

# Tick-Borne Rickettsioses, Neglected Emerging Diseases in Rural Senegal

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## Abstract

**Background:** Rickettsioses are one of the most important causes of systemic febrile illness among travelers from developed countries, but little is known about their incidence in indigenous populations, especially in West Africa.

**Methodology/Principal Findings:** Overall seroprevalence evaluated by immunofluorescence using six rickettsial antigens (spotted fever and typhus group) in rural populations of two villages of the Sine-Saloum region of Senegal was found to be 21.4% and 51% for spotted fever group rickettsiae for Dielmo and Ndiop villages, respectively. We investigated the role of tick-borne rickettsiae as the cause of acute non-malarial febrile diseases in the same villages. The incidence of rickettsial DNA in 204 blood samples from 134 (62M and 72F) febrile patients negative for malaria was studied. DNA extracted from whole blood was tested by two qPCR systems. Rickettsial DNA was found in nine patients, eight with *Rickettsia felis* (separately reported). For the first time in West Africa, *Rickettsia conorii* was diagnosed in one patient. We also tested 2,767 Ixodid ticks collected in two regions of Senegal (Niakhar and Sine-Saloum) from domestic animals (cows, sheep, goats, donkeys and horses) by qPCR and identified five different pathogenic rickettsiae. We found the following: *Rickettsia aeschlimannii* in *Hyalomma marginatum rufipes* (51.3% and 44.8% in Niakhar and Sine-Saloum region, respectively), in *Hyalomma truncatum* (6% and 6.8%) and in *Rhipicephalus evertsi evertsi* (0.5%, only in Niakhar); *R. c. conorii* in *Rh. e. evertsi* (0.4%, only in Sine-Saloum); *Rickettsia massiliae* in *Rhipicephalus guilhoni* (22.4%, only in Niakhar); *Rickettsia sibirica mongolitimonae* in *Hyalomma truncatum* (13.5%, only in Sine-Saloum); and *Rickettsia africae* in *Rhipicephalus evertsi evertsi* (0.7% and 0.4% in Niakhar and Sine-Saloum region, respectively) as well as in *Rhipicephalus annulatus* (20%, only in Sine-Saloum). We isolated two rickettsial strains from *H. truncatum*: *R. s. mongolitimonae* and *R. aeschlimannii*.

**Conclusions/Significance:** We believe that together with our previous data on the high prevalence of *R. africae* in *Amblyomma* ticks and *R. felis* infection in patients, the presented results on the distribution of pathogenic rickettsiae in ticks and the first *R. conorii* case in West Africa show that the rural population of Senegal is at risk for other tick-borne rickettsioses, which are significant causes of febrile disease in this area.

**Citation:** Mediannikov O, Diatta G, Fenollar F, Sokhna C, Trape J-F, et al. (2010) Tick-Borne Rickettsioses, Neglected Emerging Diseases in Rural Senegal. PLoS Negl Trop Dis 4(9): e821. doi:10.1371/journal.pntd.0000821

**Editor:** Pamela L. C. Small, University of Tennessee, United States of America

**Received:** April 14, 2010; **Accepted:** August 12, 2010; **Published:** September 14, 2010

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**Funding:** The authors have no support or funding to report.

**Competing Interests:** The authors have declared that no competing interests exist.

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## Introduction

Cases of tick-borne rickettsiosis have been regularly reported in North [1] and South Africa [2,3] since 1910. Despite Pijper's suggestions [4], all cases of spotted fevers in sub-Saharan Africa were considered to be Mediterranean spotted fever (MSF) with *Rickettsia conorii* as an agent [5]. *Rickettsia conorii* was isolated in Tunisia in 1932 [6]. Since that time, multiple cases of the disease and isolations of the agent have been reported, mostly in countries in the Mediterranean region. *R. conorii conorii* has also been detected in ticks in Kenya, Somalia, South Africa, and Chad [7]. In 1992, however, a case of another spotted fever group (SFG) rickettsiosis in a 36-year-old woman presenting with tick bite fever at a hospital in Zimbabwe was described [8]. Authors succeeded in isolating the etiological agent. By PCR and restriction fragment length polymorphism they proved that the obtained strain differed from all other SFG rickettsiae, including *Rickettsia conorii*. The new

strain was not, however, absolutely unique. It was indistinguishable from the strains isolated earlier from the Ixodid tick, *Amblyomma variegatum*, collected in Ethiopia [9] and from isolates recovered from another tick of the same genus, *Amblyomma hebraeum*, collected in Zimbabwe in the 1980s [10]. *Rickettsia africae*, a SFG rickettsia that causes African tick-bite fever (ATBF) officially received its name in 1996 [11]. *R. africae* seems to be very widely distributed in the continent. It has been either isolated or found by PCR in a number of African countries, including Niger, Mali, Burundi, Sudan [12], Chad, Ethiopia [13], and in most countries of equatorial and Southern Africa [14]. The majority of strains and cases are reported in South Africa [11,15]. Recently, we have reported the high prevalence of *R. africae* in *A. variegatum* in Senegal [16].

Moreover, many proven and potential rickettsial pathogens were discovered in Africa [14], mostly in ticks. *Rickettsia sibirica mongolitimonae*, the agent of lymphangitis-associated rickettsiosis

## Author Summary

Spotted fever rickettsioses are endemic diseases known since the beginning of the 21st century. They may be severe, like Rocky Mountain Spotted fever in the Americas, and are always transmitted by the tick bite. In Africa, little is known about the prevalence of these diseases; most available data is from the travelers who felt ill after coming back to Europe and USA. We have studied the distribution of bacteria causing different spotted fevers (rickettsiae) in rural Senegal, as well as the role of these bacteria in human pathology among indigenous population. We have found that up to half of tested villagers have serological evidence of contact with rickettsiae and in some cases these bacteria may be found in the blood of feverish patients. From the other side, almost all species of ticks that may be collected in the villages on domestic animals also harbor the pathogenic bacteria. In total, six different species of rickettsiae were identified in ticks. We believe that our data cast light on the problem of unexplained fevers in West Africa.

(LAR) was identified in ticks in Niger 10 years after its first isolation in China in 1991 [12]. *Rickettsia slovaca*, which causes tick-borne lymphadenopathy (TIBOLA) in Europe, was found in *Dermacentor marginatus* ticks in Morocco by PCR [17]. Two *Ixodes*-associated rickettsiae, *Rickettsia helvetica* and *Rickettsia monacensis*, were also detected in ticks in North Africa [17,18]. Both were reported several times as probable human pathogens, although more information is required regarding their pathogenicity [14]. Beginning in 1994, another SFG rickettsia, *Rickettsia massiliae*, was repeatedly detected in *Rhipicephalus* spp. ticks in Central African Republic, Mali, Algeria and Morocco [12,17,19,20]. The first human case of spotted fever caused by this rickettsia was identified in 2005 [21]. *Rickettsia aeschlimannii* was first isolated in Morocco in 1992 from the *Hyalomma marginatum marginatum* tick [22]. Genotypically similar or identical strains were reported in many regions, including Kazakhstan, Southern Europe, Zimbabwe, Mali, Niger, and Algeria [14,19]. These strains are almost always associated with almost always associated with *Hyalomma* ticks. Several human cases have been reported in Africa, including the sub-Saharan regions [14]. Many other SFG rickettsiae not previously associated with human diseases have been reported in Ixodid ticks in Africa. Some of them are genetically described and registered under *Candidatus* status [23].

