

Original Study Article

<https://doi.org/10.36233/0372-9311-557>

Current data on the circulation of the Q fever pathogen in the Republic of Guinea

Ekaterina V. Naidenova^{1✉}, Kirill S. Zakharov¹, Dmitrii A. Agafonov¹, Mikhail Yu. Kartashov², Aislu M. Senichkina¹, Erik S. Khalilov³, Abdoul B. Ibrahim⁴, Mamadou B. Bah⁴, Ibrahim Nouridine^{4,5}, Nikolai K. Tokarevich³, Sanaba Boumbaly^{4,5}, Ysuf Sidime⁶, Svetlana A. Shcherbakova¹, Vladimir V. Kuttyrev¹

¹Russian Research Anti-Plague Institute «Microbe», Saratov, Russia;

²State Scientific Center of Virology and Biotechnology «Vector», Kol'tsovo, Russia;

³Saint Petersburg Pasteur Research Institute of Epidemiology and Microbiology, St. Petersburg, Russia;

⁴Research Institute of Applied Biology of Guinea, Kindia, Republic of Guinea;

⁵Virology Research Center, Conakry, Republic of Guinea;

⁶Institute of Veterinary Medicine, Dalaba, Republic of Guinea

Abstract

Background. Q fever is the one of the best-studied zoonoses, which is widespread throughout almost the entire territory of Africa, excluding the territory of the Sahara. However, the current data on the incidence of coxiellosis and the circulation of *Coxiella burnetii* on this continent are limited and vary according different sources.

In 1980–1990, the Soviet-Guinean Research Virology and Microbiology Laboratory conducted studies to estimate the distribution of the Q fever pathogen, assess the herd immunity in humans and identify specific antibodies in the sera of livestock. However, in subsequent years, the research was suspended.

The aim of this study is to obtain up-to-date data on the distribution of *C. burnetii* in all landscape and geographical zones of the Republic of Guinea.

Materials and methods. The study was carried out in the laboratory of the Russian-Guinean Center for Epidemiology and Prevention of Infectious Diseases (Kindia, Republic of Guinea). The study involved 332 sera of febrile patients and 3156 sera from practically healthy volunteers, 1074 blood samples of livestock, 1648 suspensions of ticks, 319 specimens of small mammals and 298 of bats. The study was carried out using ELISA and PCR methods, selected samples were subjected to in-depth genetic analysis.

Results and discussion. The study of the distribution of *C. burnetii* on the territory of all landscape-geographical zones of the Republic of Guinea was carried out. For the first time, an officially registered case of human Q fever case has been identified. The role of livestock, small mammals and bats in the circulation of the pathogen has been established. It has been shown that the main vectors in Guinea are ixodid ticks of the *Amblyomma variegatum*, *Hyalomma truncatum* and *Rhipicephalus decoloratus* species. Employing molecular methods, *C. burnetii* strains carrying the QpH1 plasmid, capable of causing diseases in humans and animals were identified. For the first time, the complete nucleotide sequence of 16S rRNA of the Q fever pathogen (OQ152497–OQ152500) identified on the territory of Guinea was determined and registered in the GenBank database.

Conclusion. Taking into account the high epidemiological significance of Q fever, the study of the specifics of *C. burnetii* circulation in Guinea remains an urgent task. Regular monitoring and assessment of risk factors for diseases caused by coxiella are necessary for the development of an algorithm for laboratory diagnosis and recommendations for clinicians.

Keywords: Q fever, *Coxiella burnetii*, cases of the disease, immune stratum, carriers and vectors, Republic of Guinea

Ethics approval. The study was conducted with informed consent of patients or their official representatives. The study protocol was approved by the decision of the National Ethical Committee of the Ministry of Health of the Republic of Guinea (protocol No. 129/CNERS/16 of August 31, 2015). The authors confirm compliance with institutional and national standards for the use of laboratory animals in accordance with the “Consensus Author Guidelines for Animal Use” (IAVES, July 23, 2010). The study was approved by the Bioethics Commission of the Russian Anti-Plague Institute “Microbe” (Protocol No. 8 of November 11, 2023).

Acknowledgement. The authors are grateful to the management and staff of the Viral Hemorrhagic Fever Laboratory (Conakry), the regional hospitals of Conakry, Boké, Boffa, Coyah, Mamou, Kindia, Labé, Nzérékoré, Kankan, Dabola, Dalaba, Faranah, and the Institute of Applied Biology of Guinea (Kindia) and the Institute of Medical Veterinary Medicine (Dalaba) (Republic of Guinea) for their help in collecting the material.

Funding source. The research was conducted within the framework of the orders of the Government of the Russian Federation No. 1448-r dated July 25, 2015, No. 2904-r dated December 22, 2017 and No. 2985-r dated November 14, 2020 on Russian-Guinean scientific and technical cooperation in the field of epidemiology, prevention and monitoring of bacterial and viral infections in the Republic of Guinea.

Conflict of interest. The authors declare no apparent or potential conflicts of interest related to the publication of this article.

For citation: Naidenova E.V., Zakharov K.S., Agafonov D.A., Kartashov M.Yu., Senichkina A.M., Khalilov E.S., Ibrahim A.B., Bah M.B., Nouridine I., Tokarevich N.K., Boumbaly S., Sidime Y., Shcherbakova S.A., Kutyrer V.V. Current data on the circulation of the Q fever pathogen in the Republic of Guinea. *Journal of microbiology, epidemiology and immunobiology*. 2024;101(5):606–618.

DOI: <https://doi.org/10.36233/0372-9311-557>

EDN: <https://www.elibrary.ru/tezljr>

Оригинальное исследование

<https://doi.org/10.36233/0372-9311-557>

Современные данные о циркуляции возбудителя лихорадки Ку на территории Гвинейской Республики

Найденова Е.В.^{1✉}, Захаров К.С.¹, Агафонов Д.А.¹, Карташов М.Ю.², Сеничкина А.М.¹, Халилов Э.С.³, Ibrahim A.B.⁴, Bah M.B.⁴, Nouridine I.^{4,5}, Токаревич Н.К.³, Boumbaly S.^{4,5}, Sidime Y.⁶, Щербаклова С.А.¹, Кутырев В.В.¹

¹Российский научно-исследовательский противочумный институт «Микроб», Саратов, Россия;

²Государственный научный центр вирусологии и биотехнологии «Вектор», р.п. Кольцово, Россия;

³Санкт-Петербургский научно-исследовательский институт эпидемиологии и микробиологии имени Пастера, Санкт-Петербург, Россия;

⁴Исследовательский институт прикладной биологии Гвинеи, Киндия, Гвинейская Республика;

⁵Исследовательский центр вирусологии, Конакри, Гвинейская Республика;

⁶Институт медицинской ветеринарии, Далаба, Гвинейская Республика

Аннотация

Введение. Лихорадка Ку является наиболее изученным зоонозом, широко распространённым практически на всей территории Африки, исключая территорию Сахары. Однако сведения о заболеваемости коксиеллезом и циркуляции *Coxiella burnetii* на этом континенте являются ограниченными и неоднородными. В Гвинейской Республике в 1980–1990 гг. на базе Советско-Гвинейской научно-исследовательской вирусологической и микробиологической лаборатории проводились исследования по изучению распространения возбудителя лихорадки Ку, получены данные об иммунной прослойке населения и выявлены специфические антитела в сыворотках крови сельскохозяйственных животных. В последующие годы исследования были приостановлены.

Цель работы — получение современных данных о распространении *C. burnetii* на территории всех ландшафтно-географических зон Гвинейской Республики.

