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Prevalence of *Bartonella* spp. in rodent and shrew species trapped in Kigoma and Morogoro Regions, Tanzania: A public health concern

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***Bartonella* spp. bacteria are responsible for bartonellosis in humans and animals for which rodents are the main natural reservoirs. Common bartonellosis symptoms include fever, chills, weakness, and headache. This study aimed to determine the prevalence of *Bartonella* spp. infection in rodents and shrews of the genus *Crocidura* in the Kigoma and Morogoro regions of Tanzania. Blood culture and conventional PCR targeting a portion of the *gltA* gene were used to screen and confirm presence *Bartonella* spp. Among the 1036 small mammals tested, 999 were rodents and 37 were shrew species. The overall prevalence of *Bartonella* spp. in small mammals was 22.5%. *Bartonella* spp. was found in 13 rodent species and one *Crocidura* species. Prevalence varied significantly among host species (p <0.0001) and habitats. *Bartonella* spp. was found to be widespread in rodent species inhabiting indoor, peridomestic, farm and forest habitats. This study highlights rodents and *Crocidura* spp. as potential reservoirs of *Bartonella* spp., likely contributing to the spread of human bartonellosis due to their inevitable interactions in suitable habitats. Further research is needed to characterize zoonotic *Bartonella* spp., determine their genetic diversity, and assess ecological factors influencing the transmission cycle.**

Key words: Bartonellosis, Habitats, humans, interactions, small mammals.

INTRODUCTION

Bartonella spp. is pleomorphic rod-shaped bacteria (Minnick and Anderson, 2015) that are microaerophilic fastidious (Okaro et al., 2017). A number of species and sub species of the genus *Bartonella* isolated from small mammals have been described including *Bartonella elizabethae, Bartonella tribocorum, Bartonella phoceensis, Bartonella coopersplainsensis, Bartonella rattimassiliensis, Bartonella queenslandensis,* (Klangthong et al., 2015); *Bartonella grahamii, Bartonella taylorii and Bartonella doshiae* (Obiegala et al., 2021).

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Worldwide, studies on bartonellosis have shown that small mammals, especially rodents, serve as the primary natural reservoirs of a diverse range of *Bartonella* spp. (Yu et al., 2022). Bartonellosis in animals and humans is transmitted through bite from blood-sucking arthropod vectors including fleas, ticks, lice, and biting flies (Cheslock and Embers, 2019). Other ways of transmission for *Bartonella* spp. infections include contaminated abrasions, direct contact with infected animals (Okaro et al., 2017), and through blood transfusion or organ transplantation from infected donors (Noden et al., 2014). In mammalian hosts, *Bartonella* spp. attack erythrocytes, endothelial cells, and dendritic cells, which are important in the body's immune response (Birtles, 2005). Infections caused by *Bartonella* spp. result in various clinical manifestations, such as fever, anemia, and inflammation in organs including lymph nodes, heart, liver, spleen, and eyes in humans (Lins et al., 2019). In companion animals, clinical signs of *Bartonella* spp. infection include fever, cardiac murmurs, cough, tachypnea, lameness, and neurological symptoms in dogs, as well as endocarditis and myocarditis in cats (Sykes and Chomel, 2014).

Only a few studies have been conducted on bartonellosis in Tanzania (Gundi et al., 2012; Theonest et al., 2019). Despite being limited in number, these studies, mostly carried out in northern part of Tanzania, have been able to provide a rough picture of the disease situation in Tanzania, especially their likelihood to contribute to febrile illnesses of "unknown origin''. In the areas characterized by scattered agriculture fields with various crops, grazing, and increased human-wildlife interactions (Kimaro, 2014). This, coupled with a high diversity of synanthropic small mammals, poses a higher risk of zoonotic diseases to humans (Shilereyo et al., 2021). However, the information from these studies is too limited to fully explain the epidemiology and risk associated with bartonellosis. Therefore, this study will generate additional information which will considerably contribute towards further understanding of the epidemiology of bartonellosis in Tanzania, particularly with regards to interactions between wildlife, livestock and humans in different habitats. Consequently, this study aimed to determine the prevalence of *Bartonella* spp. in rodents and shrews from different habitats in Kigoma and Morogoro regions. This study provides insight into the presence of bartonellsis to the farmers and livestock keepers particularly in the areas with high interactions with small mammals that serve as a reservoir host for zoonotic pathogens. Understanding these implications can help raise awareness, inform preventive measures and promote early detection of the disease.