Tick-borne rickettsioses play a very important role in public health. A recent worldwide report demonstrated a 5.6% incidence of rickettsial infection in a group of travelers who developed acute febrile infections after returning from sub-Saharan Africa. It is one of the most frequently identified etiology for systemic febrile illness among travelers, following malaria [24,25].

The precise serological identification of the etiological agent of spotted fever in humans may be difficult because of the strong cross-reactivity in serological studies [26]. In some cases, cross-absorption studies and western blots may help [27], but these techniques may only work in cases in which the suspected agent is known and isolated. In all cases of new and emerging rickettsioses, the serological study may indicate only the group etiology (SFG). One of the first studies performed with *R. conorii* antigen showed the strikingly high incidence of rickettsial antibodies in human sera from many African countries, including Angola, Burkina Faso, Central African Republic, Mali, Cote d'Ivoire [28], Zambia [29], and other countries [30–40]. The percentage of seroprevalence found in different studies is shown in Figure 1.

The growing number of newly discovered rickettsial species outlines the indispensable role of molecular methods in microbiology. However, the studies are still in early stages because the distribution of many agents of rickettsioses is incompletely described. West Africa, including Senegal, remains incompletely studied in terms of tick-borne rickettsioses. Despite recent reports of high rates of infection of *A. variegatum* ticks in Senegal [16], other tick species were never studied for the presence of rickettsial agents. Thirty-three species of Ixodid ticks are known in Senegal [41]; many of them are associated with domestic animals and readily bite humans.

The present work was performed in order to enlarge the scant knowledge about tick-borne rickettsioses in Senegal.

## Materials and Methods

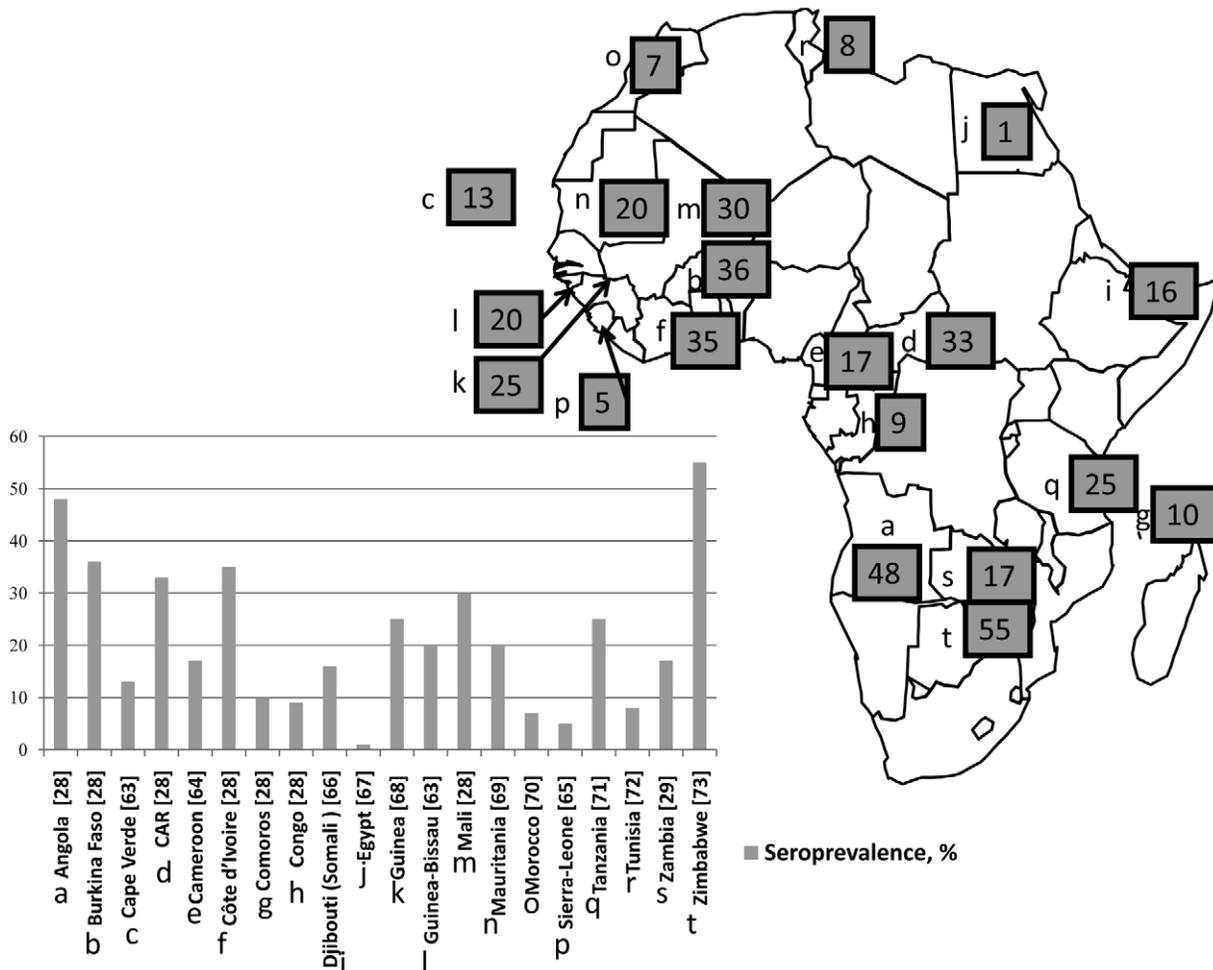
### Human sample collection and treatment

The study was performed in two Senegalese villages, Dielmo (13°43'N;16°24'W) and Ndiop (13°41'N;16°22'W), situated in the Sine-Saloum region. Since 1990, a longitudinal study of malaria and tick-borne relapsing fever has been ongoing in these villages [42,43]. The project consists of long-term investigations of host-parasite relationships in the entire village population, which was enrolled in a longitudinal prospective study. The project was approved by the National Ethics Committee of Senegal [42] and the Local Ethics Committee (Marseille, France). Written individual informed consent was obtained from each participant, including the parents or legal guardians of all children, at the beginning of the current study. Dielmo and Ndiop villagers are settled agricultural workers. Millet and peanut crops are cultivated during the rainy season, and market gardening is the main agricultural activity during the dry season.

Here we used the serological techniques to detect immune response to different rickettsial species. We tested the samples from the serological bank created for the above-mentioned longitudinal study and collected in 2008. In total, 238 serum samples collected in Dielmo in 2008 (mean age 26±18, range from 3 to 78, 117 men and 121 women) and 241 samples from Ndiop (mean age 25±17, range from 5 to 82, 112 men and 129 women) were tested.

Another part of the study was to investigate the role of tick-borne rickettsiae as the causes of acute non-malarial febrile disease in rural populations of the same villages. Interviews and sampling were conducted in the same two villages from December 2008 through June 2009. During the period between November 2008 and July 2009, a total of 204 samples from 134 patients (62M and 72F) were included in this study. In this study, we included patients who came into the dispensary with a recent fever and had negative test results for malaria; 103 (77%) were from Dielmo (468 inhabitants) and 31 (23%) from Ndiop (628 inhabitants); 90 (67.2%) were younger than 10 years, including 64 (47.8%) under five years. No one died during the study.

Medical examinations were performed by a medical attendant for each individual with fever (defined by an axillary temperature >37.5°C). A questionnaire was completed for each individual. Whole blood was collected from the fingertip by lancet stick and then applied to glass microscope slides. Thick and thin blood smears were stained with Giemsa and analyzed by microscopy for the trophozoites and gametocytes of malaria. If the malaria test was negative, 200 µl of whole blood (3–4 drops) were collected for DNA extraction. The first stages of DNA extraction (digesting, binding and washing) was performed directly in the village dispensary using the QIAamp kit (QIAGEN, Hilden, Germany). The columns with the bound and dry DNA inside were then stored at 4°C before transportation and final elution, which was performed in URMITE, Marseilles, France.