Материалы и методы. Исследования проводили в лаборатории Российско-Гвинейского центра эпидемиологии и профилактики инфекционных болезней (Киндия, Гвинейская Республика), для чего были получены 332 сыворотки крови лихорадящих больных и 3156 сывороток крови практически здоровых людей, 1074 образца крови сельскохозяйственных животных, 1648 суспензий клещей, 319 экземпляров мелких млекопитающих и 298 — рукокрылых. Исследование проводили методами иммуноферментного анализа и полимеразной цепной реакции, отдельные образцы подвергали углублённому генетическому анализу.

Результаты и обсуждение. Проведено изучение распространения *C. burnetii* на территории всех ландшафтно-географических зон Гвинейской Республики. Впервые выявлен и подтверждён лабораторными методами случай заболевания человека лихорадкой Ку. Установлена роль сельскохозяйственных животных, мелких млекопитающих и рукокрылых в циркуляции возбудителя. Показано, что основными переносчиками на территории Гвинеи являются иксодовые клещи видов *Amblyomma variegatum*, *Hyalomma truncatum* и *Rhipicephalus decoloratus*. При проведении молекулярно-генетических исследований выявлены штаммы *C. burnetii*, несущие плазмиду QpH1, способные вызывать заболевания людей и животных. Определены полные нуклеотидные последовательности 16S рРНК возбудителя лихорадки Ку, обнаруженного на территории Гвинеи, которые в последующем зарегистрированы в базе данных GenBank (OQ152497–OQ152500).

Заключение. С учётом полученных сведений о распространении возбудителя лихорадки Ку актуальной задачей остается продолжение изучения особенностей циркуляции *C. burnetii* на территории Гвинеи. Регулярный мониторинг и оценка факторов риска возникновения заболеваний, вызываемых коксиеллами, позволят разработать алгоритм лабораторной диагностики и рекомендации для врачей.

Ключевые слова: лихорадка Ку, *Coxiella burnetii*, случаи заболевания, иммунная прослойка, носители и переносчики, Гвинейская Республика

Этическое утверждение. Исследование проводили при информированном согласии пациентов или их официальных представителей. Протокол исследования одобрен решением Национального этического комитета Министерства здравоохранения Гвинейской Республики (протокол № 129/CNERS/16 от 31.08.2015). Авторы подтверждают соблюдение институциональных и национальных стандартов по использованию лабораторных животных в соответствии с «Consensus Author Guidelines for Animal Use» (IAVES, 23.07.2010). Исследование одобрено комиссией по биоэтике Российского противочумного института «Микроб» (протокол № 8 от 21.11.2023).

Благодарность. Авторский коллектив выражает благодарность за помощь в сборе материала руководству и сотрудникам лаборатории вирусных геморрагических лихорадок (Исследовательский центр вирусологии, Конакри, Гвинейская Республика), региональных госпиталей городов Конакри, Боке, Боффа, Коя, Маму, Киндиа, Лабе, Нзерекоре, Канкан, Дабола, Далаба, Фарана, а также сотрудникам Института прикладной биологии Гвинеи и Института медицинской ветеринарии (Гвинейская Республика).

Источник финансирования. Исследования проводились в рамках распоряжений Правительства РФ № 1448-р от 25.07.2015, № 2904-р от 22.12.2017 и № 2985-р от 14.11.2020 о российско-гвинейском научно-техническом сотрудничестве в области эпидемиологии, профилактики и мониторинга бактериальных и вирусных инфекций в Гвинейской Республике.

Конфликт интересов. Авторы декларируют отсутствие явных и потенциальных конфликтов интересов, связанных с публикацией настоящей статьи.

Для цитирования: Найденова Е.В., Захаров К.С., Агафонов Д.А., Карташов М.Ю., Сеничкина А.М., Халилов Э.С., Ibrahim A.B., Bah M.B., Nouridine I., Токаревич Н.К., Voumbaly S., Sidime Y., Щербакова С.А., Кутырев В.В. Современные данные о циркуляции возбудителя лихорадки Ку на территории Гвинейской Республики. *Журнал микробиологии, эпидемиологии и иммунобиологии.* 2024;101(5):606–618.
DOI: <https://doi.org/10.36233/0372-9311-557>
EDN: <https://www.elibrary.ru/tezljr>

Introduction

Q fever or coxiellosis is a common natural focal disease for humans and animals, the etiological agent of which is the bacteria *Coxiella burnetii* (family *Legionellaceae*, class *Gammaproteobacteria*), characterized by polymorphism of the clinical picture in humans and various mechanisms of transmission of the pathogen. In natural foci, the main vector of *C. burnetii* is considered to be ixodes, less frequently argas ticks, and the reservoir — wild mammals, among farm animals — small and large cattle [1, 2].

The disease in humans runs in the form of fever with general toxic symptoms with possible transition to a chronic form. Due to the widespread infection, a variety of transmission routes (contact, food, airborne and dust), Q fever is an important medical and social problem worldwide.

Furthermore, this infectious disease has an important veterinary significance, as it causes reproductive disorders (abortions and stillbirths) in small and large cattle, which causes significant economic losses, especially in those regions where livestock breeding is the main branch of agricultural production [2].

Coxiellosis is one of the best-studied zoonoses within Africa. There is emerging evidence that *C. burnetii* infection is responsible for non-malarial febrile illnesses and community-acquired pneumonia in many African countries. However, current information on the incidence of Q fever and circulation of *C. burnetii* in this continent is limited and heterogeneous [3].

Available publications on previous studies indicate a fairly high level of detection of specific antibodies to the pathogen in the population of some African countries [4–9]. For example, the study of blood serum samples from residents of some settlements of the Sin-Saloum region (Republic of Senegal) showed that specific

