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MAPPING TRYPANOSOMIASIS HOTSPOTS: A GEOSPATIAL APPROACH TO DISEASE RISK ASSESSMENT IN YANKARI GAME RESERVE

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ABSTRACT

Trypanosomiasis, a parasitic vector-borne disease, poses a serious threat to both animal and human populations, especially in areas where the convergence of vectors and their hosts is easy. The Yankari Game Reserve in northeastern Nigeria is poorly understood as an environment with complex dynamics of Trypanosomiasis transmission. Using geospatial techniques, this paper comprehensively conducted an epidemiological risk assessment and mapping of Trypanosomiasis in the Yankari Game Reserve. This was achieved through combining Geospatial tools and methods such as Geographic Information Systems (GIS), Remote Sensing, and Spatial Analysis. This way, acquired data sets were integrated and analysed to generate risk maps delineating areas of high Trypanosomiasis transmission potential. Results indicated a spatial heterogeneity in the distribution of tsetse flies and trypanosome infections within the Game Reserve – Yankari. Environmental variables, including elevation, vegetation cover and proximity to water bodies, are identified as important predictors of Trypanosomiasis risk. Risk map results provide invaluable insights that aid in focusing target interventions on curtailing and mitigating the spread of Trypanosomiasis in the Game Reserve Region. The study also demonstrated the versatility of geospatial tools and techniques in interpreting the epidemiology of Trypanosomiasis, as well as highlighting the relevance of integrating multidisciplinary approaches for disease management and surveillance in wildlife reserves. Notably, this will significantly improve our understanding of the dynamics of Trypanosomiasis transmission and enhance the decision-making process, thereby safeguarding the health of both animal and human populations within and beyond Yankari Game Reserve.

Keywords: Epidemiology, Risk Assessment and Mapping, Trypanosomiasis and Geospatial Techniques

INTRODUCTION

The epidemiology of vector-borne diseases is complex due to the ecological variation of actors involved (parasites, vectors, hosts, and the environment). The complex transmission of African Animal Trypanosomiasis (AAT) and Human African Trypanosomiasis (HAT) in the West African savannah region was excellently exemplified by Abdullahi et al. (2007). The type of species and habitat suitability for survival to a greater extent determine the heterogeneous distribution of the vectors (tsetse flies). Disease transmission occurs during feeding because tsetse flies depend solely on blood meals as their source of food. While feeding on animals or humans, pathogenic micro-organisms called ***trypanosomes*** are deposited into the host's bloodstream, causing the disease Trypanosomiasis.

This disease is considered a neglected tropical disease that affects both animal and human populations, and is endemic in 38 countries in sub-Saharan Africa (Barret *et al.,* 2003). The disease exists in two forms: Human African Trypanosomiasis (HAT), a fatal disease to humans if left untreated, and African Animal Trypanosomiasis (AAT), also a fatal disease to animals. This disease is associated with substantial economic loss to farmers, thus becoming a significant cause of poverty in the affected regions. In sub-Saharan Africa, AAT is one of the significant constraints to the development of farming and livestock production (Adewuyi *et al.,* 2020). In regions challenged by Trypanosomiasis, livestock rearing cannot be used to exploit grazing lands, where over 48 million (30.0%) African cattle, excluding other livestock species, are exposed to Trypanosomiasis (Begna *et al*., 2011).

Trypanosomiasis is associated with agricultural loss of up to USD 4.5 billion per annum, with about three million cattle dying each year globally (Abdullahi *et al.,* 2009). Furthermore, Cecchi *et al.* (2014) reported that about 70 million humans and 60 million cattle are at risk of contracting the disease. More than 10,000 cases are reported each year across Africa. Trypanosomiasis cannot be exempted from being endemic in wildlife and game reserves. Thus, Governments' current conservation strategies to turn all game reserves into government-protected national parks and game management areas provide a favourable environment for vector habitation (Bhatt & Joshi, 2012). The combination of a conducive environment for parasite, vector, and host interaction in a given geographical area, such as a game reserve ecosystem, typically provides a perfect habitat that supports a continuous disease transmission cycle.

Tsetse-transmitted Trypanosomiasis remains a significant animal health problem in Nigeria, given that changes in land cover, climate, and control interventions are modifying its epidemiological patterns. Evidence-based decision-making for progressive disease control requires spatially explicit information on its occurrence and prevalence, as well as the associated distribution and abundance of vectors. The Yankari Game Reserve's ecological niche lies within the standard tsetse fly belt, which harbours a high tsetse population density in Nigeria (Abubakar *et a*l., 2019). Ecological factors, such as climate, vegetation, and the type of wildlife found in this reserve, favour an interplay between wildlife and disease vectors.

Information technology developments led to the rapid growth of information systems for vector ecologists and controllers of vector-borne diseases. Improvements in computer hardware also support the development of sophisticated mapping software, which further aids in the graphic representation of disease distribution and vector abundance in space and time. This enables data to be correlated with environmental variables using Global Positioning Systems (GPS), Remote Sensing (RS) and Digital Database in a Geographic Information System (GIS). Over the past 25 years, the application of remote sensing techniques for mapping vector prevalence and associated disease distribution has undergone significant evolution. This indicates contemporary epidemiologists adopting the use of RS and GIS in the study of vector-borne diseases. Furthermore, associations between satellite-derived environmental variables, such as vegetation, climate, relief, and landscape data, are used to identify and characterise potential vector habitats.

Understanding the fact that convergence of factors (availability of multi-temporal satellite data and geo-referenced epidemiological data) and collaboration between remote sensing scientists and biologists, coupled with Geographic Information Systems applications' availability with sophisticated statistical and image processing algorithms on a computer, creates a fertile research environment for this study. Therefore, RS and GIS have been recognised as practical tools for predicting, monitoring, and planning control activities related to vector-borne diseases. Thus, this study aims to carry out an epidemiological risk assessment of Trypanosomiasis in Yankari Game Reserve by identifying areas where interaction between vectors of Trypanosomiasis; the tsetse fly (Glossina spp.) and wildlife are most likely to occur thereby mapping out areas with elevated risk of the disease transmission between vectors and hosts in the Study Area.