MATERIALS AND METHODS

Study sites

This study was conducted in two regions of Tanzania namely; Kigoma and Morogoro. Two districts were purposively selected from each region based on reserved natural land (game reserve/natural forest). In Kigoma region, the selected districts were Kibondo (4.1938° S, 31.0794° E) and Kakonko (3.2469° S, 30.9417° E) (Figure1). In Morogoro region, the selected districts were Kilosa (6.8343° S, 36.9917° E) and Morogoro rural (7.2009° S, 37.8511° E) (Figure 2).

Kibondo and Kankoko districts are bordered by Moyowosi game reserve. One village was selected from each district based on its closeness to the game reserve. These villages were Kigendeka (3°46'24.0"S 30°41'33.2"E) in Kibondo district and Itumbiko (3°17'16.7"S 30°58'38.9"E) in Kakonko district. The main economic activities in these villages include subsistence farming, grazing and poaching for some people from both villages (Pers communication). The other two villages are not bordered by a game reserve. The main economic activities in Kumuhama village (3°35'16.4"S 30°40'40.6"E) are subsistence farming, with all of the land being used for agriculture. In Kihomoka village (3°11'46.5"S 31°2'24.5" E), the economic activities are subsistence farming and grazing.

In the Morogoro region, Kilosa district, Mamboya village (6°18'11.5"S 37°06'23.9"E) is located near the Mamboya mount village reserve. The main economic activities in this village are subsistence farming and grazing. Another study village in Kilosa district was Magubike (6°14'52.884"S 37°9'48.084"E), situated along the Dodoma road. The main activities in this village are subsistence farming, entrepreneurship and grazing. There is no reserved land in this village. Kibuko village (6°57'12.4236" S 37°50'46.98492" E) in Morogoro rural district is engaged in subsistence farming, especially maize, rice and orchard. This village is not bordered by the Kimboza forest reserve. The other study village was Mwarazi (7°0'44.94276" S 37°48'51.27084" E). This village is closely bordered to Kimboza forest reserve on the way to Nyerere National Park. The main economic activities in Mwarazi village are subsistence farming especially maize, rice and orchard farming.

Rodents and Shrews trapping

Rodents and shrews were live trapped in eight villages from both regions. Four of them have a game reserve or reserved land where the traps were set including indoor, peridomestic, farms/fallow and the natural land (game reserve/ village reserved land). The other four villages had traps set only in indoor, peridomestic and farm/fallow land as those villages had no natural reserved land.

Rodents and shrews were trapped during the wet and dry seasons in order to capture seasonal variation. These animals were captured live indoors using modified wire cage traps and outdoors using Sherman® traps. All traps were baited with approximately 5g of peanut butter mixed with maize flour at the ratio of 2:1 (1000g of peanut butter mixed with 500g of maize flour). The indoor traps were augmented with a piece of tomato to increase their attraction to *Rattus rattus*.

In each study village, 20 to 25 houses were purposefully selected based on presence of rats and minimum recommended number of traps. Each house was provided with 2 to 3 modified local wire cage traps, depending on size of the house. These traps were used indoors purposefully because of the neophobic behavior of *Rattus rattus.* For outdoor habitats, a maximum of 100 Sherman traps were used in five trap-lines of 20 traps each. The traps were set at an interval of five meters apart from each trap station and trap lines, for a maximum of three consecutive nights in each village. Traps were checked and re-baited once per day.

