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Buffalo Parasitology: Unraveling Infections in the Digestive Scheme

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Abstract

Buffalo are big herbivores that belong to the Bovidae family; the study of parasites that impact themwhich is known as buffalo parasitology. Some intriguing tendencies in the occurrence of parasites were discovered in the research, which included 100 buffalo. The positive rate for female buffalo was 30%, somewhat higher than that of male buffalo (27%). An age-specific research found that the occurrence was more elevated in buffalo older than three years (38% vs. 30%) than in buffalo younger than one to three years (30%). Parasite species distributions showed varying levels of prevalence, with Strongyles accounting for 30% of all infections.Furthermore, monthly fluctuations were seen in the number of positive cases; December had the most excellent positivity rate (83.33%).In addition, the research examined the three categories of parasite intensity (50-200, 201-400, and 401-600). Strongyloides spp., Amphistome, and T. vitulorum were found at varying frequencies throughout these ranges, demonstrating the need to consider intensity levels in parasitological studies. The findings help shed light on the ever-changing field of buffalo parasitology and pave the way for more targeted strategies for administration and treatment. A comprehensive view of buffalo health is possible by comprehending the interactions between sex, age, months, and intensity levels. This viewpoint helps make well-informed decisions for efficient parasite control and herd management.

Keywords: Buffalo, Gastrointestinal (GI), Bovine Tuberculosis (BTB), Disease, Parasitology

INTRODUCTION

A number of potential strategies exist for mitigating the effects of nematode infections. Even if grazing control measures aren't always doable, they work when combined with anthelmintic treatment or used. The emergence of drug-resistant parasite populations and the growing concern about drug residues in food and the environment pose a danger to the efficacy of anthelmintic treatment, which has been very effective until this moment (1). Buffaloes are among many mammalian species that can get the disease complex known as animal trypanosomiasis (AT), which is caused by *Trypanosoma spp*. However, other parasite strains, like those from the African buffalo, produce minor parasitosis and parasitemia, die, and not spread between cattle (2). Wherever susceptible cattle come into contact with vector ticks that have been infected on buffalo, the principal animal carrier hosts, and this strain is known to produce more severe clinical condition known as Corridor Disease. These specific strains were first identified based on their distinct clinical presentation, which varies from typical Epidermal Cell Fates (ECF). Molecular and antigenic evidence showing commonalities between the two strain populations led to the abolition of this name (3). Many animals have the latent or carrier state of this virus, which means they don't show any symptoms but might have an impact on their productivity. The bites of insect vectors allow these parasite carriers to infect vulnerable buffaloes. There has been an uptick in clinical cases, but they are relatively low (4). Diseases in wild animals have not received the same level of attention those in domesticated and producing animals due to the inherent challenges in investigating these populations. Illnesses in domestic animals are studied because they are easier to sample and have a significant impact on the economy (5). However, a better knowledge of wildlife illnesses can help with the management of critical zoonoses and livestock diseases. For example, studies on bovine tuberculosis (BTB) and GIhelminths in buffalo

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(Synceruscaffer) demonstrated that treating co-infected buffalo with an anthelminthic agent increased the likelihood of BTB transmission to susceptible hosts, such as cattle, and prolonged host survival times (6). To control similar illnesses in domesticated animals, it is helpful to understand how infections work in nature. A lack of balanced knowledge can lead to the neglect of interrelated diseases that affect humans, domesticated animals, and wild animals. To discuss the health consequences of these infections and the factors that contributes to the dynamics of subclinical disease (7). Protozoan parasites belonging to the genus Cryptosporidium produce a severe diarrheal illness known as cryptosporidiosis. Among many parasites that infect farmed buffalo and cattle, these particular species rank high.

Cryptosporidium causes substantial economic losses due to the infections it causes in different cattle, as seen in its epidemiological profile (8). The buffalo is a vital part of the rural economy in Nepal since it provides milk, meat, manure, and drought power, making it one of the most significant domestic livestock species. (Bubalusbubalis), an Asian mammal, is vital to farmers' economics. Buffaloes are helpful for their milk, meat, and draft facilities but also for the fuel and fertilizer they produce, the hides they have, the horns and stubble they grow, and the organic waste products they produce, such as urine and feces (9). Although they move slowly, the buffaloes make no fuss as they labor. Buffalo have a longer working life than cattle, often exceeding the wild water buffalo, which is on the verge of extinction. All domestic variations and breeds can trace their ancestry back to a single common progenitor. Buffaloes are referred as the "living factor of the East" due to their exceptional pulling and draft capacities (10).The study (11) described that Updated epidemiological data is needed to understand water buffalo GI parasite etiology and vectors. It examined marshland buffalo GI parasite prevalence and risk factors. Buffaloes' high GI parasite infection rate indicates endogenous disease. The study(12) investigated the histopathological alterations and metabolic markers, such as oxidative stress indices, that occur in newborn buffalo calves as a result of a natural infection with Cryptosporidium parvum. Infected calves' intestinal and abomasal mucosa exhibited architectural abnormalities such as rounded margins and villous atrophy. The glands were significantly enlarged and packed with necrotic material, and there were many cryptosporidia at various phases of their life cycle. The study (13) found that GIP is quite common in Indian buffaloes, which might explain why Indian buffaloes had poor output. To combat this, researchers and farmers must use scientific, managerial, and therapeutic approaches backed by constant monitoring. The study (14) described the abundance of studies on buffaloes published in Bangladesh; the subject of a comprehensive assessment. To fill in any gaps and give suggestions for future academic and research plans on buffalo development, this study analyzed and summarized the existing inland research papers on buffaloes. The study (15) described the buffalo-based in-origin vaccination against Theileriaparva, which has the potential to "breakthrough" the immunity that is developed in cattle as a result of the infection and treatment process.