**Figure 1. Map of Africa showing the countries where serological studies for SFG rickettsioses were performed before our study.** The numbers on the map indicate seroprevalence in %. The diagram represents relative seroprevalence in different countries and reference [in square brackets].

doi:10.1371/journal.pntd.0000821.g001

## Ticks

In November-December 2008, ticks were collected from domestic animals (cows, goats, sheep, horses, donkeys) in two regions of Senegal: Sine-Saloum and Niakhar (Table 1, Figure 2). A total of 406 ticks were collected from four villages in the Sine-Saloum region and 2361 ticks from the Niakhar region. They were stored in 70% ethanol. Twenty adult *Hyalomma truncatum* ticks were preserved alive in a flask at 90–95% of relative humidity. The species and sex were identified according to standard taxonomic keys for adult ticks [44,45].

## Culture

Live *H. truncatum* ticks were used for bacterial culture and were not included in the overall statistics. Each was washed in a 10% water solution of a commercial disinfectant-detergent (Amphomousse, Hydenet S.A., Sainghin-en-Melantois, France), then rinsed in sterile water and placed in a 1% solution of sodium hypochlorite for 10 min. After rinsing with distilled water, they were incubated in 70% ethanol for 15 min. A final rinse in sterile phosphate buffer saline preceded inoculation. Ticks were placed in a sterile 1.5 ml plastic tube, where they were triturated with a sterile micropestle in 300  $\mu$ l of Minimum Essential Medium (MEM) supplied with 4% of fetal bovine serum (FBS). Isolation

was done according to the well-known shell-vial technique with modifications [46]. We used 300  $\mu$ l of whole tick suspension for inoculation of a vial with a monolayer of L929 cells. After centrifugation, the supernatant was removed and conserved. The cells were covered with culture media (MEM, 4% FBS). Antibiotics were not used during the cultivation.

## Molecular biology

DNA from homogenized ticks that were conserved in ethanol, supernatants collected after shell-vial inoculation, as well as supernatants of cell culture were extracted using the BioRobot MDx Workstation (Qiagen, Courtaboeuf, France) with a customized extraction protocol following the manufacturer's instructions. DNA was stored at 4°C until use in PCR amplifications. Rickettsial DNA was initially detected by *Rickettsia* genus-specific quantitative PCR (qPCR) reactions that were performed using LightCycler 2.0 equipment and software (Roche Diagnostics GmbH, Mannheim, Germany). Master mixtures were prepared by following the instructions of the manufacturer with primers RKND03F and RKND03R and a probe, whose sequences are specific for the sequence of the rickettsial citrate synthase gene. PCR cycling and melting curve conditions have been described previously [47]. A new qPCR system based on rickettsial *scal* gene and specific for *R.*

**Table 1.** Geographic coordinates of tick collection sites.

Region	Village	Coordinates
Sine-Saloum	Dielmo	13°43'N;16°24'W
	Ndiop	13°41'N;16°22'W
	Medina	13°42'N;16°24'W
	Passi	13°42'N;16°23'W
Niakhar	Ngangarlame	14°34'N-16°29'W
	Poudaye	14°32'N-16°28'W
	Toucar	14°32'N-16°28'W
	Poultok Diohine	14°31'N-16°29'W
	Ngonine	14°34'N-16°31'W
	Logdir	14°29'N-16°29'W
	Ngayokheme	14°31'N-16°26'W
	Diokoul	14°29'N-16°26'W
	Sob	14°29'N-16°26'W
	Diohine	14°30'N-16°30'W
	Kalom	14°31'N-16°25'W
	Sass-Ndiafadji	14°30'N-16°24'W
	Mboyene	14°31'N-16°27'W
	Ngan-Fissel	14°30'N-16°26'W
Ngardiamé	14°29'N-16°27'W	
Ngonine	14°34'N-16°31'W	

doi:10.1371/journal.pntd.0000821.t001

*aeschlimannii* was designed and tested for specificity and sensitivity. The sequences of the primers and probe are as follows: forward primer R\_aesSca1\_F 3'-AAGCGGCACCTTATAGGTAAAGAAA-5', reverse primer R\_aesSca1\_R 3'-CATGCTCTGCAAATGAACCA-5', probe 6-FAM®-TGGGGAAATATGCCGTATACGCAAGC-TAMRA®. Specificity was tested with 26 species and strains of different rickettsiae and sensitivity was compared with RKND03 by serial dilutions [47].

Chosen positive samples were subjected to simple PCR using primers manufactured by Eurogentec, Seraing, Belgium. They amplified almost the complete genetic sequence of rickettsial citrate synthase (*glcA*), as previously described [48,49]. Additionally, a 632 bp fragment of the *ompA* gene was amplified using Rr. 190.70 and Rr. 190.701 primers [50].

The screening of DNA from human samples for SFG rickettsiae was also performed with the Rickettsia genus-specific RKND03 qPCR system. The positive results were then confirmed by the "1029 system" based on the RC0338 gene (referenced by *R. conorii* genome AE006914) coding for hypothetical protein and present in all rickettsiae of spotted fever group [51]. A nested PCR was later used to obtain the larger portion of the rickettsial *glcA* gene for the subsequent sequencing of the amplicons derived from positive samples. For the nested PCR, CS2d and CSendR primers were used to amplify most of the full-length *glcA* gene, and the primers RpCS409p and RpCS877p were subsequently used as described above.

We used the amplification of the beta actin gene by specific qPCR [51] as the control for appropriate handling and extraction of DNA from human samples.

DNA extracted from uninfected ticks from colonies at the Unité des Rickettsies, Marseille, France and sterile cardiac valve biopsies were used as negative controls, and DNA extracted from the cell culture supernatant of *Rickettsia bellii* served as a positive control.

Polymerase chain reactions were performed in automated DNA thermal cyclers (GeneAmp 2400 and 9700; Applied Biosystems, Foster City, CA, USA). PCR products were visualized by electrophoresis on a 1.5% agarose gel, stained with ethidium bromide, and examined using an ultraviolet transilluminator. The PCR products were purified using a QIAquick Spin PCR Purification Kit (Qiagen) according to the manufacturer's instructions. Sequencing of amplicons was performed using the BigDye Terminator Cycle Sequencing Kit (Perkin Elmer Applied Biosystems) with an ABI automated sequencer (Applied Biosystems). Obtained sequences were assembled (ChromasPro 1.49 beta, Technelysium Pty Ltd, Tewantin, Australia), edited by BioEdit Sequence alignment editor v. 7.0.9.0 [52], and compared with those available in GenBank by NCBI BLAST (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>). Sequences of *glcA* genes from *Rickettsia* species chosen in GenBank for comparison were concatenated and aligned with the ClustalW program, and a neighbor-joining phylogenetic tree was constructed with Geneious 4.7.6 software (Biomatters Ltd, Australia).

### Serological studies

Titers of IgG and IgM antibodies in serum samples obtained from each person were determined using an indirect immunofluorescence assay with antigens generated in-house. We tested sera with the following antigens: *R. conorii conorii* strain Malish (ATCC VR-613), *R. africae* strain ESF-5, *R. aeschlimannii* strain MC16, *Rickettsia sibirica mongolitimonae* strain HA-91 (ATCC VR-1526), *Rickettsia felis* strain Marseille (ATCC VR-1525), and *R. typhi* strain Wilmington. All serum samples were diluted at ratios of 1:25, 1:50, and 1:100 and were screened for total immunoglobulin. If the serological screening with any rickettsial antigen was positive, final titers for IgG and IgM were determined for all anti-rickettsial antibodies.