Sample collection

Each trapped animal was euthanatized in a container containing

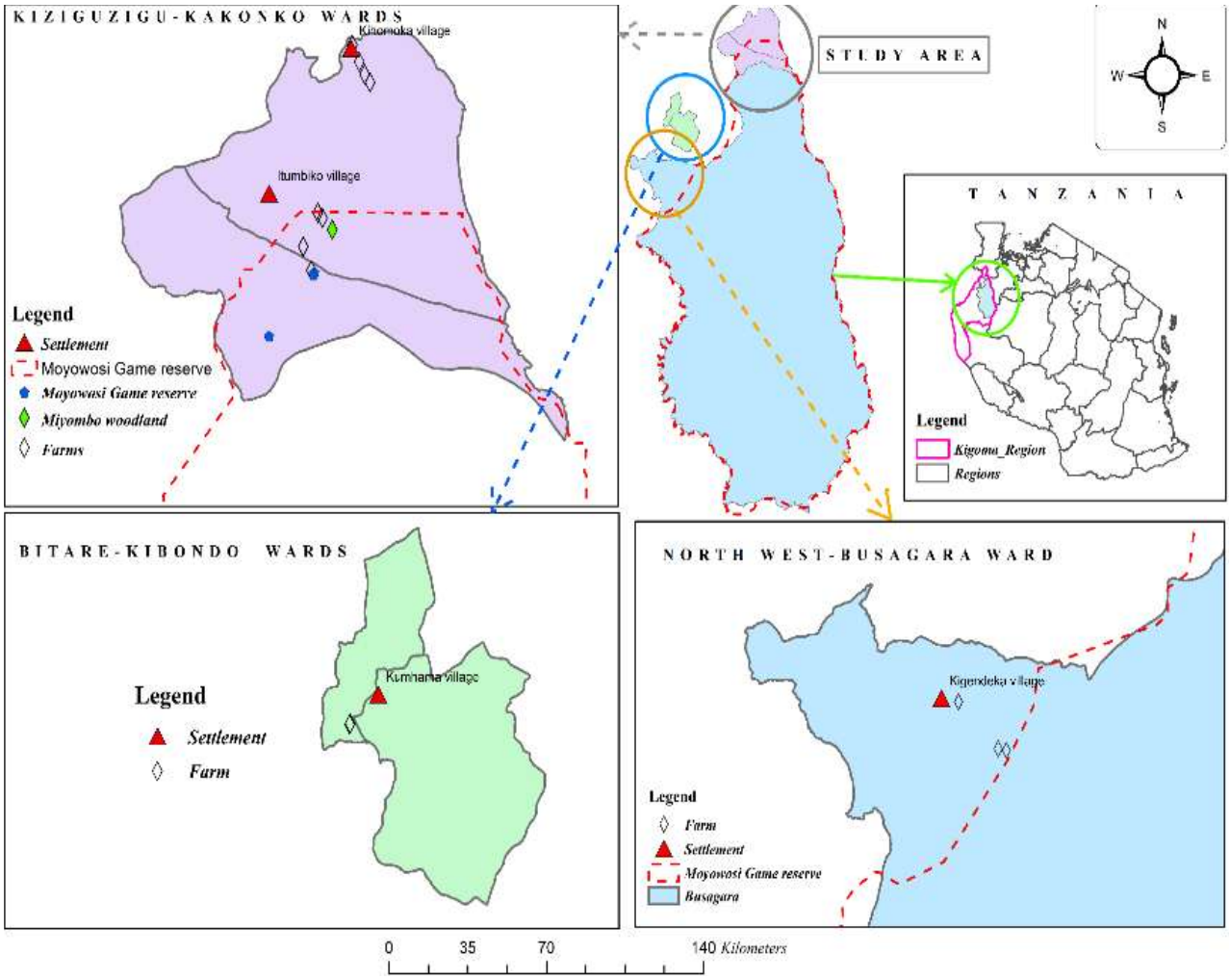

Figure 1. Kakonko and Kibondo Districts in Kigoma region. Source: Authors

cotton wool soaked in halothane. A cardiac puncture was aseptically performed on each anesthetized animal after treating it with 70% ethyl ethanol. A minimum of 250µl of blood was drawn from the heart and placed in a sterile Ethylenediaminetetraacetic acid (EDTA) micro-vial and kept at -20˚C before being transported under cold conditions using a polystyrene box containing ice packs to the Institute of Pest Management of Sokoine University of Agriculture for laboratory analysis. For all trapped animals, standard body measurements (weight, head and body length, ear length, hind feet length and tail length), sex and sexual condition were recorded for morphological identification at the genus or species level, according to Happold (2013).

Blood culture

Blood culture was conducted according to Trataris et al. (2012), with some modifications. Briefly, frozen EDTA blood was thawed at room temperature, and then 50µl of the blood was pipetted and smeared onto Columbia Blood Agar (CBA) enriched with 5% horse blood. The plates were left unturned for at least 30 min until the wet smear vaporized. Then, the plates were streaked from the dot inoculum. Plates were then placed in a candle jar and incubated at 35˚C. Fast-growing bacteria were observed after 24 h. Plates showing no growth were re-incubated and observed twice a week for up to three weeks. Purification was done for the mixed growth cultures, by picking suspected colonies and sub culturing them in another CBA medium. Presumptive *Bartonella* positive cultures were identified based on the slow-growth of different colony morphologies including small to medium in size, smooth or rough, moist and dry, self-adhesive, or easy to scrape off the surface of the medium. Other colonies that tended to pit into the medium were difficult to scrape off. Some colonies were clear or displayed faint metallic sheen. Furthermore, Gram and/ or Giemsa stain, catalase and oxidase tests were performed for the bacterial cell morphology. From the purified cultures 3 to 5 colonies were harvested and placed into a micro vial containing 95% ethanol and stored at -20˚C before confirmation by PCR. All procedures were aseptically done under the safety cabinet.