Nevertheless, there have been no reports of similar "breakthroughs" in the northern region of Tanzania, where the use of Institute of Technology and Management (ITM) in pastoralist cattle has been going for a long time and is prevalent where the Cape buffalo (Synceruscaffer) is also native. The author (16) suggested a brief overview detailing the prevalence of *G. duodenalis* and *Cryptosporidium spp* worldwide in buffaloes, as well as the genetic methods used to identify the genotypes and species/assemblages of these protozoa. To learn more about the epidemiology of *G. duodenalis* and *Cryptosporidium spp.* genetic investigations of isolates from human, animal, and environmental sources have been carried out on the species Cryptosporidium parvum in buffaloes. The study (17) provided a collection of single nucleotide polymorphisms (SNP) collected from thirteen virtually complete mitogenomes. These strains include the strains that were utilized in the inventory of live vaccines. In the coding and non-coding regions, they discovered eleven SNPs that were not preferentially distributed, all of them are synonymous, with the exception of two located in the cytochrome b gene of the buffalo-derived strains.The author (18) investigated the relationship between the faecal egg counts used to determine the gastrointestinal nematode burden (strongyles and Strongyloides spp.) and three dimensions of the social environment of elephants: the size, sex ratio, and individual solitary behavior after adjusting for personal identification, human sampler bias, sex, age, origin, and the duration since the previous deworming treatment. The study (19) described discussions encompass a wide range of topics, including the following: the role of parasites in natural selection, the influence of biodiversity and human activities on host-parasite relationships, the occurrence of parasites in different geographical areas, and the investigation of the evolution of parasites are topics that are being studied.

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MATERIALS AND METHODS

Buffalo parasitology is the study of parasites that impact the buffalo GI tract, with an emphasis on elucidating infections in that system. Many different kinds of parasites, such as protozoa and helminths (worms), attack the digestive tract. If we want buffalo herds to be healthy and productive, we need to know what causes these diseases**.**

Dataset

For the present study, faecal samples from 100 buffaloes were gathered in India across several estimations in 2021 and 2022 to determine the prevalence of GI helminths in these animals**.** Following a visual inspection for consistency, color, and the presence of adult worms, the rectum faeces samples were subjected to processing and amplification using the direct smear method, Willi's flotation, and sedimentation procedures. Parasite ova were recognized by their outward appearance. To quantify the level of parasite infection (EPG) using McMaster's approach, examine the feces. The number infected animals was determined by calculating the proportion of positive samples out of all pieces that were tested.

Sampling procedures

Among the several communities that contributed buffaloes, one hundred were chosen at random. They took considerable care to detail each participant's age, sex, and nutritional state. Period was used to categorize buffaloes into three groups: calves (less than three years old), young (12-3 years old), and adults (five years and beyond). Based on their nutritional state, buffalo were further categorized as poor (n=40) or medium (60), with 50 males and 50 females each. The buffaloes were finally classified into two groups, one for the rainy season (n=50) and another for the fall (n=50), according to the season in which their feces were collected. Examining the teeth allowed to calculate the age of the buffaloes.

The majority of buffalo were raised using a free-range method. Therefore, the animals were secured prior to collection either in the rectal area or immediately after feces was used to gather samples. For every buffalo, researchers concluded about 20–25 grams of excrement. Carefully knotted and appropriately numbered polycarbonate vials containing 10% formalin were used to store each sample. The laboratory was consulted for an examination of the correctly labeled and numbered plastic vials holding fecal samples that had the necessary information.

Analysis of samples of feces

In the lab, the samples were prepared and analyzed. Parasite ova and cysts were morphologically recognized, and quantitative measurement was performed using a modified version of Stoll's ova dilution method**.**

Statistical analysis

When statistical analysis in SPSS, the F-test was used. The data was analyzed by comparing the parasite prevalence in the sexes using a paired sample t-test.One statistical tool for comparing variations across many groups is the F-test. To learn more about the degree to which the variances in different groups of experimenters are similar or other, it determines whether the discrepancies in the sample variances are statistically significant.One standard statistical tool for determining whether variations in group averages are significant in the t-test. By dividing the difference in group means by the standard error difference, it finds the t-statistic, which is a measure of statistical significance.