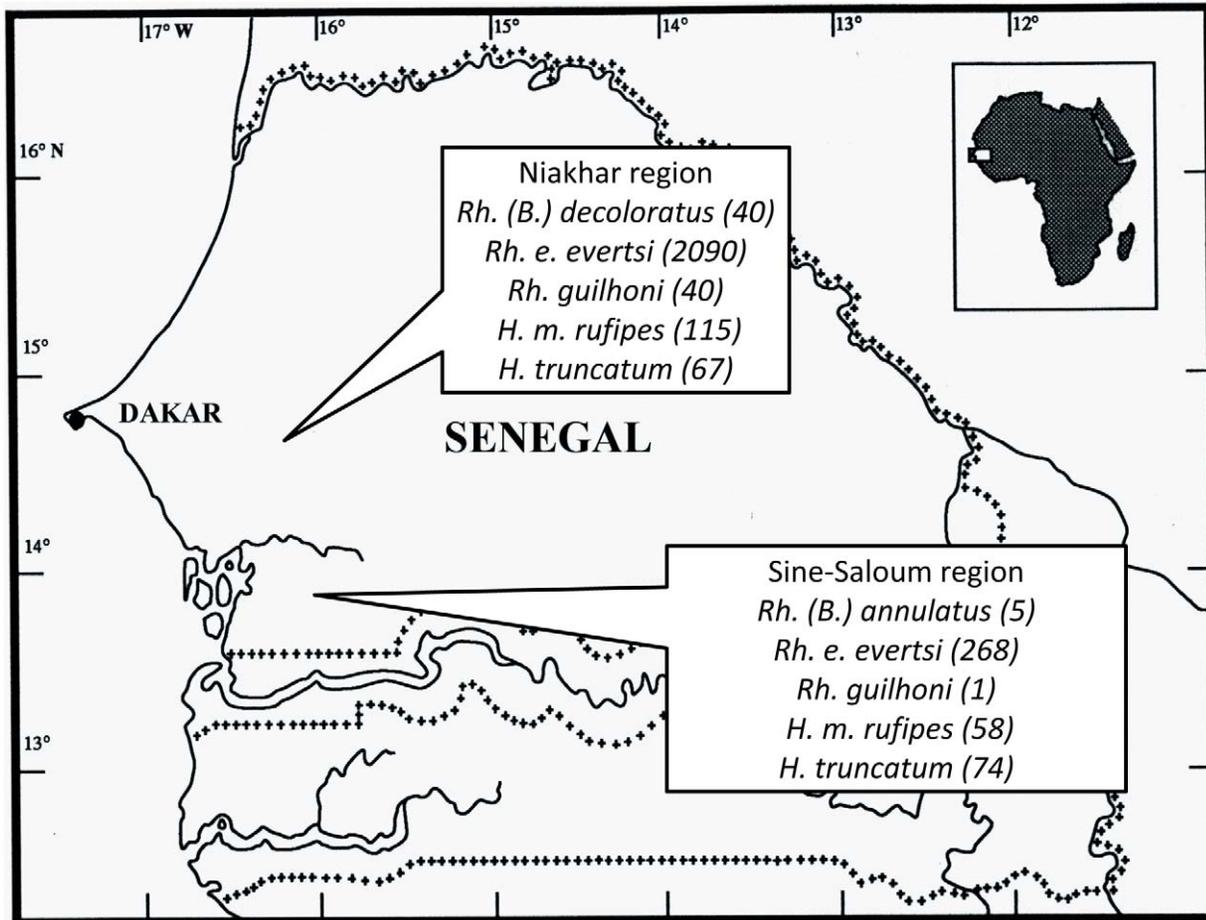
### Statistical analysis

Data were analyzed using Epi Info software, version 3.4.1 (Centers for Disease Control and Prevention, Atlanta, GA, USA). Non-parametric values were compared using a  $\chi^2$  test. Statistical significance was defined as  $p < 0.05$ .

## Results

### Human samples

We have found that that 51/238 (21.4%) and 123/241 (51%) of randomly screened healthy population of the Dielmo and Ndiop villages of Sine-Saloum region of Senegal, respectively, had serological evidence of contact with rickettsiae (Table 2). We have noted that the prevalence of anti-rickettsial antibodies in sera was higher in young villagers, with the positive ratio declining with age. This tendency was always true for Ndiop; however, in Dielmo only inhabitants older than 40 showed a higher seroprevalence compared with the younger population (Table 2). In most cases, sera reacted with several rickettsial antigens, and the titers of total Ig were low and did not exceed 1/100 (94.1% of positive results in Dielmo and 88% in Ndiop). We found IgM in 2 out of 3 sera with high antibody levels from Dielmo and in 13 of 15 from Ndiop, indicating recent infection. The highest titers for IgG and IgM were 1/256, and both sera were from Ndiop. We identified the antibodies against *R. typhi* in 6 cases (2.4%) from Dielmo and in 7 cases (2.9%) from Ndiop, but in all cases sera also reacted with rickettsiae of SFG with at least the same titers. Only one patient from Dielmo had low titer (1/50) antibodies against *R. felis*. His serum also reacted with *R. typhi* and all SFG rickettsiae. We noted that among all antigens tested, *R. africae* reacted most often with



**Figure 2. Map of Senegal with indicated locations of tick collection, species of ticks and a quantity collected.**  
doi:10.1371/journal.pntd.0000821.g002

the tested sera; 49 of 51 (96%) and 110 of 123 (89%) reacted with its antigen in Dielmo and Ndiop respectively; it constitutes 20.6% and 45.6% of tested villagers, respectively. The second most commonly reactive rickettsia was *R. sibirica mongolitimonae* with 35 sera of 51 (68.6% and 14.7% of tested villagers) positive sera from Dielmo and 93 sera of 123 (75.6% and 35.6% of tested villagers) positive sera from Ndiop.

As for rickettsial DNA, nine patients who presented in the dispensary with acute fever of non-malarial origin were positive. We considered patients positive only in samples in which the qPCRs for both rickettsial genes were positive and the subsequent standard PCR/sequencing produced the rickettsial *gltA* gene. Data for eight of the patients positive for the DNA of *R. felis* were already reported [51]. In one patient, we have successfully amplified the DNA of *Rickettsia conorii conorii*. The patient was a 4-year-old girl with tachycardia and a fever that appeared on the same day (27 March 2009). No rash or eschar was noticed during her examination. Paracetamol was prescribed and the girl was sent home. The fever resolved within several days without antibiotics.

## Ticks

We have collected ticks of seven different species on domestic animals (Table 3), 491 ticks from four villages in the Sine-Saloum region and 2494 ticks from 16 villages of the Niakhar region. The results of studies of *Amblyomma variegatum* ticks have already been reported (74/85 (87.1%) and 101/133 (79.7%) positive for *R.*

*africae*, respectively, for both regions) [16]. The majority of ticks in both regions (268 of 406 (66%) and 2090 of 2361 (88.5%)) were represented by *Rhipicephalus evertsi evertsi* (Figure 3). In our study, *Rhipicephalus guilhoni* was the predominantly collected species in the Niakhar region (49 of 50 ticks collected). Most of the ticks (85.7%) were collected from donkeys. We have collected only five *Rhipicephalus (Boophilus) annulatus* ticks and these ticks were all collected in the Sine-Saloum region. Another species, *Rhipicephalus (B.) decoloratus*, was only collected in the Niakhar region. Two species of the *Hyalomma* genus were collected in both regions. *Hyalomma marginatum rufipes* was less common than *Hyalomma truncatum* in Sine-Saloum (58 ticks collected versus 74) when compared with Niakhar (115 versus 67).