The Study Area

Yankari Game Reserve is a large wildlife park in the South-central part of Bauchi State, North-eastern Nigeria. It covers an area of approximately 2,244 square kilometres (866 square miles) and is home to several natural water bodies, as well as a diverse range of flora and fauna. It is known for its population of African elephants (the largest in Nigeria), baboons, hippos, and over 350 bird species. It also has hot springs and significant archaeological sites. Its location in the heartland of the West African savannah makes it a unique place for tourists and holidaymakers to watch wildlife in their natural habitat. Yankari was gazetted as a Game Reserve in 1956 (Abubakar *et al.,* 2019), the first in Nigeria, and later designated as a National Park in 1991. As a result of this long period of protection, the park has become the nation's foremost wildlife conservation area and a major tourist attraction in Nigeria.

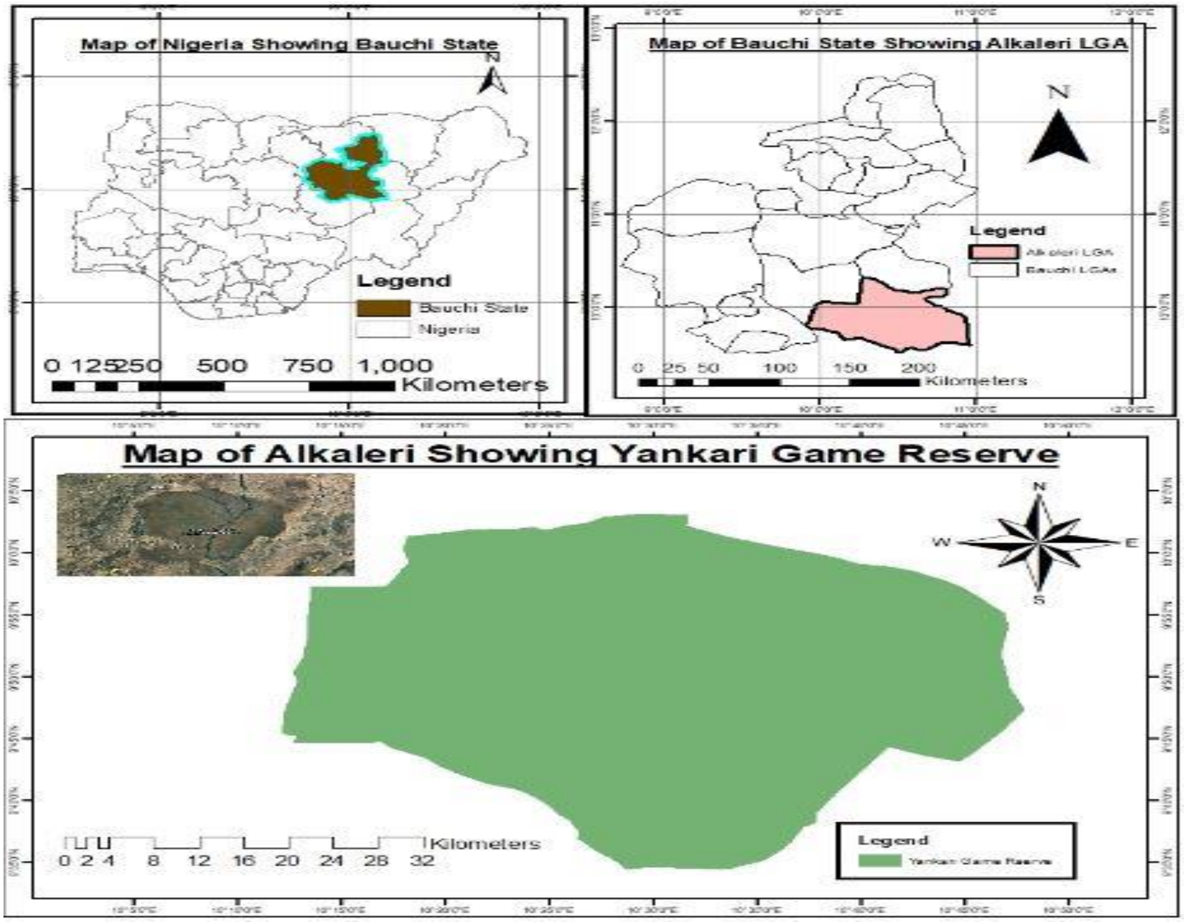


Figure 1. Location of the study Area

Yankari Game Reserve is located between latitudes 9°35′ to 10°05′N and longitudes 10°10′ to 10°50′E in Alkaleri Local Government Area of Bauchi State, Nigeria (Fig. 1). This reserve's area is in the southern part of the Sudan Savannah. It is composed of savannah grassland with well-developed patches of woodland (Adewuyi *et al*., 2020). It is also a region of rolling hills, primarily located between the ranges of 200m and 400m, with Kariyo Hill being the highest peak at 640m (Abubakar *et al.,* 2019). Two major habitat types occur in dry savannah woodlands and riparian forest vegetation, which includes areas of swamps and floodplains.

Materials and Methods

Remote Sensing Data

Spatial datasets acquired for this study include; a cloud-free Landsat 8 (OLI) satellite image scene; (LC08_L2SP_087053_20171030_ 20200902) with the following details; Source: - United States Geological Survey (USGS) website, Resolution: - 30, 30 (VNIR, SWIR), Date Acquired: - 2017/10/30, Spatial Reference: - WGS_1984_UTM_Zone32N and Datum: - D_WGS_1984. Additionally, a Digital Elevation Model (DEM) dataset of the study area is available with the following details: n09_e09_1arc_V3.tif and n10_e010_1arc_V3.tif. The source is the United States Geological Survey (USGS) website, and the resolution is 0.00027777778. The spatial reference is GCS_WGS_1984, and the datum is D_WGS_1984. The Remote Sensing data of the study area was downloaded from freely available open sources, which include Satellite images from Google Earth, Digital Elevation Models, and VNIR and SWIR data of the Landsat 8 (OLI) Satellite imagery.

The study aimed to assess epidemiological risk by mapping areas at risk of Trypanosomiasis disease transmission within Yankari Game Reserve using RS and GIS techniques. This was achieved by using environmental factors as dependent variables to identify areas within the study area that are most suitable for vector–host interaction. These included vegetation, elevation, and proximity to water sources, as these factors, observed in the reviewed literature (Aregawi et al., 2019), are known to have a strong influence on tsetse flies' habitat.

Vegetation analysis was carried out using the Normalised Difference Vegetation Index (NDVI) to identify areas with vegetation types that were most suitable for tsetse habitation. Elevation and hydrological information were derived from 30m resolution Digital Elevation Model (DEM) data obtained from the Shuttle Radar Topography Mission (SRTM) sourced from the USGS Earth Explorer website. Flow direction and flow accumulation were used as proxy river data, which were analysed using Euclidean distance to determine proximity to water sources. Each data point was reclassified and ranked according to its degree of influence on vector habitation. A weighted overlay of all three factors was carried out to identify areas where vector and wildlife interaction is most likely to occur, thereby identifying areas with different risk levels of Trypanosomiasis disease transmission.