DNA extraction and PCR verification of *Bartonella* suspected cultures

Sub samples of 100 culture positive samples were further confirmed for *Bartonella* DNA using PCR. The DNA was extracted using Zymol

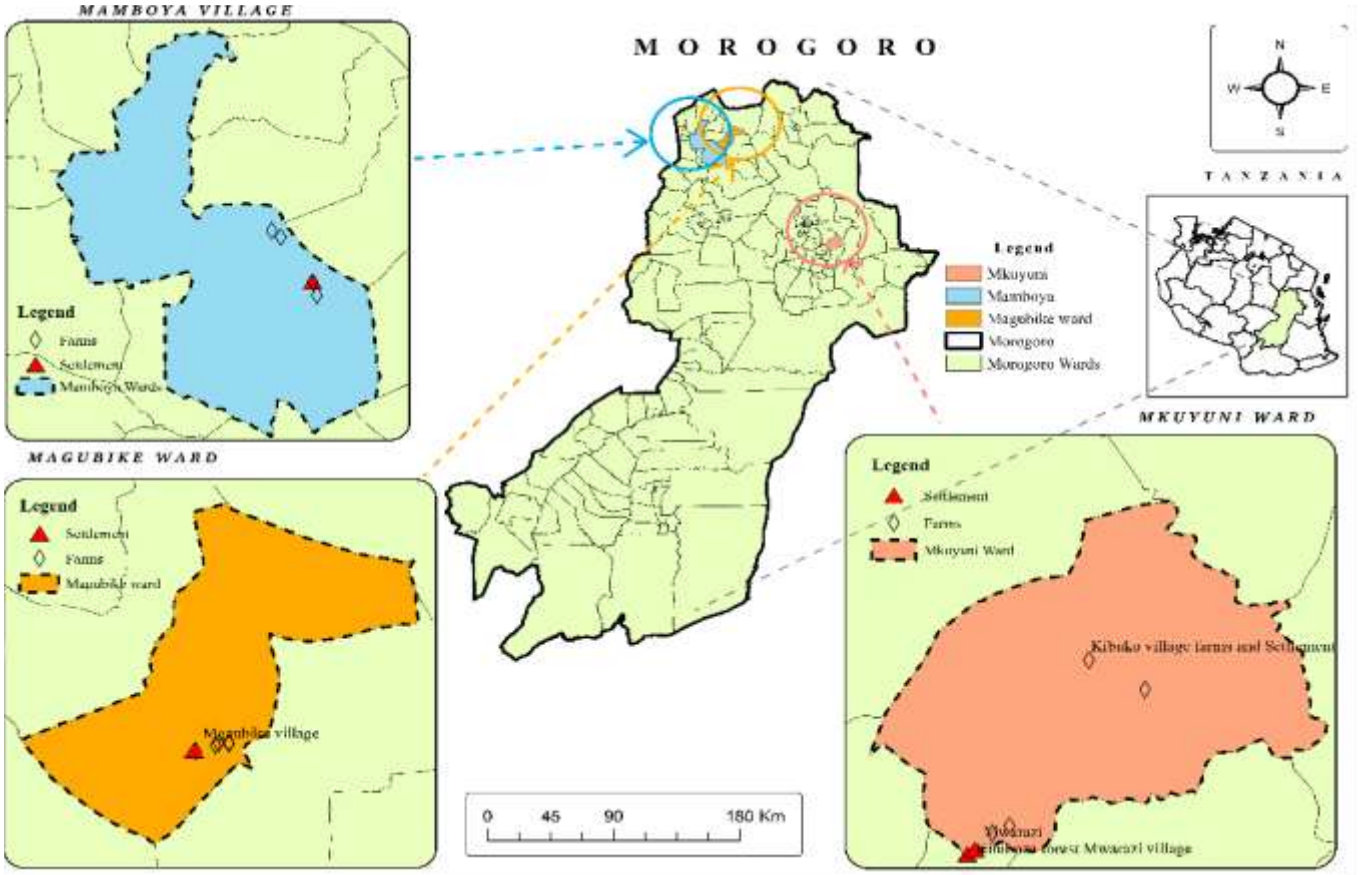

Figure 2. Kilosa and Morogoro Rural Districts in Morogoro region.
Source: Authors