## Molecular identification of rickettsiae in ticks

We found three different rickettsial species in *Rh. e. evertsi*, with a low rate of infection from 0.4 to 0.7% (Table 3). In the Sine-Saloum region, one tick collected from the horse was infected with *R. conorii conorii*, the agent of MSF. One tick from Sine-Saloum and 14/2090 (0.7%) total were infected with *R. africae*, the agent of African tick-bite fever. This finding represents the first time that it was found in *Rh. e. evertsi*. In the Niakhar region, 10 (0.5%) ticks were infected by *R. aeschlimannii*. In both regions we were able to amplify and sequence almost complete *gltA* gene (all samples positive by qPCR were subjected to standard PCR and sequencing). The *gltA* sequence was not absolutely identical to

**Table 2.** Results of serological screening of the generally healthy population of two villages (Dielmo and Ndiop) of the Sine-Saloum region of Senegal.

Dielmo				Ndiop				P value
Population screened, number of participants								
238				241				
Positive with at least one SFG rickettsial antigen at titer of 1/50 minimum, number (% of screened)								
51 (21.4%)				123 (51%)				<10 <sup>-3</sup>
Age	No. of positives	% among screened of the same age	% among positives	Age	No. of positives	% among screened of the same age	% among positives	
3–5	3	33.3	5.9	3–5	4	66.7	3.3	
6–10	11	25.6	21.6	6–10	26	57.8	21.1	
11–15	6	13.3	11.8	11–15	23	59.0	18.7	
16–20	4	14.3	7.8	16–20	22	52.4	17.9	
21–40	8	14.	15.7	21–40	27	43.5	22.0	
>40	19	33.9	37.3	>40	21	44.7	17.1	
Positive with <i>R. typhi</i> antigen at titer of 1/50 minimum, number (% of screened)								
6 (2.4%)				7 (2.9%)				0.8
Positive with <i>R. africae</i> antigen at titer of 1/50 minimum, number (% of screened; % of overall positive with rickettsial antigens)								
49 (20.6%; 96%)				110 (45.6%; 89%)				<10 <sup>-3</sup> (0.1)
Positive with <i>R. sibirica mongolitimonae</i> antigen at titer of 1/50 minimum, number (% of screened; % of overall positive with rickettsial antigens)								
35 (14.7%; 68.6%)				93 (35.6%; 75.6%)				<10 <sup>-3</sup> (0.3)
Positive with at least one SFG rickettsial antigen at titer of higher than 1/50, number (% of screened; % of overall positive with rickettsial antigens)								
3 (1.3%; 5.9%)				15 (6.2%; 12%)				0.004 (0.2)

doi:10.1371/journal.pntd.0000821.t002

the *R. africae* reference strain (ESF-5), the clonality of which was previously based on analysis of strains isolated from patients and *A. variegatum* ticks [53]. Moreover, the sequence of the *gltA* gene of *R.*

*aeschlimannii* found in *Rh. e. evertsi* differed slightly from all GenBank records. The phylogenetic positions of these rickettsiae are shown in Figure 4.

**Table 3.** Tick species collected in Senegal and studied for SFG rickettsiae.

Species	Collected	Positive for rickettsiae: number (%)			Species of rickettsial identified	Animals from which positive ticks were collected
		In total in region	Dielmo	Ndiop		
<b>Niakhar region</b>						
<i>Rhipicephalus (Boophilus) decoloratus</i>	40	0			-	-
<i>Hyalomma marginatum rufipes</i>	115	60 (51.3%)			<i>Rickettsia aeschlimannii</i>	Cows, donkeys, sheep, goats, horses
<i>Hyalomma truncatum</i>	67	4 (6%)			<i>Rickettsia aeschlimannii</i>	Cows, donkeys, sheep, goats, horses
<i>Rhipicephalus evertsi evertsi</i>	2090	14 (0.7%) 10 (0.5%)			<i>Rickettsia africae</i> <i>Rickettsia aeschlimannii</i>	Cows, donkeys, sheep, goats, horses
<i>Rhipicephalus guilhoni</i>	49	11 (22.4%)			<i>Rickettsia massiliae</i>	Predominantly donkeys (9), cows (2)
<b>Sine-Saloum region</b>						
		In total in region	Dielmo	Ndiop		
<i>Rhipicephalus (Boophilus) annulatus</i>	5	1 (20%)	0/1 (0%)	0/2 (0%)	<i>Rickettsia africae</i>	Cow
<i>Hyalomma marginatum rufipes</i>	58	26 (44.8%)	0/2 (0%)	19/43 (44%)	<i>Rickettsia aeschlimannii</i>	Cows, donkeys, sheep, goats, horses
<i>Hyalomma truncatum</i>	74	5 (6.8%)	1/25 (4%)	1/30 (3%)	<i>Rickettsia aeschlimannii</i>	Cows, donkeys, sheep, goats, horses
		10 (13.5%)	5/25 (20%)	3/30 (10%)	<i>Rickettsia sibirica mongolitimonae</i>	Cows, donkeys, sheep, goats, horses
<i>Rhipicephalus evertsi evertsi</i>	268	1 (0.4%)	0/21 (0%)	0/151 (0%)	<i>Rickettsia conorii</i> ssp.	Horse
		1 (0.4%)	0/21 (0%)	1/151 (0.7%)	<i>Rickettsia africae</i> 99%	Sheep
<i>Rhipicephalus guilhoni</i>	1	0	0	0	-	-

Separate columns represent data for two villages in the Sine-Saloum region (Dielmo and Ndiop) where serological and molecular studies in humans were performed. doi:10.1371/journal.pntd.0000821.t003



*Rhipicephalus evertsii evertsii*, ♂

- *Rickettsia africae* (0.4%, Sine-Saloum; 0.7% Niakhar)
- *Rickettsia aeschlimannii* (0.5%, Niakhar)
- *Rickettsia conorii* (0.4%, Sine-Saloum)



*Rhipicephalus guilhoni*, ♂

- *Rickettsia massiliae* (22%, Niakhar)



*Rhipicephalus (Boophilus) annulatus*, ♀

- *Rickettsia africae* (5%, Sine-Saloum)



*Hyalomma truncatum*, ♂

- *Rickettsia aeschlimannii* (6.8%, Sine-Saloum; 6% Niakhar)
- *Rickettsia sibirica mogolitimona* (13.5%, Sine-Saloum)