Data analysis was conducted on a laptop computer with ArcGIS 10.3 and Global Mapper software.

For vegetation analysis, the VNIR and SWIR bands of Landsat 8 (OLI) data, covering the study area's extent, were used. A Normalised Difference Vegetation Index (Buscher et al., 2017) analysis was carried out to identify different vegetation types using the formula; NDVI = (NIR - RED)/ (NIR + RED) = (Band 5 - Band 4) / (Band 5 + Band 4) NDVI raster was reclassified into five (5) classes using the Natural Breaks method (Abubakar *et al.,* 2019). Ranks were assigned to each class range, where "5" was assigned to the class range with the highest NDVI and "1" to the class range with the lowest NDVI. Then, the area of each NDVI class range was calculated.

Table 1: Ranks of Reclassified NDVI

NDVI Values	Ranking
0.229012 – 0.13427	1
0.13427 – 0.182146	2
0.182146 – 0.213124	3
0.213124 – 0.249735	4
0.249735 – 0.486297	5

Source: (Lab work, 2024)

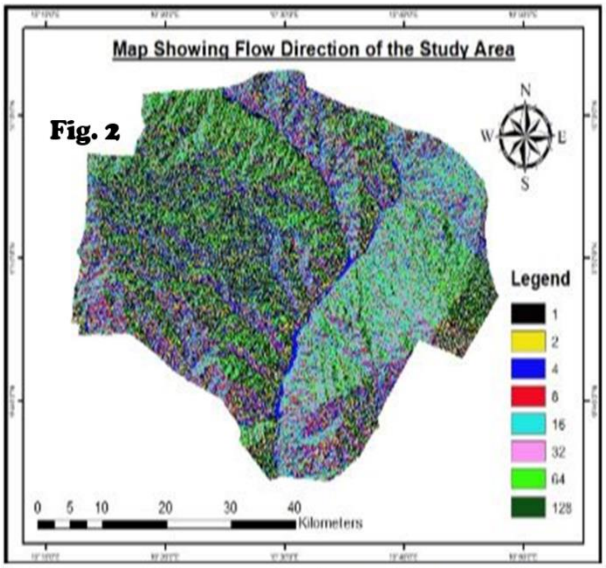
Elevation within the study area was analysed using the Digital Elevation Model (DEM). To carry out this analysis, two (2) tiles of DEM raster datasets were downloaded from the USGS website (it required two overlapping tiles to cover the study area). DEM datasets were added to the ArcGIS environment for processing. The two tiles of DEM raster datasets were merged using the "Mosaic to New Raster" tool from the Arc Toolbox. The mosaicked raster was used for further data analysis. The mosaicked raster was further corrected using the "Fill" tool to remove imperfections in the raster image. Spatial resolution was converted from decimal degrees (x = 0.00027777778, y = 0.00027777778) to meters (x = 30, y = 30) using Global Mapper software.

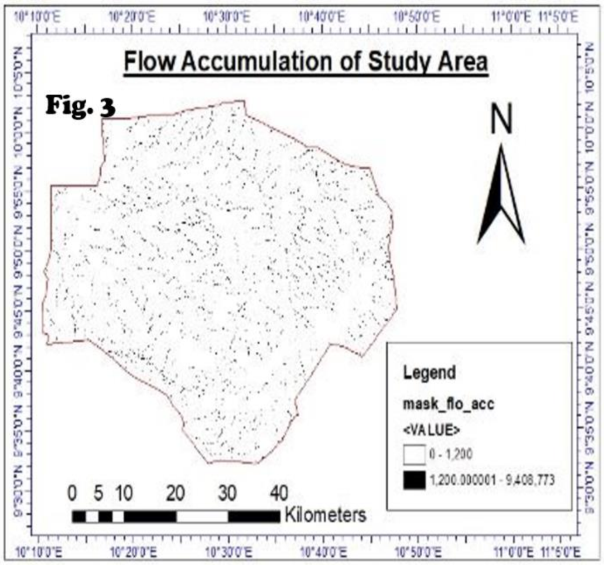
DEM raster was reclassified using the Natural Breaks Jenks method (Abubakar et al., 2019) Into five (5) classes, where areas at the lowest elevation were given the highest rank "5", and areas with the highest elevation were assigned "1".

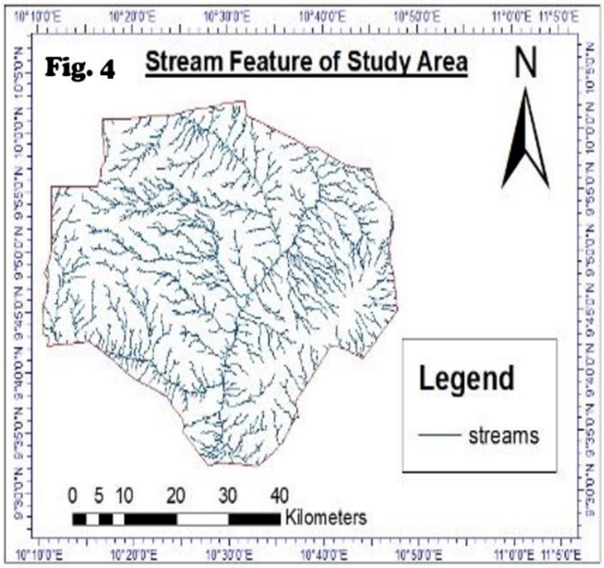
Proximity to water bodies was analysed using the Euclidean distance tool from the Arc Toolbox. The Euclidean distance tool calculates the Euclidean distance for each cell to the closest source, which in this case is the drainage of the study area generated as a stream feature. The stream feature was generated using DEM data through the following steps:

i. *Flow Direction*: - creates a raster of flow direction from each cell to its steepest downslope neighbour. Flow direction was computed using the "Flow Direction" tool from the Arc toolbox (Fig. 2).

ii. *Flow Accumulation*: - Flow accumulation creates a raster of accumulated flow into each cell, where a weight factor can optionally be applied. Flow accumulation was computed using the "Flow Accumulation" tool from the Arc Toolbox (Fig. 3).