kit (Quick-DNA^{TM} Miniprep Plus Kit), according to manufacturers' instructions and PCR was done according to Norman et al. (1995), with some modifications. Briefly, forward primer BhCS871.p (5'-GGGGACCAGCTCATGGTGG-3') and reverse BhCS1137.n (5'-AATGCAAAAAGAACAGTAAACA-3') targeting a 379 bp of the genus- specific *gltA* gene were used. Three microliters of DNA templates were added into a PCR reaction tube containing 12.5µl of 2x master mix, 0.5µl of 10µM of each primer, and 8.5µl of nuclease-free water. Amplification was done by a thermal cycler by the following parameters: an initial denaturing at 95˚C for five minutes, and 35 cycles of denaturation at 95˚C for one minute, annealing at 56˚C for one minute, and elongation at 72˚C for one minute.

Amplification was finalized by holding the reaction mixture at 72˚C for 10 min. The amplified product was confirmed for the proper size of amplicon by electrophoresis in 1.5% agarose gel.

Statistical data analysis

The overall prevalence of *Bartonella* was estimated by the number of positive samples over the total number of samples subjected to culture. The frequencies of captured individuals were summarized and counted for each genus/species using Microsoft excel and verified in SAS software version 9.1. The prevalence from different variables including regions, habitats, land use category, species, sex and sex condition were calculated as the proportion of positives out of the total number of individuals tested. Chi-square was used to compare prevalence rates between the above variables. Differences of compared small samples sizes ($n < 30$) were tested with Fisher's exact test. All tests were done using SAS software; $p < 0.05$ was considered significant.

RESULTS

Captured animals

In total, 1147 small mammals were captured during this study, out of which 616 (53.7%) were captured in Kigoma and 531 (46.3%) were captured in Morogoro. The captured animals belonged to different species including *Acomys* spp., *Arvicanthis nairobae, Arvicanthis neumanii, Dendromus* spp., *Aethomys kaiseri, Aethomys chrysophilus, Dasmys* spp., *Tatera,*spp,, *Grammomys* spp,, *Graphuris* spp,, *Lophuromys sikapus, Lophuromys laticeps, Lemniscomys rosalia, Lemniscomys striatus, Lemniscomys zebra, Mastomys natalensis, Mus* spp., *Praomys* spp., *Rattus rattus,* and *Crocidura* spp. These species were examined for prevalence of *Bartonella* spp. Samples collected from 1036 animals (566 from Kigoma and 470 from Morogoro) representing 90.2% of the total

Table 1. Prevalence (%) of *Bartonella* spp. in different rodent and shrew species collected from different habitats across the study villages in Kigoma region.