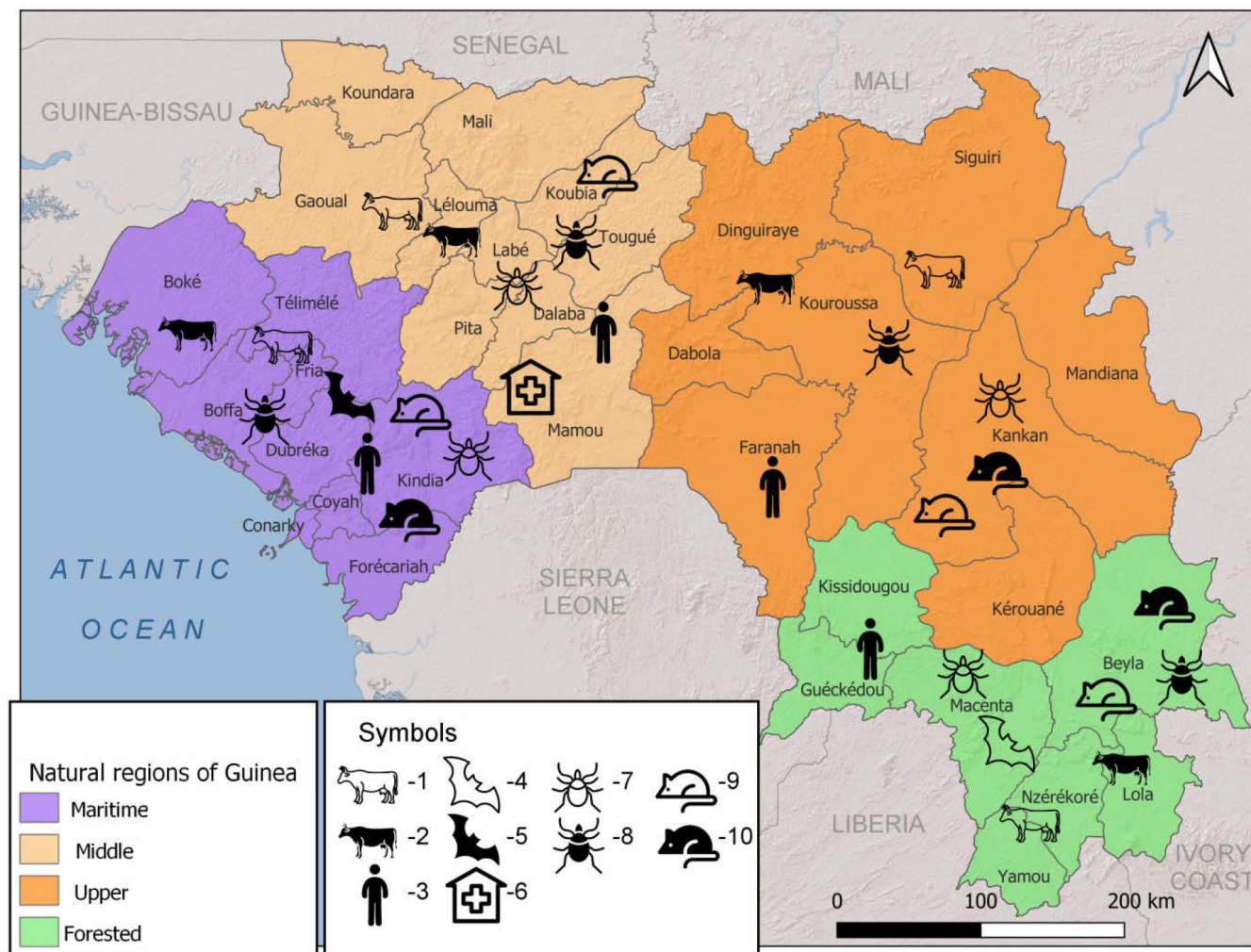
antibodies to *C. burnetii* were detected in 3.7–24.8% of samples (depending on the place of residence of the subjects) [5]. Similar data were obtained during serosurvey in pastoralist communities in Marsabit County, northern Kenya, when positive results were obtained in 13.2% of cases [6]. Males in Kenya were significantly more likely than females to have immunologic markers identified [7].

It has been shown that pastoralist tribes are at the highest risk of contracting coxiellosis because of their nomadic lifestyle and well-preserved traditions, which increase the likelihood of eating unboiled dairy products and raw meat from infected animals. It is also possible that infection occurs through contact with urine, feces, and blood of infected animals, as well as amniotic fluid after abortion or premature birth [6–9].

It is also known that Q fever causes significant losses among not only farm animals but also wild animals such as antelopes, giraffes, lions and cheetahs, causing irreparable damage to the numbers of these rare mammals [10].

This infectious disease is also becoming relevant as a “travelers' disease” due to the popularization of the African continent and rapidly developing tourism in this territory. An outbreak of Q fever was described in the literature, when during a safari in a natural park in Kenya, 4 (8%) out of 50 participants of the tourist route were infected, which caused importation of cases to Europe [11].

Most of the information published in the open press on the circulation of the Q fever pathogen relates to East Africa. There is much less information on the situation in the western part of the continent. There are data on studies conducted in natural foci of coxiellosis in Ghana, Nigeria, Mali [12–14], as well as in Senegal, where in 2023 two new genotypes of *C. burnetii* were



Landscape and geographical zones of the Republic of Guinea, where markers of the Q fever pathogen were identified.

1 — DNA in blood sera of cattle; 2 — IgG antibodies in blood sera of cattle; 3 — IgG antibodies in blood sera of residents; 4 — DNA in suspensions of bat organs; 5 — antigens in suspensions of bat organs; 6 — cases of human disease; 7 — DNA in suspensions of ixodes ticks; 8 — antigens in suspensions of ixodes ticks; 9 — DNA in suspensions of organs of small mammals; 10 — antigens in suspensions of organs of small mammals.

identified in samples from small mammals, the pathogenicity of which remains to be studied [15].

The Republic of Guinea is located in West Africa, on the coast of the Atlantic Ocean. The population of the country, as of the end of March 2024, is about 14.5 million people [16]. Based on geographical and natural-climatic features, the territory of the state is conditionally divided into 4 landscape-geographical zones: Lower (Maritime), Middle, Upper and Forested (Figure) [17].

In 1980–1990, the Soviet-Guinean Research Virology and Microbiology Laboratory conducted a large number of studies to investigate the spread of the Q fever pathogen in the Republic of Guinea, including data on the immunity of the country's population and the detection of specific antibodies in the blood sera of farm animals [18]. In the following decades, due to the prevailing economic and political conditions, research was suspended, and the significance of Q fever in the overall morbidity has not been determined. In 2017, as

part of the research work of the Russian-Guinean Center for Epidemiology and Prevention of Infectious Diseases (hereinafter referred to as the Center), established on the basis of orders of the Government of the Russian Federation on the premises of the Institute of Applied Biology of Guinea (Kindia), research was continued [19–21].

The aim of the study was to obtain up-to-date data on the distribution of *C. burnetii* and the features of natural foci of Q fever in different landscape and geographical zones of Guinea.

Materials and methods

Collection of samples of clinical and biological material and subsequent diagnostic work was carried out on the basis of the Center's laboratory by Russian and Guinean specialists, guided by the requirements of sanitary rules and regulations 3.3686-21 “Sanitary and Epidemiological Requirements for the Prevention of Infectious Diseases”.

Human blood serum

Blood serum of practically healthy people was collected in regional hospitals in Guinea and by local specialists. Fasting blood sampling was performed in the morning hours from the ulnar vein in the amount of 5–10 ml into a disposable sterile vacuum tube with a clot activator in compliance with the rules of asepsis.

Then the obtained samples were delivered to the laboratory of the Center in compliance with the rules of biological safety and temperature regime. All serum samples were preliminarily analyzed by immunochromatographic analysis for detection of malaria plasmodium antigens with the SDBIOLINE Malaria Ag P.f./Pan reagent kit (Standart Diagnostics, Inc.). To exclude the possibility of nonspecific reactions, samples containing antigens of malaria pathogens were not included in subsequent studies.

A panel of 3156 sera from virtually healthy individuals living in all 4 landscape-geographic zones of Guinea was compiled to study the herd immunity to the Q fever pathogen in the Guinean population. Different age groups were included: 1519 (48.2%) women and 1637 (51.8%) men. The work was carried out using the enzyme-linked immunosorbent assay (ELISA) reagent kit “Enzyme-linked immunosorbent assay for detection of class G antibodies to *C. burnetii* antigens” (Pasteur Research Institute of Epidemiology and Microbiology, Russia). The sera were tested at a dilution of 1 : 100.

To clarify the possibility of human disease with Q fever, 332 sera from febrile patients who sought medical help in regional hospitals in Guinea with complaints of prolonged fever and other symptoms not excluding coxiellosis were collected and examined. The material was also collected by Guinean specialists using the methodology described above. For molecular genetic studies, blood was also collected in an amount of 5–10 ml in a disposable sterile vacuum tube with 3.8% sodium citrate.

Samples were examined by polymerase chain reaction (PCR) to detect *C. burnetii* DNA with the AmpliSens *Coxiella burnetii*-FL reagent kit (Central Research Institute of Epidemiology, Russia) and ELISA using the diagnostic kit *Coxiella burnetii* ELISA IgM (Vircell) to detect IgM antibodies to the pathogen.