Figures 2, 3, and 4 show: Flow Direction, Flow Accumulation and Drainage network/ tributaries within the study area, Yankari Game Reserve

iii. *Stream Feature:* The stream feature raster was computed from a resampled DEM using Arc's "Hydrology" tool (Figure 4).

Table 2: Stream Class by Length

Stream Class	Length (m)
1	1189060
2	597261
3	206972
4	104542
5	13585
6	39943
Total	**2151363**

The stream feature was further dissolved using the dissolve tool to identify major streams. The "Euclidean Distance" tool analysed the proximity of the water bodies. The resulting proximity raster was reclassified into five classes, with the highest rank assigned to values representing the shortest distance to water bodies (5), and the score decreasing with increasing distance from water bodies, culminating in the lowest score (1).

A Weighted Overlay Analysis was carried out with all three variables as criteria for analysis, i.e. ***NDVI, elevation, and proximity to water bodies***. The weighted overlay tool overlays several Raster datasets using a standard measurement scale (reclassification) and weighs each according to its importance or influence.

Table 3: Level of Influence by Each Criterion

CRITERIA	INFLUENCE (%)
NDVI	40
Elevation	20
Proximity to stream	40
Total	**100**

Source: (Lab work, 2024)

The result of the weighted overlay analysis was reclassified into three (3) classes to identify areas as ***High, Medium, or Low-risk*** disease transmission areas based on the extent and level of influence of each criterion on a given geographical location.

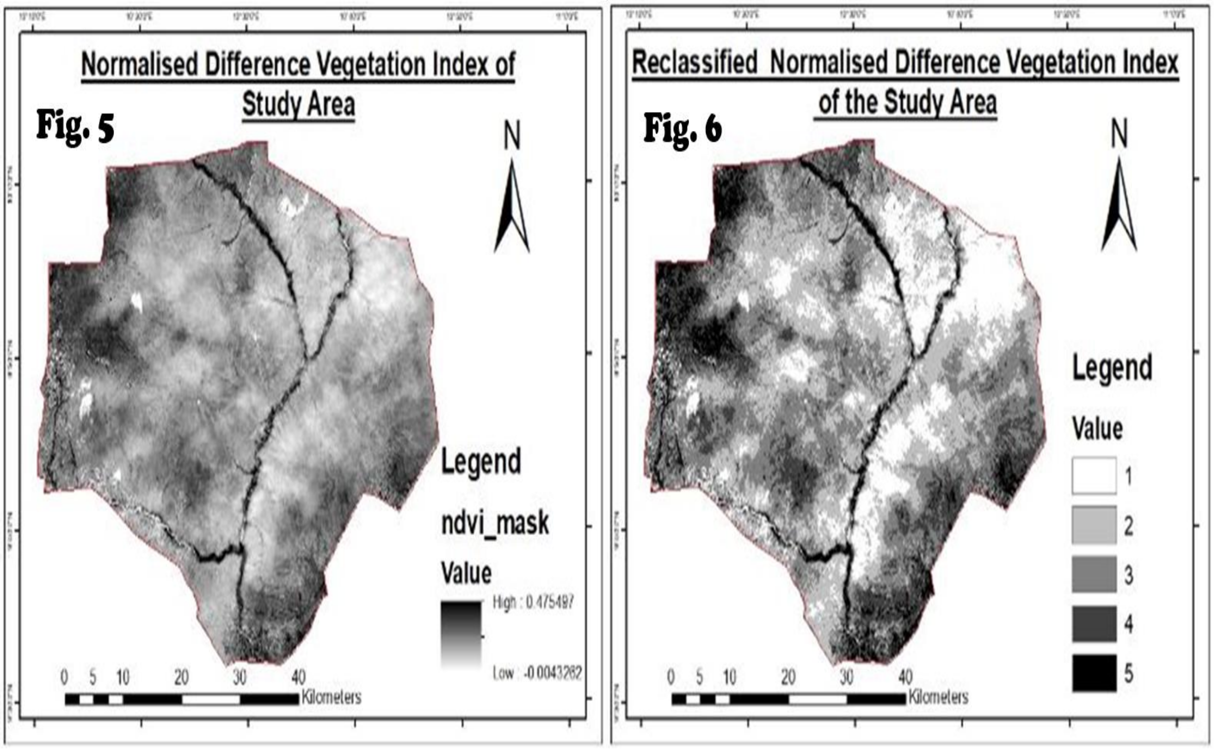
Results and Discussions

The results of data analysis are presented in the form of maps, tables, and charts. Maps were used to illustrate information on the location and distribution of environmental data graphically, as the analysis was based on spatial data, demonstrated in figures 5 and 6 for vegetation, figures 7, 8, 9, 10, and 11 for elevation, and figures 12, 13, 14 for proximity to water sources. Others include maps showing results of weighted overlay and reclassified weighted overlay of the three variables used as criteria in this study, in figures 15 and 16, respectively. Tables were used to display the quantities and results of spatial analysis, including area and percentage coverage of each vegetation category, elevation, stream class length, and disease transmission risk areas. A pie chart was also used to present the final result of the data analysis (Figure 17).

Result of Vegetation Analysis

The Normalised Difference Vegetation Index (NDVI) analysis carried out indicated that the vegetation in the study area ranged between 0.475497 and -0.0043262 as the highest and lowest NDVI values, respectively. High NDVI values were recorded in areas close to water bodies, at very low altitudes (<200m above sea level), and at very high altitudes (>500m above sea level), which are inaccessible to wildlife grazing. Low NDVI values were recorded in areas farther away from water bodies and planes used as grazing fields by wildlife.

Vegetation distribution within the study area indicates three (3) major layers of vegetation cover, including thick forest vegetation, shrub layer, and riparian forest-type vegetation. However, there exist some areas of bare land.



Figures 5 and 6: NDVI and Reclassified NDVI of Yankari Game Reserve Study Area

Thick forest vegetation is found at the fringes of the study area, along the reserve boundary to the east and west. Patches of thick forests also occur in the middle of the study area, to the west of the Gaji River. A canopy cover created by forest-type vegetation serves as a seasonal refugia for vectors when located further away from water sources and resting places. However, when it occurs near water bodies, the availability of shade allows vectors to take refuge during hot afternoons. The shrub layer occupies the highest percentage of the study area and serves as a feeding site for vectors due to the availability of grazing wildlife, which provides a source of blood meals for vectors. Riparian forests occur along the Gaji River and its tributaries. Vectors most prefer this vegetation type as it is close to water sources which increase the humidity of its immediate environment, and fertile soil that supports the growth of thick vegetation creating gallery forests that serve as resting sites for vectors. Water bodies also serve as sources of water for wildlife, thereby creating a favourable environment for vector–host interaction.