Study village	Habitat	Rodent spp.															Shrew spp.	Prevalence per village/habitat
		Avna	Den	Ak	Ds	Ta	Gr	Lops	Lopl	Lr	Ls	Lz	Mn	Ms	Pr	Rr	Cr	
Itumbiko	Indoor	-	-	-	-	-	-	-	-	-	-	-	1/3 (33.3)	-		1/32 (3.1)	-	2/35 (5.7)
	Peridomestic	1/1 (100)	-	-	-	-	-	-	-	2/2 (100)	1/3 (33.3)	0/1	2/8 (25)	0/1	-	-	0/1	6/17 (35.3)
	Farms	1/2 (50)	-	2/9(22.2)	7/14 (50)	-	0/1	-	-	2/7 (28.6)	9/25(36)	0/5	14/58 24.1)	0/9	-	-	0/2	35/132 (26.5)
	Forest/Bush	1/1 (100)	-	-	1/2 (50)	-	-	-	-	2/3 (66.7)	6/9 (66.7)	-	0/1	1/2 (50)	-	-	-	11/18 (61.1)
	Sub total	3/4 (75)	-	2/9 (22.2)	8/16 (50)	-	0/1 (0)	-	-	6/12 (50)	16/37 43.2)	0/6(0)	17/70 24.3)	1/12(8.3)	-	1/32 (3.1)	0/3 (0)	54/202 (26.7)
Kihomoka	Indoor	-	-	-	-	-	-	-	-	-	0/1	-	0/1	-	-	1/11 (9.1)	-	1/13 (7.7)
	Peridomestic	-	-	2/9 (22.2)	-	-	-	-	-	0/1	1/5 (20)	0/1	7/12 (58.3)	-	-	-	0/2	10/30 (33.3)
	Farm	1/3 (33.3)	-	8/11 (72.7)	1/4 (25)	0/1	-	-	-	0/1	7/13 (53.8)	0/1	15/33 45.5)	0/2	-	-	0/2	32/71 (45)
	Forest/Bush	NA	NA	NA	NA	NA	NA	NA	-	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Sub total	1/3 (33.3)		10/20(50)	1/4 (25)	0/1(0)	-	-	-	0/2 (0)	8/19(42.1)	0/2(0)	22/46(47.8)	0/2 (0)	-	1/11 (9.1)	0/4 (0)	43/114 (37.7)
Kigendeka	Indoor	-	-	-	-	-	-	-	-	-	0/1	-	2/6 (33.3)	-	-	0/5	-	2/12 (16.7)
	Peridomestic	-	-	-	-	-	-	1/1 (100)	-	-	1/3	-	0/2	-	-	-	-	2/6 (33.3)
	Farm/Fallow	2/4 (50)	-	9/17 (52.9)	1/1 (100)	0/1	0/1	-	-	4/5(80)	12/20 (60)	-	18/43 41.9)	0/2	0/1	-	0/3 (0)	46/98 (46.9)
	Forest/bush	-	0/1	2/2 (100)	-	-	-	1/1 (100)	-	1/3 (33.3)	1/4 (25)	-	1/1 (100)	0/3	2/6 (33.3)	-	-	8/21 (38.1)
	Sub total	2/4 (50)	0/1(0)	11/19(58)	1/1 (10)	0/1(0)	0/1 (0)	2/2(100)	-	5/8(62.5)	14/28(50)		21/52(40.4)	0/5(0)	2/7 (28.6)	0/5(0)	0/3 (0)	58/137 (42.3)
Kumhama	Indoor	-	-	-	-	-	0/3	-	-	-	-	-	9/9 (100)	0/1	-	0/6	0/1 (0)	9/20 (45)
	Peridomestic	NA	NA	NA	NA	NA	NA	NA	-	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Farm/Fallow	-	-	3/3 (100)	7/7 (100)	-	0/5	-	0/5	-	12/47 25.5)	-	7/21 (33.3)	1/5 (20)	-	-	-	30/93 (32.3)
	Forest/Bush	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Sub total	-	-	3/3 (100)	7/7 (100)	-	0/8(0)	0/5 (0)	-	-	12/47(25.5)	-	16/30 53.3)	1/6 (16.7)	-	0/6(0)	0/1 (0)	39/113 (34)
Total % per host species		6/11(54.5)	0/1(0)	26/51(51)	17/28(60.7)	0/2(0)	0/10(0)	2/7(28.6)	-	11/22(50)	50/131(38.2)	0/8(0)	76/198(38.4)	2/25(8)	2/7 (28.6)	2/54 (3.7)	0/11 (0)	194/566 (34.3)

Avna-Arvicanthis nairobae, Den-Dendromus, Ak-Aethomys kaiseri, Ds-Dasmys, Ta-Tatera, Gr-Grammomys, Lops-Lophuromys sikapus, Lopl-Lophuromys laticeps, Lr-Lemniscomys rosalia, Lz- Lemniscomys zebra, Ls-Lemniscomys striatus, Pr-Praomys spp., Rr- Rattus rattuss, Ms-Mus spp., Mn-Mastomys natalensis, Cr-Crocidura NA-Not applicable for trapping.
Source: Authors

number of captured animals, were analyzed. Other samples could not be cultured because the animals died in the traps before collection and/or lack of enough blood

The prevalence of *Bartonella* spp

Out of 1036 rodents and shrews tested, 234(22.5%) turned out to be positive for the bacteria on culture. Among them, 231 were rodents (n=999), and 3 were shrews (n=37). For the representative cultures confirmed by PCR, 86 out of 100 cultures were found to be positive. *Bartonella* spp. was detected in 14 host species out of 20 species/ genus of the small mammals investigated. The prevalence of *Bartonella* spp. differed significantly ($p < 0.0001$) among the host species tested, with except for *Gramommys,* spp., *Lemniscomys zebra, Dendromus* spp.*, Graphuris* spp., *Lophuromys sikapus* and *Tatera* spp. whose samples tested negative (Table 1). However, there were no significant differences ($p > 0.05$) in the prevalence of the organisms between seasons, habitats, land category, sex and sexual condition of the hosts from both regions. Furthermore, no significant difference was found in the prevalence of *Bartonella* spp. ($\chi^2 = 24.2297$, df = 11, $p = 0.118$) between hosts in the Morogoro region (Table 2). The prevalence of *Bartonella* spp. was significantly higher in the Kigoma region 34.3%, (n=566) (Table 1) compared to the Morogoro region at 8.5% (n=470) ($\chi^2 = 96.4463$, df = 1, $p <$

Table 2. Prevalence (%) of *Bartonella* spp. in different rodent and shrew species collected from different habitats across the study villages in Morogoro region.