*Hyalomma marginatum rufipes*, ♂

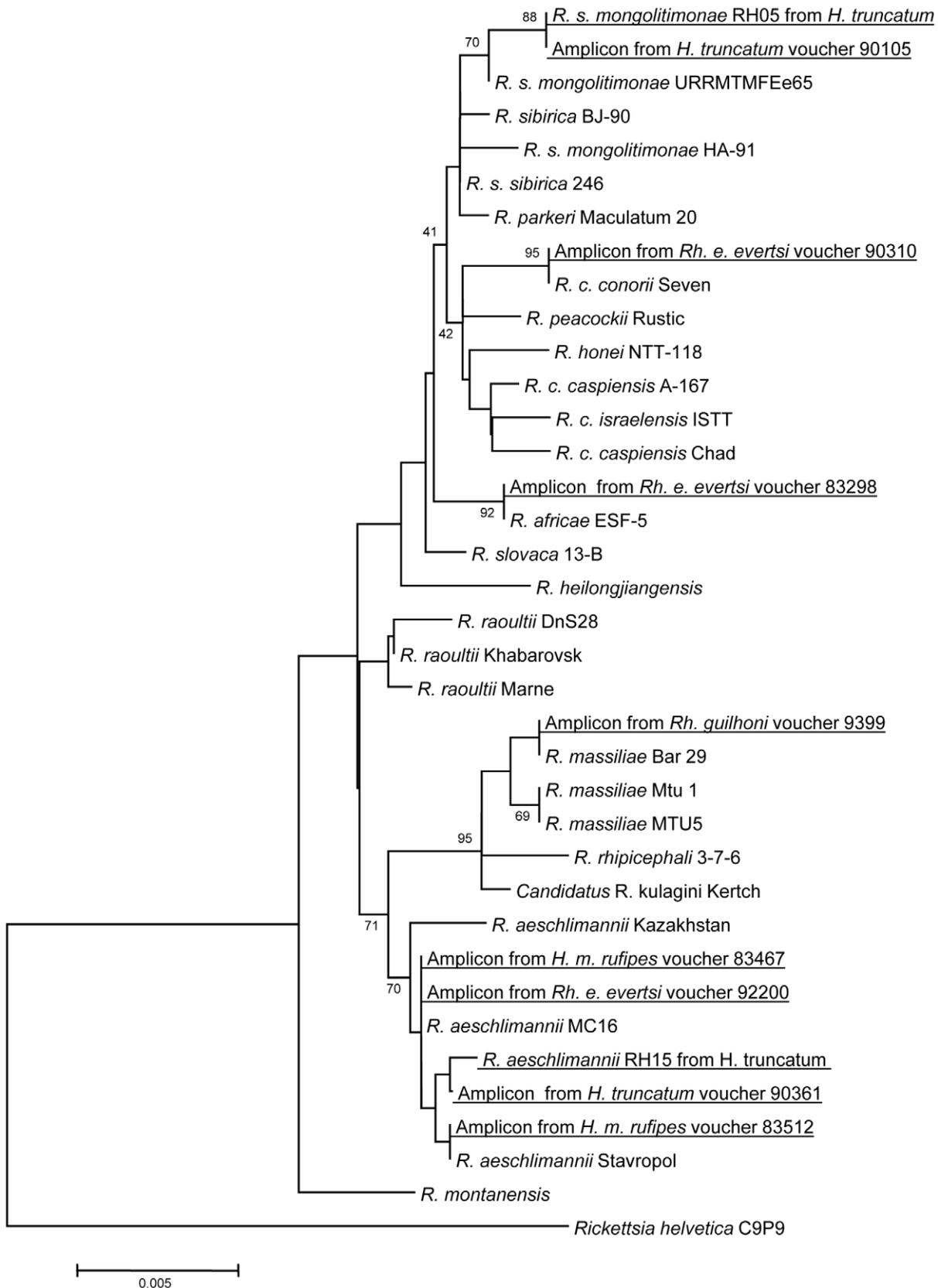
- *Rickettsia aeschlimannii* (44.8%, Sine-Saloum; 51.3% Niakhar)

**Figure 3. Photos of ticks studied with indication of rickettsiae found by PCR.**

doi:10.1371/journal.pntd.0000821.g003

We have identified only one rickettsia in *Rh. guilhoni* and only in the Niakhar region. All samples positive by qPCR were subjected to a standard PCR (*ompA* and *gltA* genes) and amplicons were sequenced. Both genes showed 100% identity

with *R. massiliae* strain Bar29 isolated from *Rh. sanguineus* from Spain. The rate of infection in the Niakhar region is 22.4%; in Sine-Saloum the only collected tick was negative by PCR.



**Figure 4. Phylogenetic tree based on aligned complete sequences of *gItA* gene and constructed by neighbor-joining method. Numbers in nodes represent bootstrap values.** The tree shows the position of isolates and amplicons from ticks collected in Senegal.  
doi:10.1371/journal.pntd.0000821.g004

We have also tested two species of *Rhipicephalus* (*Boophilus*) ticks; *R. africana* was also detected in one *Rh. (B.) annulatus* tick from Sine-Saloum. The *gltA* and *ompA* sequences were identical to the reference strain, ESF-5. All of our *Rhipicephalus (B.) decoloratus* ticks were negative when tested by rickettsial genus-specific qPCR. We found that 44.8% and 51.3% of *H. marginatum rufipes* ticks in the Sine-Saloum and Niakhar regions, respectively, are infected with *R. aeschlimannii*. In our study, it was the only species of rickettsiae identified in this species of tick. All ticks positive by genus-specific qPCR were subjected to a *R. aeschlimannii*-specific qPCR and all were found to be positive. In 6.8% and 4.6% of *H. truncatum* ticks from the Sine-Saloum and Niakhar regions, respectively, we found a variant of *R. aeschlimannii* that insignificantly differed from the one found in *Rh. e. evertsi* and *H. m. rufipes* (Figure 4). We also identified *R. s. mongolitimonae* in 13.5% of ticks, but only in the Sine-Saloum region. All ticks positive by genus-specific qPCR were tested for *R. aeschlimannii*-specific qPCR. Positive ticks were considered to harbor *R. aeschlimannii* and all negative ticks were subjected to a standard PCR with sequencing. The *gltA* gene of *R. s. mongolitimonae* was identified in all positive ticks.

### Rickettsial strains

We have also succeeded in isolating two strains of rickettsiae from *Hyalomma truncatum* collected in Dielmo village, in the region of Sine-Saloum. Both strains were deposited in official collection of Unité des Rickettsies, Medical Faculty, Marseilles, France ([http://ifr48.timone.univ-mrs.fr/portail2/index.php?option=com\\_content&task=view&id=96](http://ifr48.timone.univ-mrs.fr/portail2/index.php?option=com_content&task=view&id=96)) under the following references: CSUR R175 for *R. s. mongolitimonae* strain RH05 and CSUR R176 for *R. aeschlimannii* strain RH15. Sequences of the *rrs*, *gltA*, *ompA*, *ompB*, and *sca4* genes of *R. sibirica mongolitimonae*, strain RH05, were deposited in GenBank under the accession numbers HM050271, HM050296, HM050272, HM050273, and HM050295, respectively. Sequences of the *rrs*, *gltA*, *ompA*, *ompB*, and *sca4* genes of *R. aeschlimannii*, strain RH15, were deposited in GenBank under the accession numbers HM050274, HM050276, HM050277, HM050278, and HM050275, respectively. According to the proposed criteria for species definition in rickettsiology [54], the isolated bacteria do not belong to a new species. Strain RH05 was close but not identical to *R. s. mongolitimonae*. Strain RH15 was also close but not identical to *R. aeschlimannii*. The degree of divergence of the five above-mentioned genes from the closest relative (*R. s. mongolitimonae* for RH05 and *R. aeschlimannii* for RH15) was less than that required for the definition of a new species. Genes of both strains were almost completely identical with sequenced amplicons from *H. truncatum* ticks.