RESULT AND DISCUSSION

Out of the 100 buffaloes that were examined, 56 had tests that were positive for parasitology GI parasite eggs. The results could vary from previous reports because of differences in the amount of feces samples tested, the length of time the study was conducted, and the climatic conditions (such as temperature and humidity) that allow the parasites' infectious stage and intermediate hosts to survive, as well as differences in management

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practices and deworming methods. Nevertheless, the disparity in eating habits and habitats between buffaloes and cattle might explain the former has a significant frequency.

Table (1) show that out of the buffaloes 50 females and 50 males had GI parasites. There was no considerable change (p>0.05) in this case. Although the specific cause of the more excellent infection rates in male animals remains unknown, one possible explanation is that farmers pay less attention to the care and management of male animals. Table 1 show that the data were further analyzed by age group. It was found that 60 of the buffaloes older than three years old had GI parasites, compared to 40 of the buffaloes younger than 12 months to 3 years old. However, the differences between the two groups were not statistically significant (p>0.05). However, it was said that older animals are less vulnerable than younger ones. It is not known that, why parasite prevalence changes with age. However, it might be due to variations in grazing regions, management strategies, or the innate immunity of the individuals.

Table (1). Prevalence of GI parasites in buffaloes by sex and age
(Source: Author)

Species	Factor level	
Buffalo (n=100)	**Examined**	**Positive (%)**
Sex		
Male	50	27
Female	50	30
Age		
12 months -3 years	40	30
> 3 years	60	38

In Table (2), we can see the findings for the parasite prevalence in the GI tract broken down by location. In the nematode kingdom, the incidence rates were *Strongyloides spp*.17 in buffalo. *Moniezia spp*., the sole cestode found in this investigation, accounted for ten buffaloes, *Trichuris spp*.12 in buffalo, and *Strongyles* 30 in buffalo. Possible explanations for the observed variance in prevalence include the different pastures' exposure to intermediate hosts, and free-living soil mites were *Eimeria spp*.4 in buffalo, *F. gigantic* 6 in buffalo, *Amphistome* 15 in buffalo, and *T. vitulorum* 20 in buffalo.

Table (2). Parasite-wise prevalence of GI parasites in buffaloes
(Source: Author)

Parasite/ Species (%)	Buffalo (n=100)
Strongyloides spp.	17
Moniezia spp.	10
Trichuris spp.	12
Strongyles	30
Eimeria spp.	4
F. gigantica	6
Amphistome	15
T. vitulorum	20

According to Table (3), the monthly prevalence of GI parasites in buffaloes shows that the environmental conditions can be ideal for the growth of larvae, which might explain this phenomenon. It thought that the EPG/OPG of feces in buffaloes was a good indicator of the GI parasite load. The frequency of a particular disease in buffalo throughout several months is shown in the table. Included in the table are the total buffalo examined and the number of positive instances, expressed as a percentage. The most significant proportion of positive cases is seen in December at 83.33%, with a total positivity rate of 56.00% for all months. This reflects the fact that the ailment occurs at different rates among the buffalo population on a monthly basis.

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Table (3). Buffaloes' GI parasite prevalence broken down by month
(Source: Author)

Months	Buffalo	positive
June	17	6 (35.29)
July	10	7 (70.00)
August	12	8 (66.67)
September	30	12 (40.00)
November	4	2 (50.00)
December	6	5 (83.33)
January	15	7 (46.67)
February	20	9 (45.00)
Total	100	56 (56.00)

The prevalence of several parasites in three distinct intensity groups (50-200, 201-400, and 401-600) among buffalo is shown in the table. The numbers indicate the frequencies each intensity range for each parasite species. Researchers can learn a lot about buffalo population health and management from this data, which shows, where parasite infections are most prevalent. The EPG/OPG found in the majority of stool samples fell somewhere between 50and 200, as shown in Table (4). The majority of the animals examined had EPGs that showed signs of a mild infection, indicating the need for treatment.

Table (4). EPG/OPG of GI parasites in buffaloes
(Source: Author)

Parasites	Buffalo		
	50-200	**201-400**	**401-600**
Strongyloides spp.	6	5	6
Moniezia spp.	3	3	4
Trichuris spp.	7	3	2
Strongyles	15	12	3
Eimeria spp.	1	2	1
F. gigantica	2	3	1
Amphistome	9	2	4
T. vitulorum	10	4	6

CONCLUSION

This study's findings support the idea that buffaloes get GI parasites. More research is required to assess the monetary effect of GI parasites. The rates of GI parasite prevalence changed from month to month; treatment was necessary for the majority of animals due to the moderate EPG of infection; evaluating the economic effect of GI parasites in the study region requires further research. Finally, the complex dynamics and frequency of parasite infections may be better understood via the study of buffalo parasitology. The research provides valuable information for developing tailored intervention techniques to reduce parasites and implement sustainable herd management practices by variables like sex, age, months, and intensity levels. To establish focused breeding strategies, future research in buffalo parasitology should investigate genetic markers that impact parasite resistance. Parasite management tactics may be improved with the use of precision medicine and cutting-edge diagnostic technologies, leading to more sustainable and resilient buffalo heads that can adapt to new parasite threats

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