Study village	Habitats	Rodent spp.											Shrew spp	Prevalence per habitat/village
		Ac	Aech	Avneu	Ta	Gr	Graph	Lr	Lz	Mn	Pr	Rr	Cr	
Mwarazi	Indoor	-	-	-	-	-	-	-	-	0/1	-	0/16	-	0/17
	Peridomestic	0/1	-	-	-	-	-	-	-	-	-	-	-	0/1
	Farms	1/4 (0.25)	-	-	0/1	-	-	-	-	14/46 (30.4)	-	0/1	2/14 (14.3)	17/66 (25.8)
	Forest/Bush	1/18 (5.6)	1/1 (100)	-	-	-	0/1	-	-	0/7	1/1	-	0/3	3/31
	Sub total	2/23 (8.7)	1/1 (100)	-	0/1	-	0/1	-	-	14/54 (27)	1/1(100)	0/17	2/17 (11.8)	20/115 (17.4)
Kibuko	Indoor	-	-	-	-	-	-	-	-	-	-	0/4	-	0/4
	Peridomestic	-	-	-	-	-	-	-	-	1/11(9)	-	-	-	1/11 (9)
	Farm	-	-	-	-	-	-	0/2	-	0/68	-	-	1/2 (50)	1/72 (1.4)
	Forest/Bush	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Sub total	-	-	-	-	-	-	0/2	-	1/79 (1.3)	-	0/4	1/2 (50)	2/87(2.3)
Mamboya	Indoor	-	-	-	-	-	-	-	-	0/1	-	11/36 (30.6)	-	11/37 (30.6)
	peridomestic	0/1	-	-	-	-	-	-	-	0/11	-	-	-	0/12
	Farm/Fallow	-	0/1	-	-	-	-	-	-	0/78	-	-	0/2	0/81
	Forest/bush	0/2	0/2	-	-	0/1	-	1/1 (100)	-	-	-	-	-	1/6 (6.25)
	Sub total	0/3	0/3	-	-	0/1	-	1/1 (100)	-	0/90	-	11/36(30.6)	0/2	12/136(8.8)
Magubike	Indoor	-	-	-	-	-	-	-	-	0/1	-	1/14 (7.1)	-	1/15 (6.7)
	Peridomestic	NA	NS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Farm/Fallow	0/1	0/7	3/19 (15.8)	0/2	0/1	-	0/1	0/2	2/79 (2.5)	-	-	0/5	5/117 (4.3)
	Forest/Bush	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	Sub total	0/1	0/7	3/19 (15.8)	0/2	0/1	-	0/1	0/2	2/80(2.5)	1/1 (100)	1/14 (7.1)	0/5	6/132(4.5)
Total (%) per host species		2/27 (7.4)	1/11 (9.1)	3/19 (15.8)	0/3	0/2	0/1	1/4 (25)	0/2	17/303 (5.6)	1/1 (100)	12/71 (16.9)	3/26(11.5)	40/470 (8.5)

Ac-Acomys, Aech-Aethomys chrysophilus, Avneu-Arvicanthis neumanii, Ta-Tatera, Gr-Gramommys, Graph-Graphuris, Lr-Lemniscomys rosalia, Lz-Lemniscomys zebra, Mn-Mastomys natalensis, Pr-Praomys, Rr-Rattus rattus, Cr-Crocidura. NA-Not applicable for trapping.
Source: Authors

0.0001) (Table 2). Furthermore, significant differences (χ^2=13.1703, df = 3, p = 0.0043) in prevalence were observed among habitats in Kigoma region, where thenatural habitat had a higher prevalence of 48.72% compared to farm/fallow (36.02%), peridomestic (36%), and indoor habitats (16.25%) (Table 1).