Sequenced amplicons from the ticks were registered in GenBank under the following accession numbers: *gltA* and *ompA* genes of *R. s. mongolitimonae* from *H. truncatum* voucher #90105 (HM050279 and HM050280); *gltA* and *ompA* genes of *R. aeschlimannii* from *H. truncatum* voucher #90361 (HM050282 and HM050281); *gltA* and *ompA* genes of *R. aeschlimannii* from *H. m. rufipes* voucher #83512 (HM050283 and HM050284); voucher #83467 (HM050285 and HM050286); *gltA* and *ompA* genes of *R. africana* from *Rh. e. evertsi* voucher #83298 (HM050288 and HM050287); *gltA* and *ompA* genes of *R. aeschlimannii* from *Rh. e. evertsi* voucher #92200 (HM050289 and HM050290); *gltA* and *ompA* genes of *R. massiliae* from *Rh. guilhoni* voucher #93995 (HM050293 and HM050294); and *gltA* and *ompA* genes of *R. conorii* from *Rh. e. evertsi* voucher #90310 (HM050292 and HM050291).

### Discussion

Entomological studies performed in two regions of Senegal confirmed that Ixodid ticks, the potential vectors of spotted fevers

in Senegal, are highly prevalent in domestic animals and that the close contact of humans with ticks is continual and permanent. Seven different tick species of 33 known in Senegal were collected in the studied regions. The most abundant species, *Rhipicephalus evertsi evertsi*, is one of the most common ticks that feed not only on domestic animals, but also many species of wild animals in Africa [41,55]. The species is confined to the Afrotropical zoogeographical region in sub-Saharan Africa [44]. This species, although very common and prevalent, has not been frequently studied as the vector of agents of humans and animal diseases. To date, it has been known to transmit the protozoa *Babesia bigemina* [56], Crimean-Congo hemorrhagic fever virus (CCHFV) [57], and *Ehrlichia ruminantium* [58]. Rickettsial agents have not been previously reported in these ticks, although tick hemolymph tests showed the presence of rickettsial-like organisms [10]. Here, we report the first identification of *R. conorii* in Senegal and in this tick. This report also provides the first evidence of the role of this tick species in the epidemiology of MSF. Despite its very low infection rate (that is, in fact, always very low for all vectors of MSF [7]), the abundance of this tick and its close contact with humans who take care of and often live close to animals increases the probability of infection. Two other rickettsial species, *R. africana* and *R. aeschlimannii*, were not previously reported in *Rh. e. evertsi*.

*Rh. guilhoni* is a member of the *Rhipicephalus sanguineus* group. It can be a common tick in the drier areas in a horizontal band south of the Sahara. Cattle, sheep, horses, and dogs, as well as wild carnivores and birds are the preferred hosts of adult *Rh. guilhoni* [44]. The only previously known pathogenic agent associated with this species is CCHFV [57], although the disease itself has never been reported to result from a bite by this tick. *R. massiliae*, a recently emerged pathogen [21], was found in our study of this tick. Interestingly, this rarely studied species was collected from donkeys and ruminants and not from dogs, which are the usual hosts for ticks of the *R. sanguineus* group.

Ticks of the *Boophilus* sub-genus of *Rhipicephalus* are one-host ticks with a monotropic type of behavior. *Rhipicephalus (Boophilus) annulatus* transmits the protozoans *Babesia bigemina* and *Babesia bovis* to cattle, both of which cause bovine babesiosis. It also transmits *Anaplasma marginale* and *Eh. ruminantium* to cattle [44]. *R. africana* has also been found in the closely related species, *Rhipicephalus (B.) microplus* [59]. *Rhipicephalus (B.) decoloratus* was already shown to harbor *R. africana* in Botswana [60]. Our finding of typical *R. africana* in *Rh. (B.) annulatus* is not surprising. The low percentage of infection compared with *A. variegatum* collected in the same region from the same animals may be explained by lower genus/species susceptibility to *R. africana*.

*H. marginatum rufipes* is the most widespread *Hyalomma* in Africa and is notorious as a vector of the CCHF virus [61]. The feeding of adults on cattle often causes large lesions at the attachment sites, leading to the formation of severe abscesses. It has also been identified as a host of *R. aeschlimannii* [22], which our data supported. *H. truncatum* is found predominantly in sub-Saharan Africa where it may be the most common *Hyalomma*. This species of tick is notorious for causing many types of direct damage to its hosts. Certain strains of *H. truncatum* have a toxin in their saliva that causes the skin disease known as sweating sickness in cattle [62], particularly calves. *H. truncatum* also transmits the protozoan *Babesia caballi* to horses [44]. Rickettsia-like organisms have been previously observed microscopically in this species [10]. We found *R. s. mongolitimonae*, which causes lymphangitis-associated rickettsiosis, in this aggressive tick that readily bites humans. Interestingly, the reported clinical picture of the illness caused by this rickettsia strikingly resembles the description of the disease of “young shepherds” mentioned by the village chiefs. The theory

that rickettsiae are responsible for this disease is also supported by the highest seroprevalence in the younger members of the village population.

Finally, we have identified five different pathogenic rickettsial species in tick vectors with an incidence up to 51.3% (*R. aeschlimannii* in *H. marginatum rufipes*). *R. africae* is a pathogen known to be responsible for African tick-bite fever. The high incidence (87.1%) of this rickettsia in *A. variegatum* ticks was previously reported. We have found that, although to a lesser degree, two other species of ticks, *Rh. e. evertsi* and *Boophilus (Rhipicephalus) annulatus*, may harbor this pathogen. *R. aeschlimannii* is a recently recognized pathogen [63]. The properties of aggressivity, abundance, and the high rate of infection of vectors that are characteristic of ticks of the *Hyalomma* genus may enhance the probability of this infection.

We suppose that ticks in Senegal may play an important role in the transmission of vector-borne diseases, primarily because of the elevated probability of contact with humans and because of high levels of rickettsial infection in ticks. Indirect evidence of the role of Ixodid ticks in vector-borne diseases may be obtained from local populations. The village chiefs of Dielmo and Ndiop told us, for instance, that the beginning of the field activities of children coincides with the appearance of multiple eschar-like lesions on the child's ankles that is often associated with a fever. This description perfectly corresponds with many rickettsial diseases, including African tick-bite fever (Table 4). Several publications from other regions confirm that Ixodid ticks, and especially tick larvae, may be a serious pest, causing "skin disease" [64,65]. Here and in previous works [16], we have shown that *A. variegatum*, *H. marginatum rufipes*, *H. truncatum*, and *Rh. evertsi evertsi* are among the most important species that may have a contact with humans.

The results of the serological screening confirmed our assumption. They showed a very high prevalence (21.4% and 51% in Dielmo and Ndiop, respectively) of sera that react with rickettsial antigens (spotted fever group) in a generally healthy population of rural Senegal. Generally, our results correspond with the previous data from Burkina Faso, Central African Republic, Mali, Cote d'Ivoire, and Guinea-Bissau where an incidence of rickettsial antibodies in human sera of up to 36% was shown [28]. Preliminary results show that two rickettsial species, *R. africae* and *R. sibirica mongolitimonae*, which show a greater affinity with human

sera may play a more important role in human pathology in the studied regions. *R. aeschlimannii*, which is most prevalent in ticks, is not as pathogenic as two above-mentioned rickettsiae, however, because of cross-reactivity among rickettsiae of spotted-fever group and *R. felis*, based on performed serological studies we may not say exactly which species of rickettsia play the most important role in elevated seroprevalence in West Africa.

We have also studied the role of rickettsial infections as possible causes of acute fevers in the indigenous population of rural Senegal. It was found that rickettsioses may be responsible for up to 6.7% of cases of recent acute non-malarial fever in the rural dispensary. Although most of the cases were found to be caused by flea-borne rickettsiosis caused by *R. felis* [51], in 0.7% the origin of the fever was tick-borne rickettsia. The identified case was from Dielmo village, and the tick positive for *R. conorii* (*Rh. e. evertsi*) was collected in Medina, a small village not far from Ndiop. Despite the very low percentage of infected ticks, we succeeded in the identification of this rickettsia in the blood of a febrile girl that was evidently ill with Mediterranean spotted fever.