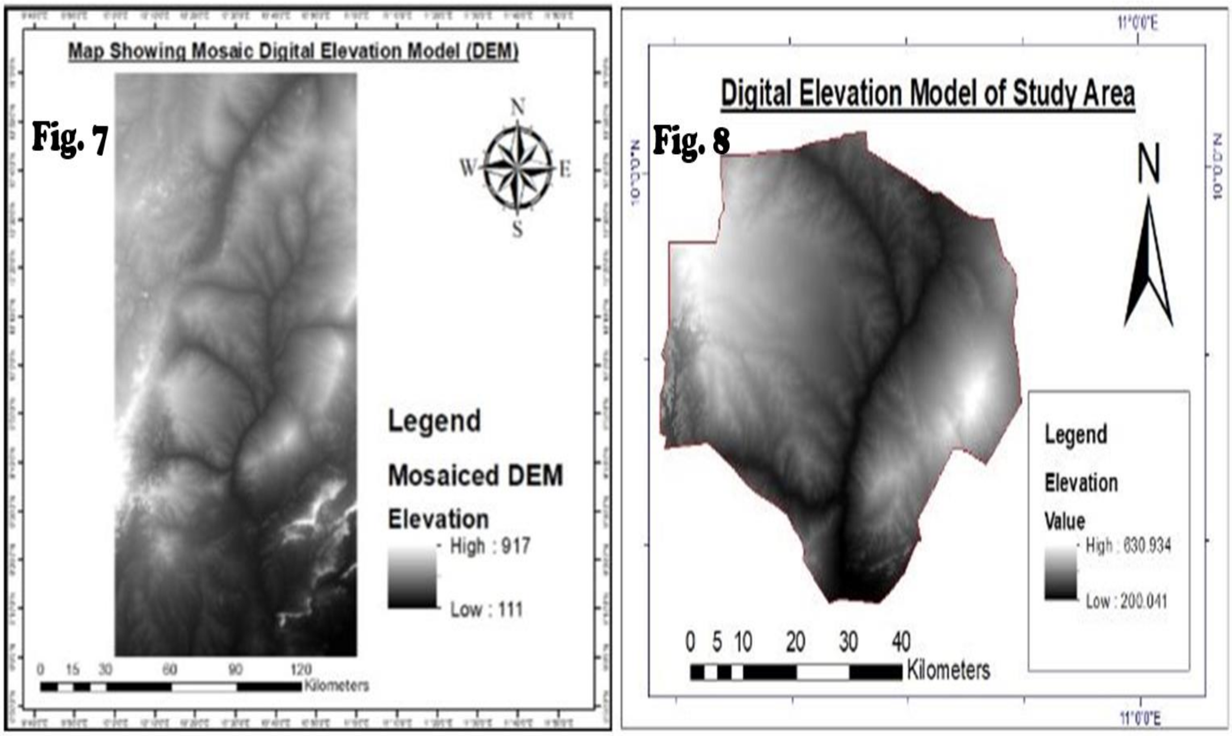
Table 4: Vegetation Class by Area (km^2) and Percentage Coverage

RANKS	AREA (sqkm)	Percentage (%)
1	8.34	0.33
2	338.68	13.23
3	1099.40	42.94
4	820.98	32.06
5	293.02	11.44
Total	**2560.41**	**100**

Source: (Lab work, 2024)

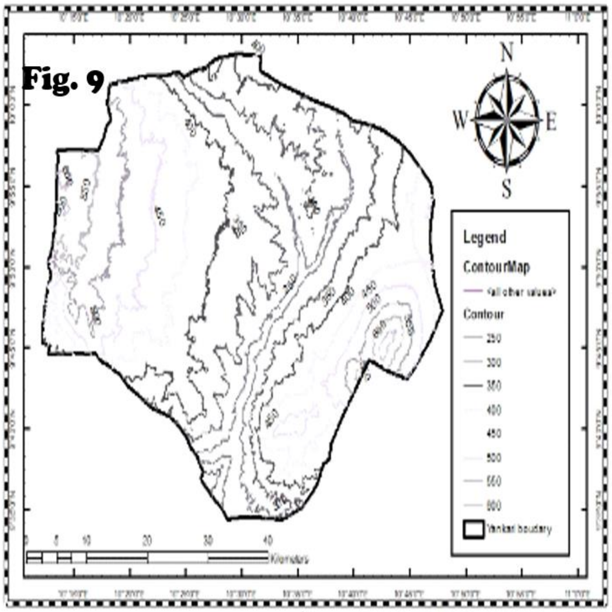
Result of Elevation Analysis

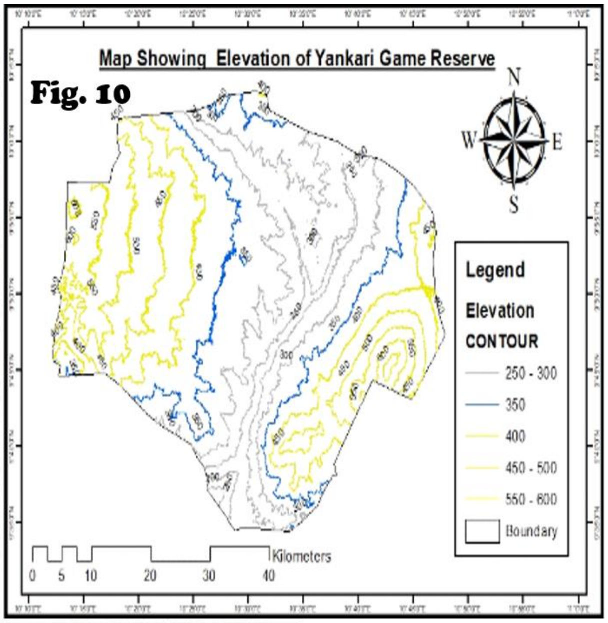
Mosaicked Digital Elevation Model datasets revealed the highest point at 917 m above sea level (a.s.l.) and the lowest point at 111 m a.s.l., as shown in Fig. 7.