The study of samples of clinical and biological material from humans was conducted with informed consent of patients, for minors — with the permission of parents (official representatives). The study protocol was approved by the decision of the National Ethical Committee of the Ministry of Health of the Republic of Guinea (protocol No. 129/CNERS/16 of August 31, 2015).

Blood serum of farm animals

Blood samples were obtained at slaughterhouses, using generally accepted methods, from adult animals (more than 1.5 years old) without signs of infectious diseases after their examination by a veterinarian. In total, a panel of 1074 cattle blood samples was formed

for the work. The obtained sera were tested by ELISA and PCR methods using “ID Screen Q Fever Indirect Multi-species” reagent kits for detection of IgG antibodies specific to *C. burnetii* (ID Screen), which is recommended as a veterinary assay, and *C. burnetii* DNA was detected by the AmpliSens *Coxiella burnetii*-FL reagent kit (Central Research Institute of Epidemiology, Russia).

Tick suspensions

Ixodes ticks were collected in all 4 landscape-geographical zones of Guinea. Ectoparasites were removed manually, using personal protective equipment, from humans, farm animals, domestic and stray dogs and cats, small mammals, and reptiles. A total of 4709 specimens of ticks were collected during the studies, which were classified into 11 species based on morphological features: *Amblyomma variegatum* Fabricius, 1794; *Haemaphysalis leachi* Audouin, 1826; *Hyalomma rufipes* Koch, 1844; *Hyalomma truncatum* Koch, 1844; *Rhipicephalus (Boophilus) decoloratus* Koch, 1844; *Rhipicephalus (Boophilus) geigy* Aeschliman & Morel, 1965; *Rhipicephalus (Boophilus) annulatus* Say, 1821; *Rhipicephalus (Boophilus) microplus* Canestrini, 1888; *Rhipicephalus lunulatus* Neumann, 1907; *Rhipicephalus sanguineus* Latreille, 1806; *Rhipicephalus senegalensis* Koch, 1844 according to the identification guide [22]. Further, 1648 pools were formed taking into account species, sex, developmental phase and fatness of individual mites, as well as places of ectoparasite collection. Ectoparasites were washed twice with 70% ethanol to remove external contaminants and external microflora. Samples were prepared using a TissueLyser II laboratory homogenizer (Qiagen) in 500 µl of sterile phosphate-salt buffer solution.

The obtained material was tested by PCR and ELISA methods using the AmpliSens *Coxiella burnetii*-FL reagent kit (Central Research Institute of Epidemiology) and ELISA-Qu-antigen (kit N1) test system for detection of *Coxiella burnetii* antigens (Pasteur Research Institute of Epidemiology and Microbiology), respectively. Some samples containing both DNA and antigens of *C. burnetii* were analyzed using high-throughput sequencing on the Ion S5 platform (Thermo Scientific); further reads were mapped to the 16S rRNA sequence from the NCBI GenBank database using the BWA algorithm [23]. The plasmid profile with specific primers to the QpH1, QpRS and QpDV plasmid loci was also studied.

Small mammal organ suspensions

During epizootological monitoring on the territory of Guinea, 319 specimens of small mammals (Rodentia, Eulipotyphla) were captured. The species spectrum of rodents was represented by 13 species: *Arvicanthis ansorgei* Thomas, 1910 (Sudan grass mouse); *Heliosciurus gambianus* Ogibly, 1835 (Gambian squirrel);

Cricetomys gambianus Waterhouse, 1840 (Gambian hamster rat); *Lemniscomys striatus* Linnaeus, 1758 (striped mouse); *Lophuromys sikapusi* Temminck, 1853 (rusty-bellied stiff-necked mouse); *Mastomys erythro-leucus* Temminck, 1853 (Guinean multispotted mouse); *Mastomys natalensis* A. Smith, 1834 (Natal mouse); *Mus minutoides* A. Smith, 1834 (dwarf mouse); *Mus musculooides* Temminck, 1853 (Temminck's mouse); *Praomys daltoni* Thomas, 1892 (Dalton's mouse); *Rattus rattus* Linnaeus, 1758 (black rat); *Crocidura olivieri* Lesson, 1827 (African giant whitetooth); *Crocidura* sp. Wagler, 1832 (whiteteeths) [24–28].

We obtained 298 specimens of bats (Chiroptera) of 14 species: *Eidolon helvum* Kerr, 1792 (palmate wing); *Epomophorus gambianus* Ogilby, 1835 (great epaulet wing); *Lissonycteris angolensis* Bocage, 1898 (Angolan flying dog); *Rousettus aegyptiacus* E. Geoffroy, 1810 (Egyptian flying dog); *Chaerephon pumilus* Cretzschmar, 1830 (dwarf folding spoonbill); *Mops condylurus* A. Smith, 1833 (Angolan folding spoonbill); *Hipposideros caffer* Sundevall, 1846 (South African leafhopper); *Hipposideros jonesi* Hayman, 1947 (Jones' leafhopper); *Hipposideros ruber* Noack, 1893 (red leafhopper); *Nycteris hispida* Schreber, 1775 (shaggy slitmouth); *Neoromicia guineensis* Bocage, 1889 (Guinean leatherback); *Scotophilus dinganii* A. Smith, 1833 (African smooth-nosed platypus); *Scotophilus leucogaster* Cretzschmar, 1830 (white-bellied house smooth-nosed platypus); *Rhinolophus alcyone* Temminck, 1853 (Ghanaian horseshoe) [24–27].

Mammals were dissected in compliance with the rules of biological safety no later than 3 h after capture. In the absence of such an opportunity, animal carcasses were frozen at -20°C and delivered to the laboratory, where they were subsequently dissected and organ samples were taken. Combined suspensions of lungs and kidneys were used as material for work, in which markers of the coxiellosis pathogen (DNA and antigens) were searched with the reagent kits mentioned above.

The authors confirm compliance with institutional and national standards for the use of laboratory animals in accordance with the “Consensus author guidelines for animal use” (IAVES July 23, 2010). The study was approved by the Bioethics Commission of the Russian Anti-Plague Institute “Microbe” (protocol No. 8 of November 21, 2023).

During statistical processing of the material we calculated the proportion of detected pathogen markers in each sample, 95% confidence intervals (CI) for the proportions using Wilson's method.

Results and discussion

Identification of human cases of Q fever in Guinea

To date, there has been no detection of suspected cases of Q fever in Guinea. This can be explained by the lack of alertness of health workers in local hospitals

to this infectious disease. In this regard, a case of the disease reported for the first time in the country is of great interest.

Patient D., 28 years old, living in Mamou (Middle Guinea), was admitted to the infectious disease department of a regional hospital. At hospitalization, the patient had prolonged (more than 1 month), subfebrile fever, muscle and joint pains and breathing difficulties. The results of immunochemistry and microscopy tests for detection of malaria pathogens were negative.

For further differential diagnosis, the patient's blood serum was sent to the Center's laboratory. The obtained material was analyzed by reverse transcription PCR to detect RNA of Ebola, yellow fever, West Nile, dengue, Zika, Crimean-Congo hemorrhagic fever, hepatitis C, 16S RNA of leptospirosis pathogens, DNA of hepatitis B virus, pathogens of Q fever and rickettsioses. Based on the results, *C. burnetii* DNA was detected in the patient's serum. The material was also tested using ELISA and specific IgM antibodies to coxiellae were detected in a titer of 1 : 400. Subsequently, the obtained blood sample was used to determine the nucleotide sequence of the DNA of the Q fever pathogen. Partial sequencing with specific primers revealed 99% identity of the tested sample with the genome of *C. burnetii*. Phylogenetic analysis using the BLAST algorithm¹ showed 96% homology with strains isolated in Namibia.