The prevalence of five tick-borne and one flea-borne rickettsiae in the same region poses a question about cross-protection. To the best of our knowledge, no other region in the world has yet been found to present such a variety of pathogenic rickettsiae. The model studies that have been performed in animals since the beginning of 20th century often showed opposite results (Table 5), even when the same animals and rickettsiae were tested, for instance *R. conorii* and *R. africae* on guinea pigs [66,67]. Usually, broader cross-protection was seen when sublethal doses of live rickettsiae were used for immunization [68,69] when compared with inactivated bacteria. No studies in humans have been performed. In Senegal, the natural condition favors simultaneous contact of the rural population with different rickettsiae, so further studies on the dynamics of antibody levels over several years and their protective significance should be performed. Moreover, the prevalence Q fever in humans and its causative agent, *C. burnetii*, in ticks in the same regions [70] shows that these regions of rural Senegal present a natural reservoir of at least several emerging zoonoses.

In conclusion, we have to emphasize that the pathogenic spotted fever rickettsiae are very common in rural Senegal. Both occasional travelers and local villagers have a very high probability of being infected. Unfortunately, the modern reader is familiar

**Table 4.** Clinical and epidemiological characteristics of spotted fevers caused by rickettsiae found in this study.

Species	Disease	Tick species associated (literature data)	Tick species associated (present study)	Fever, %	Diffuse rash, %	Eschar, %	Lymphadenopathy	Lymphangitis	Reported mortality rates, %
<i>R. conorii conorii</i>	Mediterranean spotted fever	<i>Rh. sanguineus</i> , <i>Rh. simus</i> (?)	<i>Rh. e. evertsi</i>	100	97	72	Rare	No	1–5
<i>R. africae</i>	African tick-bite fever	<i>A. variegatum</i> , <i>A. hebraeum</i> , <i>Rh. (B.) microplus</i> , <i>Rh. (B.) decoloratus</i>	<i>Rh. e. evertsi</i> , <i>Rh. (B.) annulatus</i>	92	43	98%, often multiple	Yes	No	Very low
<i>R. sibirica mongolitimonae</i>	Lymphangitis-associated rickettsiosis	<i>H. truncatum</i> , <i>H. asiaticum</i> , <i>H. anatolicum excavatum</i> , <i>Rh. pusillus</i>	<i>H. truncatum</i>	100	78	89%	55%	Yes, up to 44%	0
<i>R. aeschlimannii</i>	Unnamed	<i>H. m. marginatum</i> , <i>H. m. rufipes</i> , <i>H. aegyptium</i> , <i>Haemaphysalis inermis</i>	<i>H. truncatum</i> , <i>H. m. rufipes</i> , <i>Rh. e. evertsi</i>	Yes	Yes	Yes	?	?	0
<i>R. massiliae</i>	Unnamed (one case)	<i>Rh. sanguineus</i> , <i>Rh. turanicus</i> , <i>Rh. muhsamae</i> , <i>Rh. lunulatus</i> , <i>Rh. sulcatus</i>	<i>Rh. guilhoni</i>	Yes	Yes	Yes	?	?	0

doi:10.1371/journal.pntd.0000821.t004

**Table 5.** Selected literature data on serological cross-protection among different spotted fever group rickettsiae in animal models.

Compared rickettsiae	Animal model	Antigen	Results of the study	Reference
<i>R. africae</i> vs. <i>R. conorii</i>	Guinea pigs	Sublethal doses alive rickettsiae	Absence of cross-immunity	[66]
	Guinea pigs	Sublethal doses alive rickettsiae	Reciprocal cross-protection	[67]
<i>R. conorii</i> vs. <i>R. rickettsii</i>	Guinea pigs	Sublethal doses alive rickettsiae	Reciprocal cross-protection	[69,73]
<i>R. rickettsii</i> vs. <i>R. australis</i>	Guinea pigs	Sublethal doses alive rickettsiae	Absence of cross-immunity	[74]
<i>R. parkeri</i> vs. <i>R. rickettsii</i> vs. <i>R. conorii</i>	Guinea pigs	Sublethal doses alive rickettsiae	Reciprocal cross-protection	[75]
<i>R. sibirica</i> vs. <i>R. heilongjiangensis</i> vs. <i>R. conorii</i>	Guinea pigs	Sublethal doses alive rickettsiae	Absence of cross-immunity	[76]
<i>R. rickettsii</i> vs. <i>R. montanensis</i>	Guinea pigs	Sublethal doses alive rickettsiae	Reciprocal cross-protection	[77]

doi:10.1371/journal.pntd.0000821.t005

almost exclusively with rickettsioses as the cause of returning travelers' fever [25]. The fevers in returning travelers are easy to identify, because these people are usually intently observed after returning. In contrast, little is known about rickettsioses in the local indigenous African population. The only known report is from Cameroon [71], where seven cases were described based on the molecular identification of *R. africae* in the blood of febrile patients. The integral approach applied in our work (studies of vectors, seroprevalence, and causes of acute fevers) allowed us to reveal the important role of rickettsial diseases in public health in Western Africa.

Our results are compatible with previously reported data, and the very high prevalence of spotted fevers may be explained by the surprising number of pathogenic rickettsiae identified in the studied region (*R. conorii conorii*, *R. africae*, *R. sibirica mongolitimonae*, *R. aeschlimannii*, and *R. massiliae*). We have summarized the clinical and epidemiological data concerning spotted fevers caused by all five tick-borne rickettsiae (Table 4). In addition, our study contributes to the discovery of the origin of unexplained fevers in Africa. We showed that up to 6.7% (9 of 134) of acute non-malarial fevers in rural Africa may have rickettsial (*R. felis* and *R. conorii*) origin.

Based on these data, we concluded that tick-borne rickettsioses together with Q fever [70], flea-borne rickettsiosis caused by *R. felis* [51], *Tropheryma whippelii* infection [72], and tick-borne relapsing fever [43] are major public health problems in West Africa. Taking into consideration that the role of tick-borne fevers in West Africa was previously underestimated, it is very important to perform long-term surveys on the distribution of vector ticks and rickettsiae, as well as screening targeted groups, both tourists and the indigenous population. We suggest implementing diagnostic

procedures and adapted treatments in the field to enhance the health of the people living in rural sub-Saharan Africa.

### Supporting Information

**Alternative Language Abstract S1** Translation of the abstract of the article Tick-borne rickettsioses, neglected emerging diseases in rural Senegal into Russian language by author O. Mediannikov Found at: doi:10.1371/journal.pntd.0000821.s001 (0.00 MB DOC)

**Alternative Language Abstract S2** Translation of the abstract of the article Tick-borne rickettsioses, neglected emerging diseases in rural Senegal into French language by author O. Mediannikov Found at: doi:10.1371/journal.pntd.0000821.s002 (0.02 MB DOC)

**Checklist S1** STROBE checklist Found at: doi:10.1371/journal.pntd.0000821.s003 (0.10 MB DOC)

### Acknowledgments

We thank Denis Pyak and Geetha Subramanian for the technical assistance.

### Author Contributions

Conceived and designed the experiments: OM GD FF J-FT DR. Performed the experiments: OM GD. Analyzed the data: OM GD FF CS J-FT. Contributed reagents/materials/analysis tools: CS J-FT DR. Wrote the paper: OM DR.

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