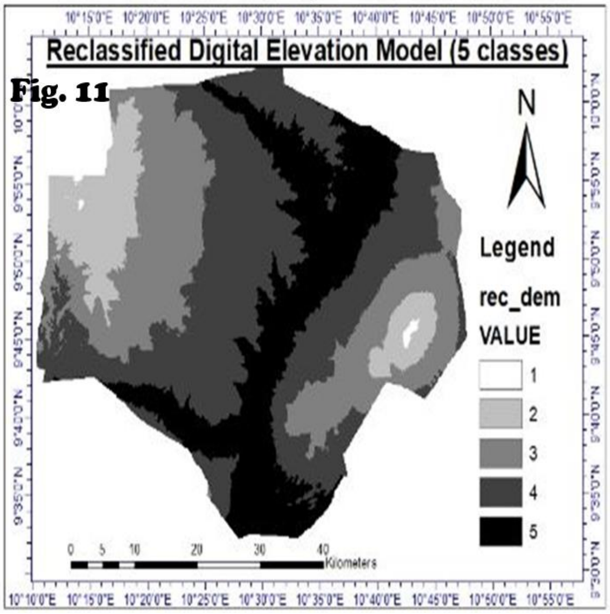


Figures 7 and 8: Mosaicked DEM Datasets & Masked DEM Raster of the Study Area

However, after extracting the extent of the study area from the mosaicked DEM, the highest elevation point within the study area was found to be 630.934 m a.s.l. In comparison, the lowest point was 200.014 m a.s.l., as illustrated in the DEM of the study area shown below (Figure 8).







Figures 9, 10, and 11. Showing Contour Map, Reclassified Contour Map, and Reclassified Digital Elevation Model of the study area

The topography of the study area is characterised primarily by rolling hills ranging between 200m a.s.l. and 500m a.s.l., with Kariyo Hill as the highest point rising above 600m a.s.l. Located in the south-eastern part of the study area (See the Contour maps in Figures 9, 10, and 11), the Gaji River is the lowest point at 200m a.s.l., situated in the middle of the study area, stretching from north to south. Also within the study area are floodplains and river swamps along the Gaji River and its tributaries, located at an elevation ranging between 300m and 450m above sea level, which comprise approximately 40% of the study area (Figures 9, 10, and 11).

These conditions create a favourable environment for vector habitation, as vectors tend to dwell well in areas of low land in thickets around water sources (Cayla et al., 2019). Floodplains are typically fertile, resulting in lush green vegetation throughout the year, which attracts a variety of wildlife and grazing animals. Additionally, water bodies in these areas serve as sources of drinking water and thermal regulation sites for wildlife. These conditions create a suitable environment for vector–host interaction, thereby resulting in disease transmission.

Table 5. Showing Area (km^2) and Percentage Coverage of Each Elevation Class

Rank	Area	Percentage (%)
1	5.7	0.2
2	255.5	10.0
3	654.6	25.6
4	1028.2	40.2
5	616.3	24.1
Total	**2560.3**	**100**

Results of Proximity to Water Body

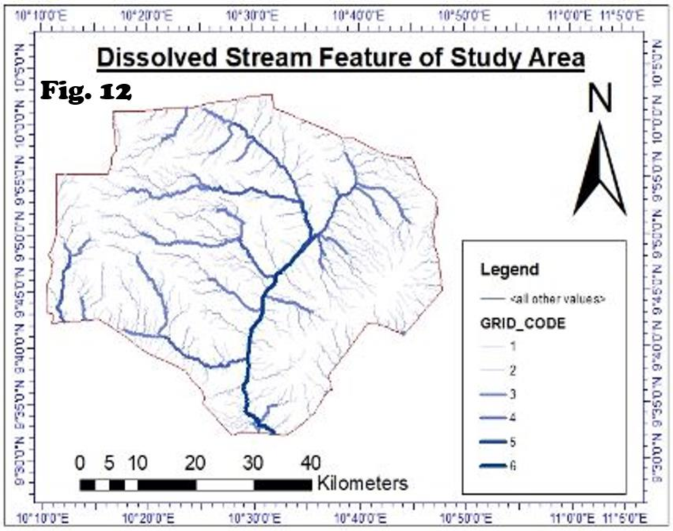
Stream Feature

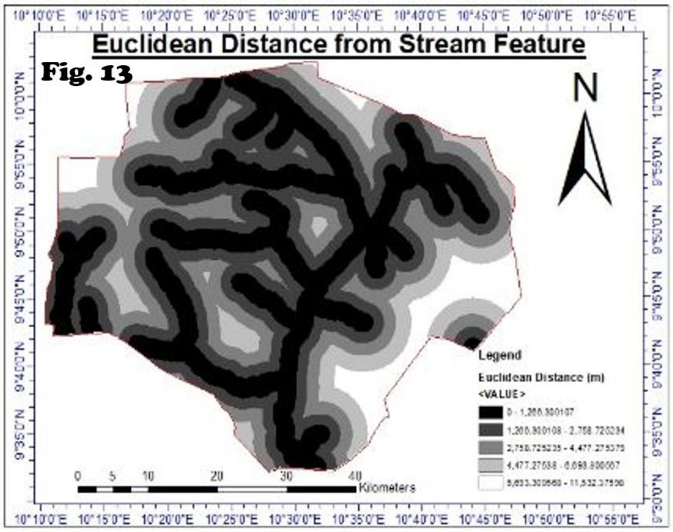
The stream feature was dissolved into six (6) classes according to the flow accumulation of each class. Stream classes labelled 3, 4, 5, and 6 (see Table 6) were designated as major stream features, as they had the highest flow accumulation and represented the primary stream network within the study area.

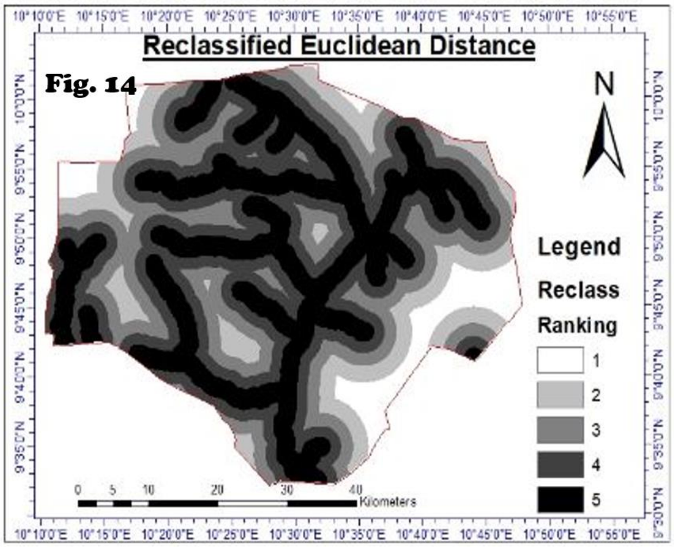
The study area comprises a single watershed, consisting of a vast network of tributaries that empty into the Yashi and Gaji Rivers. This structure of the stream network enables the creation of several wetlands within the study area, which serve as important habitats that sustain wildlife populations. Furthermore, gallery forests formed along river beds also serve as favourable habitats for vector breeding. This is due to the availability of soft soils for depositing pupae, the vegetation canopy cover that provides shade from direct sunlight, and high humidity resulting from the presence of water bodies.