When interviewed, patient D. mentioned close contact with farm animals, specifically owned cattle, and also indicated that there had been cases of spontaneous abortions of cattle in the patient's village.

Neither genetic markers of *C. burnetii* nor specific IgM antibodies to coxiellae were detected in the remaining serum samples from febrile patients transported from Guinea hospitals.

Determination of the herd immunity of Guineans to the Q fever pathogen

In the present study, specific IgG antibodies to the Q fever pathogen were detected in sera of participants of all age groups living in different zones of Guinea, and there was no dependence of the antibody detection rates on the sex of the examined persons (Table 1). In the whole country, specific immunoglobulins to *C. burnetii* were registered in 366 out of 3156 serum samples, which amounted to 11.6% (95% CI 10.5–12.8).

Determination of the herd immunity of farm animals to the Q fever pathogen

One of the indicators of circulation of pathogens of naturally occurring infectious diseases in a certain area is the detection of specific IgG immunoglobulins in blood sera of farm animals living in this region.

As a result of this work, antibodies to the Q fever pathogen were detected in 172 samples, which amount-

¹ URL: <https://blast.ncbi.nlm.nih.gov/Blast.cgi>

Table 1. Identification of specific IgG antibodies to the Q fever pathogen in the blood sera of residents of the Republic of Guinea

Age, years	Number of samples						
	total	men			women		
		total	positive	% (95% CI)	total	positive	% (95% CI)
< 10	197	108	8	7.4 (3.8–13.9)	89	6	6.7 (3.1–13.9)
10–20	498	275	26	9.4 (6.5–13.4)	223	27	12.1 (8.4–17.0)
20–30	699	340	32	9.4 (6.7–12.9)	359	29	8.1 (5.7–11.4)
30–40	595	300	39	13.0 (9.7–17.3)	295	33	11.2 (8.1–15.3)
40–50	559	285	35	12.3 (8.9–16.6)	277	29	10.5 (7.4–14.6)
50–60	339	230	37	16.1 (11.9–21.4)	109	26	23.8 (16.8–32.6)
> 70	269	102	20	19.6 (13.1–28.3)	167	19	11.4 (7.4–17.1)
Total	3156	1637	197	12.1 (10.5–13.7)	1519	169	11.3 (9.6–12.8)

ed to 16.0% (95% CI 13.9–18.3). Positive results were recorded in all landscape-geographical zones).

Detection of specific markers (DNA and antigens) of the Q fever pathogen in tick suspensions

PCR and ELISA methods were used to examine suspensions of ixodid ticks of various species, which are the main vectors of *C. burnetii*, collected in all landscape and geographical zones of Guinea. The pathogen DNA was detected in 294 (17.9%) samples and antigen in 307 (18.7%). Positive findings were noted among all ixodid tick species represented in the work, but the majority were attributed to *Am. variegatum*, *Hy. truncatum*, *Rh. decoloratus* (Table 2).

Analysis of plasmid profiles is an important tool for studying the spread of Q fever and determining the type of the pathogen. For genetic typing of *C. burnetii*, a panel of 20 samples from different tick species was created, in which both DNA (Ct level not more than 15) and antigen of the pathogen were detected simultaneously. PCR with specific primers to the QpH1, QpRS and QpDV plasmid loci revealed the presence of QpH1 alone in 5 samples. Sequences of QpRS and QpDV plasmid fragments were not detected in any of the samples. In the course of analyzing the results obtained and literature data, it was found that strains carrying the QpH1 plasmid are widespread in Equatorial Africa and are capable of causing diseases in humans and animals

Table 2. Identification of *C. burnetii* markers in suspensions of ixodid ticks of different species collected in the territory of the Republic of Guinea

Tick species	Number of samples (copies)	The number of positive samples; % (95% CI)	
		PCR	ELISA
<i>Am. variegatum</i>	872 (2493)	159; 18.2 (15.8–20.9)	193; 22.1 (19.5–25.0)
<i>Ha. leachi</i>	16 (56)	0	0
<i>Hy. truncatum</i>	52 (95)	14; 26.9 (16.8–40.3)	16; 30.8 (19.9–44.3)
<i>Rh. annulatus</i>	58 (161)	36; 62.1 (49.2–73.4)	29; 50 (37.5–62.5)
<i>Rh. decoloratus</i>	391 (1104)	47; 12 (9.2–15.6)	37; 9.5 (6.9–12.8)
<i>Rh. geigy</i>	210 (668)	36; 17.1 (12.7–22.8)	29; 13.8 (9.8–19.1)
<i>Rh. microplus</i>	18 (47)	0	1; 5.6 (1.0–25.8)
<i>Rh. sanguineus</i>	10 (42)	0	1; 10 (1.8–40.4)
<i>Rh. senegalensis</i>	18 (29)	2; 11.1 (3.1–32.8)	1; 5.6 (1.0–25.8)
<i>Rh. lunulatus</i>	2 (11)	0	0
<i>Hy. rufipes</i>	1 (3)	0	0
Total	1648 (4709)	294; 17.8 (16.1–19.8)	307; 18.6 (16.8–20.6)

[29, 30], which does not exclude the possibility of their circulation in Guinea.

The generated panel of samples was analyzed using high-throughput sequencing methods on the Ion S5 platform (Thermo Scientific). As a result, the nucleotide sequence of 16S rRNA of the Q fever pathogen was determined in 8 samples, which coincides 99.9% with the reference strain presented in the NCBI GenBank database. When comparing the obtained consensus sequence with the NCBI BLAST database, *C. burnetii* strains isolated in Namibia were found to show homology (96%) with the studied sample. Furthermore, the obtained reads were classified by the kraken2 algorithm using the Greengenes 16S RNA base, which also showed that the investigated sample belonged to the *C. burnetii* species. Some of the obtained 16S rRNA nucleotide sequences with the highest quality reads were deposited in the international GenBank database under the numbers OQ152497-OQ152500.

Detection of specific markers (DNA and antigens) of the Q fever pathogen in organ suspensions of small mammals

As a result of PCR and ELISA tests, markers of the Q fever pathogen were detected in the material collected in all zones of Guinea. Antigen was detected in 0.9% of samples and DNA in 5.1%. The maximum number of positive findings was obtained when samples from *Mastomys erythroleucus* rodents was examined (Table 3). These data may indicate the participa-

tion of animals of this systematic group in the spread of *C. burnetii* in Guinea.

Detection of specific markers (DNA and antigens) of the Q fever pathogen in organ suspensions of bats

Examination of pooled samples of lungs and kidneys obtained from bats revealed both *C. burnetii* antigens (1% of cases) and DNA (2%). The majority of positive samples were formed from organs of *Scotophilus leucogaster* (Table 4). Representatives of this species are widely distributed throughout sub-Saharan Africa. The data obtained confirm the role of bats in the circulation of the Q fever pathogen, which indicates the need for additional studies to determine the role of these mammals in the ecology of the pathogen.

