsina Abattoir

Age group (years)	No. Examined	No. Infected	Prevalence (%)	P value
0-1	00	00	00	0.086
2-3	04	01	25	
3-4	29	02	6.89	
4-5	42	00	00	
>5	59	01	1.74	
TOTAL	134	05	3.73	

($P<0.05$)

Table 4: Breed Specific Distribution of Fascioliasis in Katsina Abattoir

Breed	No. Examined	No. Infected	Prevalence (%)	P value
WF	81	04	4.93	0.17
RB	38	00	00	
WD	05	01	20.00	
AZ	10	00	00	
TOTAL	134	05	3.73	

($P<0.05$)

Table 5: Body Condition Score Specific Distribution of Fascioliasis in Katsina Abattoir

Bcs	No. Examined	No. Infected	Prevalence (%)	P value
Good	73	01	1.37	0.32
Medium	30	02	6.67	
Poor	31	02	6.45	
Total	**134**	**05**	**3.73**	

(P<0.05)

Table 6: Mean±SD of heamatological changes between infected and un infected cattle at Katsina abattoir

Haematological Parameters	Infected(n=5)	Range	Uninfected(n=5)	Range
WBC X 10^3/UL	4.8 ± 3.18^{a}	9600 – 17500	6.7 ± 1.13a	6300 – 12100
RBC X 10^6/UL	6.3 ± 4.64^{a}	3.0 – 4.89	7.4 ± 0.45^{b}	5.51 –8.9
HGB (g/dl)	9.8 ± 8.70^{a}	5.7 –9.6	13.2 ± 3.39^{b}	8.5 –13.6
HCT (%)	27.8 ± 21.43^{a}	19.5 –29	36.6 ± 9.83^{b}	30 – 50
MCV (μm^3)*	43.5 ± 1.97^{a}	61 –69	48.8 ± 10.27^{a}	46 –56
MCH (pg)*	14.3 ± 3.26^{a}	17 –22	17.6 ± 3.50^{a}	12 –18
MCHC (%)	32.8 ± 6.00^{a}	28 –36	36.2 ± 0.44^{a}	26 –33

Values in rows with different superscripts are significantly different (P<0.05).
SD=Standard deviation
^{b} *n* Size of sample

Table 7: Mean±SD of differentials changes between infected and un infected cattle at Katsina abattoir

Differential counts (%)	Infected(n=5)	Range	Uninfected(n=5)	Range
Lymphocytes	32.8 ± 1.34^{a}	29 – 68	46.4 ± 12.94a	45 – 63
Esonophils	8.6 ± 4.03^{a}	2 – 8	18.2 ± 9.76^{a}	0.49 – 1.11
Neutrphils	77.6 ± 31.68^{a}	36 – 59	38.5 ± 8.56^{b}	26 – 40.5
Monocytes	4.3 ± 2.02^{a}	0.4 – 3	9.1 ± 4.88^{b}	0.83 – 8.58
Basophils	2.1 ± 1.01^{a}	00	5.7 ± 0.80^{a}	00

Values in rows with different superscripts are significantly different (P<0.05).
SD=Standard deviation
^{b} *n* Size of sample

Table 8: Mean±SD of biochemical changes between infected and un infected cattle at Katsina abattoir

Biochemical parameter	Infected cattle	un infected cattle
ALT	62.93±18.86	61.68±30.66
AST	203.53±97.60	78.93±2.72
ALB	7.69±13.23	31.51±8.10
ALP	43.38±16.70	32.891±17.84
TP	43.38±16.70	49.66±40.40
CB	0.5±0.30	1.08±0.73
TB	5.61±3.20	2.61±0.28

ALT = Alanine aminotransferase, AST = Aspartate aminotransferase, ALB= Albumin ALP = Alkaline phophatase, TP = Total protein, CB= Conjugated bilirubin and TB = Total bilirubin

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