Table 6: Dissolved Stream Class by Length

Stream Class	Length (m)
3	206971.9
4	104542.1
5	13585.2
6	39943.0
Total	**365042.2**







Figures 12, 13, 14: showing major stream Networks, Euclidean distance from water bodies (Stream feature) and Reclassified Euclidean Distance from streams in the study area

Euclidean Distance

Euclidean Distance was used to analyse the influence of distance from water bodies on disease vector habitat. The result of the Distance from water bodies analysis carried out on the study area using the dissolved stream feature is shown in Figure 12, highlighting the water bodies. The distance from the streams as water bodies was also determined using the Euclidean distance, as shown in the maps in Figures 13 and 14, as ranked in Table 7.

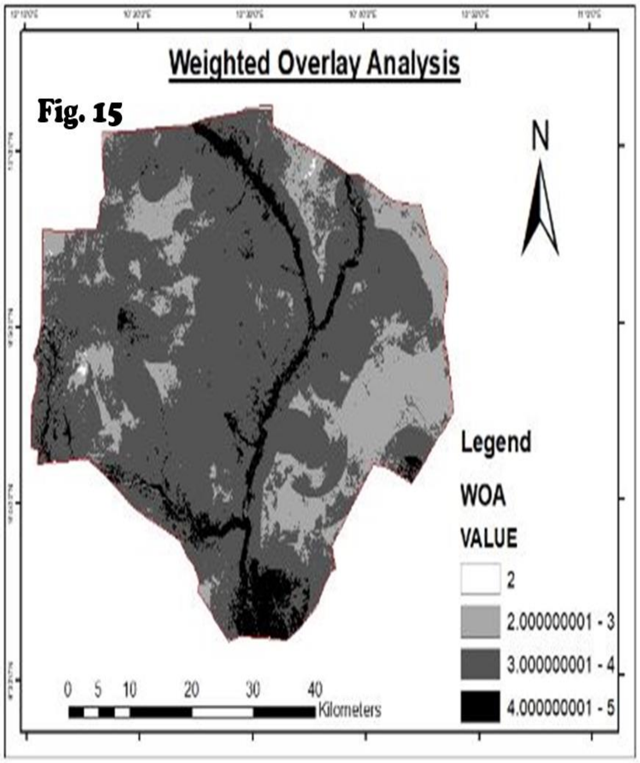
Table 7: Ranking of Euclidean by Distance from Stream Feature

Rank	Distance from Stream (m)
5	0 – 1,291.777856
4	1,291.777856 – 2,806.27603
3	2,806.27603 – 4543,49450
2	4543,49450 – 6,726.15366
1	6,726.15366 – 11,358.73633

Source: (Lab work, 2024)

Weighted Overlay

The result of weighted overlay analysis using all three (3) factors as criteria displayed four (4) categories of disease transmission risk zones, i.e. where interaction between wildlife and disease vector is most likely to occur at varying intensities. This result was further reclassified into three (3) categories of disease transmission risk zones: High, Medium, and Low disease transmission risk areas.



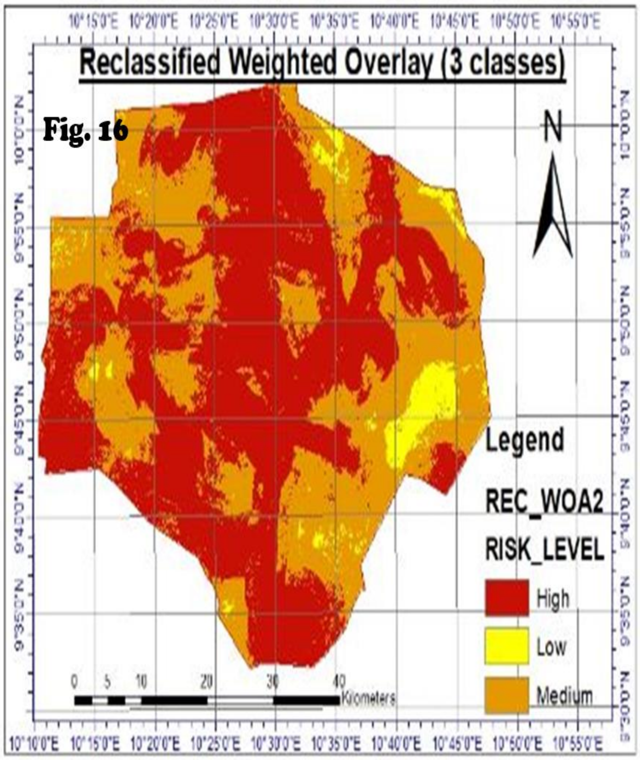


Figure 15. Weighted Overlay of Reclassified NDVI, Elevation, and Proximity to Stream.

Figure 16. Reclassified Weighted Overlay Analysis into (3 Classes) High, Medium and Low Risk

Table 8. Showing Weighted Overlay Classes, Area, and Percentage Coverage

WOA Class	Area (Sq. km)	Percentage
2	2.23	0.09
3	520.20	20.34
4	1817.81	71.06
5	217.74	8.51
Total	**2557.99**	**100**

Table 9. Showing Area and Percentage Coverage of High, Medium, and Low Disease Transmission Risk Areas

Risk Level	AREA (sqkm)	Percentage (%)
Low Risk	95	3.7
Medium Risk	1044	40.8
High Risk	1419	55.5
Total	**2558**	**100**

According to the spatial data analysis, approximately 2,560 km² of the study area appear to be at various levels of trypanosomiasis disease transmission risk, categorised as ‘high’, ‘medium’, and ‘low’ risk zones.