Conclusion

As a result of this work, the distribution of *C. burnetii* in all landscape-geographical zones of Guinea was studied, including the first case of human case of Q fever identified and laboratory confirmed (Table 5). The role of farm animals, small mammals and bats in the circulation of *C. burnetii* has been established. It was shown that the main vectors of the pathogen on the territory of Guinea are ixodes ticks of *Am. variegatum*, *Hy. truncatum* and *Rh. decoloratus* species. Molecular genetic studies of the material collected in Guinea revealed *C. burnetii* strains carrying the QpH1 plasmid, which are capable of causing disease in humans and animals, and for the first time for this region the com-

Table 3. Identification of *C. burnetii* markers in suspensions of organs of small mammals of different species collected on the territory of the Republic of Guinea

Small mammal species	Number of samples (copies)	The number of positive samples; % (95% CI)	
		PCR	ELISA
<i>Arvicanthis ansorgei</i>	3	0	0
<i>Heliosciurus gambianus</i>	4	0	0
<i>Cricetomys gambianus</i>	7	1; 14.3 (2.6–51.3)	0
<i>Lemniscomys striatus</i>	3	0	0
<i>Lophuromys sikapusi</i>	1	0	0
<i>Mastomys erythroleucus</i>	124	8; 6.5 (3.3–12.2)	2; 1.6 (0.4–5.7)
<i>Mastomys natalensis</i>	32	2; 6.3 (1.7–20.1)	0
<i>Mus minutoides</i>	5	0	0
<i>Mus musculoides</i>	16	1; 6.3 (1.1–28.3)	0
<i>Praomys daltoni</i>	6	0	0
<i>Rattus rattus</i>	96	4; 4.2 (1.6–10.2)	1; 1.0 (0.2–5.7)
<i>Crocidura olivieri</i>	7	0	0
<i>Crocidura</i> sp.	15	0	0
Total	319	16; 5.0 (3.1–8.0)	3; 0.9 (0.3–2.7)

Table 4. Identification of *C. burnetii* markers in organ suspensions of bats of various species collected on the territory of the Republic of Guinea

Bat species	Number of samples (copies)	The number of positive samples; % (95% CI)	
		PCR	ELISA
<i>Eidolon helvum</i>	1	0	0
<i>Epomophorus gambianus</i>	4	0	0
<i>Lissonycteris angolensis</i>	4	0	0
<i>Rousettus aegyptiacus</i>	15	0	0
<i>Chaerephon pumillus</i>	3	0	0
<i>Mops condylurus</i>	26	1; 3.8 (0.7–18.9)	0
<i>Hipposideros caffer</i>	32	0	0
<i>Hipposideros jonesi</i>	25	0	0
<i>Hipposideros ruber</i>	41	1; 2.4 (0.4–12.6)	1; 2.4 (0.4–12.6)
<i>Nycteris hispida</i>	5	0	0
<i>Neoromicia guineensis</i>	23	1; 4.3 (0.8–21.0)	0
<i>Scotophilus dinganii</i>	1	0	0
<i>Scotophilus leucogaster</i>	117	3; 2.6 (0.9–7.3)	2; 1.7 (0.5–6.0)
<i>Rhinolophus alcyone</i>	1	0	0
Total	298	6; 2.0 (0.9–4.3)	3; 1.0 (0.3–2.9)

plete nucleotide sequence of the 16S rRNA gene of the Q fever pathogen was determined and registered in the international GenBank database.

Our study allowed us to expand the data on the circulation and distribution of *C. burnetii* in West Africa. The study of the specifics of *C. burnetii* circulation in Guinea remains an urgent task. Systematically obtained data on the detection of the pathogen and assessment of risk factors for outbreaks of diseases

caused by coxiellae are necessary for the development of an algorithm for laboratory diagnosis and recommendations for clinicians. Regular monitoring of the spread of Q fever, carried out with the participation of both medical and veterinary services in Guinea, will make it possible to forecast the epidemiological situation and coordinate preventive (anti-epidemic) measures within the framework of the One Health concept².

² WHO. One health. URL: https://www.who.int/health-topics/one-health#tab=tab_1 (дата обращения: 26.05.2024).

Table 5. Identification of markers of the Q fever pathogen in various materials collected on the territory of the Republic of Guinea

Type of the studied samples	Number of samples	The number of positive; % (95% CI)		
		PCR	ELISA	
		DNA	antigen	IgG
Lower (Maritime) Guinea				
Blood serum of practically healthy people	943	N. i.	N. i.	106; 11.2 (9.4–13.4)
Blood serum of cattle	371	6; 1.6 (0.7–3.5)	N. i.	64; 17.2 (13.7–21.4)
Suspensions of ticks	624	111; 17.8 (15.0–21.0)	131; 21.0 (18.0–24.4)	N. i.
Suspensions of organs of small mammals	149	8; 5.4 (2.7–10.2)	0; 0 (0–2.5)	N. i.
Suspensions of bat organs	107	0; 0 (0–3.4)	3; 2.8 (0.9–7.9)	N. i.
Middle Guinea				
Blood serum of practically healthy people	778	N. i.	N. i.	82; 10.5 (8.6–12.8)
Blood serum of cattle	257	3; 1.2 (0.4–3.4)	N. i.	49; 19.2 (14.7–24.3)
Suspensions of ticks	402	71; 17.7 (14.2–21.7)	77; 19.1 (15.6–23.3)	N. i.
Suspensions of organs of small mammals	55	3; 5.4 (1.9–14.8)	0; 0 (0–6.5)	N. i.
Suspensions of bat organs	61	0; 0 (0–5.8)	0; 0 (0–5.8)	N. i.
Upper Guinea				
Blood serum of practically healthy people	655	N. i.	N. i.	77; 11.8 (9.5–14.4)
Blood serum of cattle	182	2; 1.1 (0.3–3.9)	N. i.	35; 13.2 (9.6–17.8)
Suspensions of ticks	245	53; 21.6 (16.9–27.2)	28; 0.8 (0.3–2.9)	N. i.
Suspensions of organs of small mammals	43	2; 4.6 (1.3–15.4)	1; 2.3 (0.4–12.1)	N. i.
Suspensions of bat organs	54	0; 0 (0–6.6)	0; 0 (0–6.6)	N. i.
Forest Guinea				
Blood serum of practically healthy people	780	N. i.	N. i.	101; 12.9 (10.7–15.5)
Blood serum of cattle	264	3; 1.1 (0.4–3.3)	N. i.	35; 13.2 (9.6–17.8)
Suspensions of ticks	377	59; 15.6 (12.3–19.7)	61; 16.2 (12.8–20.2)	N. i.
Suspensions of organs of small mammals	72	3; 4.2 (1.4–11.5)	2; 2.8 (0.8–9.5)	N. i.
Suspensions of bat organs	76	6; 7.9 (3.7–16.1)	0; 0 (0–4.8)	N. i.
General by country				
Blood serum of practically healthy people	3156	N. i.	N. i.	366; 11.6 (10.5–12.7)
Blood serum of cattle	1074	14; 1.3 (0.8–2.1)	N. i.	172; 16.0 (13.9–18.3)
Suspensions of ticks	1648	294; 17.8 (16.1–19.8)	307; 18.6 (16.8–20.6)	N. i.
Suspensions of organs of small mammals	319	16; 5.0 (3.1–8.0)	3; 0.9 (0.3–2.7)	N. i.
Suspensions of bat organs	298	6; 2.0 (0.9–4.3)	3; 1.0 (0.3–2.9)	N. i.

Note. N. i. — not investigated.