DISCUSSION

This study reports the presence of *Bartonella* spp. from rodents and shrews from different habitats in the study regions. An overall prevalence of 22.5% of *Bartonella* spp. was found in rodents and shrews collected from indoor, peridomestic, farm/fallow and natural forests. This occurrence could be explained by the widespread nature of *Bartonella* bacteria among rodents and shrews in all sampled habitats, as previously described by Divari et al. (2021). The presence of *Bartonella* spp. in different rodents and shrews from various habitats could be attributed to the abundance and distribution of each host species and vectors in a particular habitat, as suggested by Assefa and Chelmala (2019). This could be further explained by the presence of suitable habitats in the study areas that support the breeding of various small mammals, as highlighted by Mayamba et al. (2019).

However, it is important to note that the habitat features were not the same across all regions. For instance, the Kigoma region observed large natural bushes around farms and houses, which are more favorable for different species of rodents, as noted by Nunn et al. (2021).

Nevertheless, typical field rodents, including Aethomys spp., Lemniscomys spp. and Mastomys spp. were trapped indoors in some villages, possibly due to the presence ofnatural bushes surrounding certain houses. This interaction between field rodents and indoor environments could potentially increase the rate and risk of pathogen transmission from outdoor to indoor and vice versa.

The occurrence of the Bartonella spp. in rodents and shrews from indoors and agricultural fields holds public health importance because bartonellosis is a zoonotic disease and more than 10 rodents related Bartonella spp. are known to be zoonotic (Demoncheaux et al., 2022).

In the current study, prevalence of Bartonella spp. in rodents varied substantially among the genus/species detected. This variation could be explained by the observed differences in the abundance and diversity of rodents from different sampled habitats, as earlier explained by Mardosaitė et al. (2021). Additionally, close contacts between rodent species, humans and other animals in human-related activities may contribute to the variation in prevalence (Islam et al., 2021).

Furthermore, the variation in ectoparasite types among rodent species, as observed by Peterson et al. (2017), along with the ecological behaviors such as burrowing and nesting in different rodent species, create favorable microhabitats for ectoparasites to breed (Böge et al., 2021). Grooming behavior is also important in the spread of *Bartonella* spp. within the same host species, which may influence the prevalence of *Bartonella* spp. infection in rodent communities (Bordes et al., 2007).

The presence of *Bartonella* spp. found in this study was comparable to some previous studies. Kamani et al. (2013), reported prevalence of 26% in Nigeria, while Theonest et al. (2019), and Diarra et al. (2020) detected prevalence of 17% and 17.7% in Tanzania and Mali respectively. This similarity in prevalence could be attributed to the high prevalence of *Bartonella* spp. in small mammals from various countries, as explained by several authors globally (Krügel et al., 2022).

On the contrary, zero prevalence was reported in some sylvatic rodent species including *Lemniscomys zebra*, *Tatera* spp. and *Gramommys* spp. Failure to detect *Bartonella* spp. from these rodents could be attributed to the host specificity of *Bartonella* species (Vayssier-Taussat et al., 2009) and the likelihood of host genotypes differing in their vulnerability and ability to support the replication of certain pathogens (Ostfeld and Keesing, 2012). It is worth noting that these rodent species were trapped in the same locations and habitats where other rodent species tested positive.

Nevertheless, small sample size of these rodent species investigated may have influenced the prevalence of *Bartonella* spp. in them. Further studies are encouraged to investigate the status of immunity against *Bartonella* spp. in these rodent species.

Moreover, this study detected *Bartonella* spp. from small mammals inhabiting habitats characterized by human activities including in houses, agricultural farms, and the human-wildlife interface habitats. Therefore, it implies that small mammals could carry the pathogens to human habitations, thereby increasing the risk of *Batonella* spp. infection in humans and domestic animals. However, due to unclear clinical signs and unfamiliar, bartonellosis could be underestimated risk factor contributing to some medically important diseases.

Conclusions

The study identified considerable prevalence of *Bartonella* spp. in rodents and shrews collected from different habitats across all studied districts. This implies considerable distribution of health risks to humans and domestic animals due to close contact and interactions with those small mammals particularly around the agricultural fields and human settlements. The findings of this study raise awareness of the disease among communities living in close proximity to small mammals. From these findings upcoming studies should focus on characterizing the zoonotic *Bartonella* spp., their genetic diversity and ecological factors that influence the transmission cycle. Additionally, investigations on the occurrence of *Bartonella* spp. infections in humans and the identification of risk factors for such infections should be conducted. This information will be crucial in developing control strategies to protect public health.

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CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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