High disease transmission risk zones occupy 55% of the study area, concentrated at the centre, extending from the northern to the southern part of the study area, particularly along the Gaji River valley, which cuts across the middle of the reserve, as indicated in red on the reclassified weighted overlay map. Patches of high disease transmission risk zones also occur in areas farther away from the main river to the east and west. This is due to the presence of satisfactory environmental conditions that support both vector and wildlife habitation. This means that there is a very high probability of both vector and wildlife activity occurring within these zones at any one time, which may result from wildlife movement along riverbanks in search of food and water, thereby increasing the chances of vector-host interaction and disease transmission. Patches of medium disease transmission risk areas, indicated as green, occur in the middle of the reserve and along the fringes of the boundaries, making up 40% of the study area. Areas with a low disease transmission risk constitute 4% of the study area. They are predominantly located at high elevations east of the River Gaji, as well as along the northern and northeastern borders of the reserve. Small patches of low disease transmission risk areas also occur in the southern and western parts of the reserve.

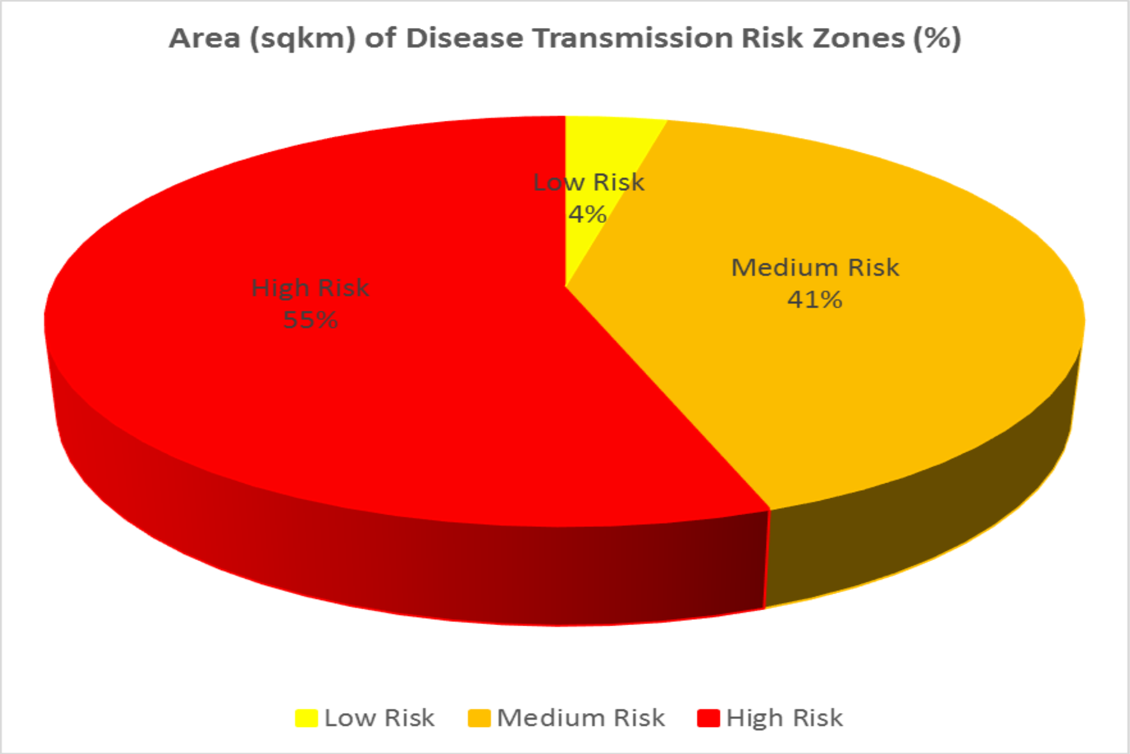


Figure 17. Pie Chart Showing Percentage of Areas at Risk of Trypanosomiasis Disease Transmission.

Areas with a very high risk of disease transmission between disease vectors and wildlife hosts account for 1,419 km² (55%) of the study area, whereas areas at medium risk account for 1,044 km² (41%), and the remaining 95 km² (4%) account for areas with a low disease transmission risk.

Discussion of Results

Out of the three (3) criteria used as dependent variables for spatial analysis to carry out an epidemiological risk assessment of Trypanosomiasis in Yankari Game Reserve (vegetation, elevation, and proximity to water sources), vegetation and proximity to water sources appear to be the strongest determinants of vector habitation, which was consistent with the works of Bhatt & Joshi (2012), and Buscher et al., (2017). This was achieved through the use of exploratory spatial analysis in ArcGIS. The weighted overlay tool in the Arc toolbox requires reclassifying environmental data to determine the degree and level of influence of each criterion on the outcome of the data analysis. Reclassification was used to simplify or change the interpretation of Raster data by changing a single or a group of values into a single value. In this study, the assignment of ranks to individual ranges of environmental data, as it relates to their suitability for vector occurrence, was based on investigations made in the existing literature on the subject matter.

Well-documented literature is abundant with research works that correlate vegetation and the availability of water bodies with vector occurrence, as seen in the works of Cecchi et al. (2008), Bukhombe et al. (2017), and Begna et al. (2011). This was taken into consideration when assigning ranks and percentages of influence (40% for vegetation, 40% for proximity to water sources, and 20% for elevation) for each criterion. On the contrary, a gap appears in published relevant research works on the effect of elevation on vector occurrence. In works where it was considered, there was very little or no correlation, as reported by Shikanai Yasuda (2022) and Rogers and Franco et al.

(2014). However, elevation is a determining factor in the distribution of the other 2 two factors (vegetation and proximity to water sources), and possibly other factors which may not have been included in this study.

Due to the rolling hill nature of the study area, streams of spring water from rocks create a network of tributaries that make the study area a watershed, as well as form gallery forests along rivers and tributaries. The nature of the elevation, whether mountainous or rocky, with steep or gentle slopes, also determines the distribution and nature of the drainage network and the resulting vegetation cover within the study area.

Conclusion

Trypanosomiasis remains a significant socio-economic threat in Africa, especially at the wildlife–livestock interface, where wildlife serves as a reservoir, sustaining the disease cycle. Yankari Game Reserve exemplifies such an ecosystem, providing a conducive environment for parasite–vector–host interactions.

This study utilised remote sensing and GIS to analyse environmental and spatial factors influencing disease distribution. These tools effectively integrated geographic and disease data, revealing patterns and enabling risk assessment models that are otherwise difficult to achieve.

Findings reaffirm the value of geospatial technologies in trypanosomiasis surveillance and control, offering cost-effective support for informed decision-making. Future research should incorporate additional variables, such as seasonal climate and entomological data, to deepen the understanding of the disease's epidemiology in the reserve.

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