СПИСОК ИСТОЧНИКОВ | REFERENCES

- Онищенко Г.Г., Кутырева В.В., ред. *Специфическая индикация патогенных биологических агентов*. М.; 2014. Onishchenko G.G., Kutuyev V.V., eds. *Specific Indication of Pathogenic Biological Agents*. Moscow; 2014. EDN: <https://elibrary.ru/qlnqhv>
- Лукин Е.П., Мищенко О.А., Борисевич С.В. Лихорадка Ку в XXI в.: материал для подготовки лекции. *Инфекционные болезни: новости, мнения, обучение*. 2019;8(4):62–77. Lukin E.P., Mishchenko O.A., Borisevich S.V. Ku fever in the XXI century: material for preparing a lecture. *Infectious Diseases: News, Opinions, Training*. 2019;8(4):62–77. DOI: <https://doi.org/10.24411/2305-3496-2019-14009> EDN: <https://elibrary.ru/houbuj>
- Vanderburg S., Rubach M.P., Halliday J.E., et al. Epidemiology of *Coxiella burnetii* infection in Africa: a OneHealth systematic review. *PLoS Negl. Trop. Dis.* 2014;8(4):e2787. DOI: <https://doi.org/10.1371/journal.pntd.0002787>
- Dupont H.T., Brouqui P., Faugere B., Raoult D. Prevalence of antibodies to *Coxiella burnetii*, *Rickettsia conorii*, and *Rickettsia typhi* in seven African countries. *Clin. Infect. Dis.* 1995;21(5):1126–33. DOI: <https://doi.org/10.1093/clinids/21.5.1126>
- Mediannikov O., Fenollar F., Socolovschi C., et al. *Coxiella burnetii* in humans and ticks in rural Senegal. *PLoS Negl. Trop. Dis.* 2010;4(4):e654. DOI: <https://doi.org/10.1371/journal.pntd.0000654>
- Muema J., Nyamai M., Wheelhouse N., et al. Endemicity of *Coxiella burnetii* infection among people and their livestock in pastoral communities in northern Kenya. *Heliyon*. 2022;8(10):e11133. DOI: <https://doi.org/10.1016/j.heliyon.2022.e11133>
- Mwololo D., Nthiwa D., Kitala P., et al. Sero-epidemiological survey of *Coxiella burnetii* in livestock and humans in Tana River and Garissa counties in Kenya. *PLoS Negl. Trop. Dis.* 2022;16(3):e0010214. DOI: <https://doi.org/10.1371/journal.pntd.0010214>
- Crump J.A., Morrissey A.B., Nicholson W.L., et al. Etiology of severe non-malaria febrile illness in Northern Tanzania: a prospective cohort study. *PLoS Negl. Trop. Dis.* 2013;7(7):e2324. DOI: <https://doi.org/10.1371/journal.pntd.0002324>
- Larson P.S., Espira L., Grabow C., et al. The sero-epidemiology of *Coxiella burnetii* (Q fever) across livestock species and herding contexts in Laikipia County, Kenya. *Zoonoses Public Health*. 2019;66(3):316–24. DOI: <https://doi.org/10.1111/zph.12567>
- Mangena M.L., Gcebe N., Thompson P.N., Adesiyun A.A. Q fever and toxoplasmosis in South African livestock and wild-life: a retrospective study on seropositivity, sporadic abortion, and stillbirth cases in livestock caused by *Coxiella burnetii*. *BMC Vet. Res.* 2023;19(1):168. DOI: <https://doi.org/10.1186/s12917-023-03645-w>
- Njeru J., Henning K., Pletz M.W., et al. Febrile patients admitted to remote hospitals in Northeastern Kenya: seroprevalence, risk factors and a clinical prediction tool for Q-Fever. *BMC Infect. Dis.* 2016;16:244. DOI: <https://doi.org/10.1186/s12879-016-1569-0>
- Dione M.M., Séry A., Sidibé C.A.K., et al. Exposure to multiple pathogens — serological evidence for Rift Valley fever virus, *Coxiella burnetii*, *Bluetongue virus* and *Brucella* spp. in cattle, sheep and goat in Mali. *PLoS Negl. Trop. Dis.* 2022;16(4):e0010342. DOI: <https://doi.org/10.1371/journal.pntd.0010342>
- Addo S.O., Bentil R.E., Baako B.O.A., et al. Occurrence of *Rickettsia* spp. and *Coxiella burnetii* in ixodid ticks in Kasse-na-Nankana, Ghana. *Exp. Appl. Acarol.* 2023;90(1-2):137–53. DOI: <https://doi.org/10.1007/s10493-023-00808-0>
- Kamani J., Baneth G., Gutiérrez R., et al. *Coxiella burnetii* and *Rickettsia conorii*: Two zoonotic pathogens in peridomestic rodents and their ectoparasites in Nigeria. *Ticks Tick Borne Dis.* 2018;9(1):86–92. DOI: <https://doi.org/10.1016/j.ttbdis.2017.10.004>
- Mangombi-Pambou J., Granjon L., Labarrere C., et al. New genotype of *Coxiella burnetii* causing epizootic q fever outbreak in rodents, Northern Senegal. *Emerg. Infect. Dis.* 2023;29(5):1078–81. DOI: <https://doi.org/10.3201/eid2905.221034>
- Черч Гаррисон Р.Дж. *Западная Африка. Природная среда и ее хозяйственное использование*. М.;1959. Church Harrison R.J. *West Africa. A study of the environment and of man's use of it*. New York;1957.
- Каливоги С., Буаро М.Е., Константинов О.К., Плотникова Л.Ф. Иммуная структура населения и домашних животных Гвинейской Республики в отношении риккетсиозов группы клещевой пятнистой лихорадки и лихорадки Ку. *Медицинская паразитология и паразитарные болезни*. 2013;(1):28–30. Kalivogi S., Boiro M.E., Konstantinov O.K., Plotnikova L.F. The immune structure of the population and domestic animals of the Republic of Guinea in relation to rickettsioses of the tick-borne spotted fever and Ku fever group. *Medical Parasitology and Parasitic Diseases*. 2013;(1):28–30. EDN: <https://elibrary.ru/tvzcbv>
- Найденова Е.В., Каливоги С., Карташов М.Ю. и др. Новые данные об уровне иммунной прослойки населения Гвинейской Республики к возбудителю лихорадки Ку. *Инфекция и иммунитет*. 2021;11(1):165–70. Naidenova E.V., Kalivogui S., Kartashov M.Y., et al. New data on the level of immune stratum against Q fever agent in population of the Republic of Guinea. *Russian Journal of Infection and Immunity*. 2021;11(1):165–70. DOI: <https://doi.org/10.15789/2220-7619-NDO-1485> EDN: <https://elibrary.ru/wzsxmv>
- Найденова Е.В., Захаров К.С., Карташов М.Ю. и др. Выявление генетических маркеров возбудителей природно-очаговых инфекционных болезней в пробах искодовых клещей, собранных на территории Гвинейской Республики. *Проблемы особо опасных инфекций*. 2023;(4):115–24. Naidenova E.V., Zakharov K.S., Kartashov M.Yu., et al. Genetic Marker Detection of Natural-Focal Infectious Disease Pathogens in Samples of Ixodidae Ticks, Collected on the Territory of the Republic of Guinea. *Problems of Particularly Dangerous Infections*. 2023;(4):115–24. DOI: <https://doi.org/10.21055/0370-1069-2023-4-115-124> EDN: <https://elibrary.ru/lnomas>
- Найденова Е.В., Карташов М.Ю., Шевцова А.П. и др. Определение уровня иммунной прослойки сельскохозяйственных животных к возбудителям зоонозных инфекционных болезней в Гвинейской Республике. *Проблемы особо опасных инфекций*. 2022;(2):101–6. Naidenova E.V., Kartashov M.Yu., Shevtsova A.P., et al. Identification of the farm animals immune to pathogens of zoonotic infectious diseases in the Republic of Guinea. *Problems of Particularly Dangerous Infections*. 2022;(2):101–6. DOI: <https://doi.org/10.21055/0370-1069-2022-2-101-106> EDN: <https://elibrary.ru/bssaaq>
- Walker A.R., Bouattour A., Camicas J.L., et al. *Ticks of Domestic Animals in Africa: A Guide to Identification of Species*. Edinburgh;2014.
- Li H., Durbin R. Fast and accurate short read alignment with Burrows–Wheeler transform. *Bioinformatics*. 2009;25(14):1754–60. DOI: <https://doi.org/10.1093/bioinformatics/btp324>
- Wilson D.E., Reeder D.M., eds. *Mammal Species of the World. A Taxonomic and Geographic Reference*. Baltimore;2005.
- Happold D.C.D., ed. *Mammals of Africa. Volume III: Rodents, Hares and Rabbits*. London;2013.

25. Happold M., Happold D.C.D., eds. *Mammals of Africa. Volume IV: Hedgehogs, Shrews and Bats*. London;2013.
26. Соколов В.Е. *Пятиязычный словарь названий животных. Млекопитающие. Латинский — русский — английский — немецкий — французский*. М.;1984. Sokolov V.E. *A Five-Language Dictionary of Animal Names. Mammals. Latin — Russian — English — German — French*. Moscow;1984.
27. Luo S., Lu S., Fan H., et al. The *Coxiella burnetii* QpH1 plasmid is a virulence factor for colonizing bone marrow-derived murine macrophages. *J. Bacteriol.* 2021;203(9):e00588–20. DOI: <https://doi.org/10.1128/jb.00588-20>

Information about the authors

Ekaterina V. Naidenova[✉] — Cand. Sci. (Biol.), senior researcher, Department of infectious disease diagnostics, Russian Anti-Plague Institute "Microbe", Saratov, Russia, katim2003@mail.ru, <https://orcid.org/0000-0001-6474-3696>

Kirill S. Zakharov — Cand. Sci. (Biol.), senior researcher, Department of infectious disease epidemiology, Russian Anti-Plague Institute "Microbe", Saratov, Russia, <https://orcid.org/0000-0002-4726-309X>

Dmitry A. Agafonov — Cand. Sci. (Biol.), senior researcher, Department of infectious diseases, Russian Anti-Plague Institute "Microbe", Saratov, Russia, <https://orcid.org/0000-0001-9273-6063>

Mikhail Yu. Kartashov — Cand. Sci. (Biol.), senior researcher, Department of molecular virology of flaviviruses and viral hepatitis, State Research Center of Virology and Biotechnology "Vector", Koltsovo, Russia, <https://orcid.org/0000-0002-7857-6822>

Aislu M. Senichkina — Cand. Sci. (Biol.), senior researcher, Department of diagnostics of infectious diseases, Russian Anti-Plague Institute "Microbe", Saratov, Russia, <https://orcid.org/0000-0003-1026-2680>

Erik S. Khalilov — junior researcher, Laboratory of zoonotic infections, Pasteur Research Institute of Epidemiology and Microbiology, St. Petersburg, Russia, <https://orcid.org/0000-0002-0599-4302>

Abdoul B. Ibrahim — researcher, Laboratory of viral hemorrhagic fevers of Guinea, Guinea Research Institute of Applied Biology, Kindia, Republic of Guinea, <https://orcid.org/0009-0003-2547-8705>

Mamadou B. Bah — researcher, Guinea Research Institute of Applied Biology, Kindia, Republic of Guinea, <https://orcid.org/0000-0002-4565-269X>

Ibrahim Nourdin — Cand. Sci. (Biol.), researcher, Research Institute of Applied Biology of Guinea, Kindia, Republic of Guinea; researcher, Laboratory of viral hemorrhagic fevers of Guinea, Virology Research Center, Conakry, Republic of Guinea, <https://orcid.org/0000-0002-2970-9676>

Nikolai K. Tokarevich — D. Sci. (Med.), Professor, Head, Laboratory of zoonanthropotic infections, Pasteur St. Petersburg Research Institute, St. Petersburg, Russia, <https://orcid.org/0000-0001-6433-3486>

Sanaba Boumbaly — Cand. Sci. (Biol.), Professor, consultant, Research Institute of Applied Biology of Guinea, Kindia, Republic of Guinea; Director, Laboratory of viral hemorrhagic fevers of Guinea, Virology Research Center, Conakry, Republic of Guinea, <https://orcid.org/0000-0002-4506-6033>

Sidime Yusuf — Cand. Sci. (Vet.), Professor, Director, Institute of Veterinary Medicine, Dalaba, Republic of Guinea, <https://orcid.org/0000-0002-0742-0468>

Svetlana A. Shcherbakova — D. Sci. (Biol.), Deputy director, Russian Anti-Plague Institute "Microbe", Saratov, Russia, <https://orcid.org/0000-0003-1143-4069>

Vladimir V. Kutyrav — D. Sci. (Med.), Professor, Academician of the RAS, Director, Russian Anti-Plague Institute "Microbe", Saratov, Russia, <https://orcid.org/0000-0003-3788-3452>

Author contribution: Naidenova E.V. — planning, organization and conduct of research, analysis of literature data, presentation of results, writing the text of the article; Zakharov K.S. — conducting research, presenting results, statistical processing of data, preparing illustrations; Agafonov D.A. — conducting research, presenting results; Kar-

28. Панферова Ю.А., Фрейлихман О.А., Токаревич Н.К. и др. Детекция *Coxiella burnetii* в клещах, собранных с крупного рогатого скота, на территории некоторых провинций Гвинейской Республики. *Эпидемиология и инфекционные болезни*. 2019;24(5-6):234–9. Panferova Yu.A., Freylikhman O.A., Tokarevich N.K., et al. Detection of *Coxiella burnetii* in ticks collected from cattle in several provinces of the Republic of Guinea. *Epidemiology and infectious diseases*. 2019;24(5-6): 234–9. EDN: <https://elibrary.ru/twsemw>

Информация об авторах

Найденова Екатерина Владимировна[✉] — к. б. н., в. н. с. отдела диагностики инфекционных болезней Российского противочумного института «Микроб», Саратов, Россия, katim2003@mail.ru, <https://orcid.org/0000-0001-6474-3696>

Захаров Кирилл Сергеевич — к. б. н., с. н. с. отдела эпидемиологии инфекционных болезней Российского противочумного института «Микроб», Саратов, Россия, <https://orcid.org/0000-0002-4726-309X>

Агафонов Дмитрий Алексеевич — к. б. н., с. н. с. отдела диагностики инфекционных болезней Российского противочумного института «Микроб», Саратов, Россия, <https://orcid.org/0000-0001-9273-6063>

Карташов Михаил Юрьевич — к. б. н., с. н. с. отдела молекулярной вирусологии флавивирусов и вирусных гепатитов ГНЦ вирусологии и биотехнологии «Вектор», р.п. Кольцово, Россия, <https://orcid.org/0000-0002-7857-6822>

Сеничкина Айслу Мухаматовна — к. б. н., с. н. с. отдела диагностики инфекционных болезней Российского противочумного института «Микроб», Саратов, Россия, <https://orcid.org/0000-0003-1026-2680>

Халилов Эрик Серкалиевич — м. н. с. лаб. зооантропонозных инфекций Санкт-Петербургского НИИ эпидемиологии и микробиологии им. Пастера, Санкт-Петербург, Россия, <https://orcid.org/0000-0002-0599-4302>

Ибрагим Абдул Бастои — н. с. лаб. вирусных геморрагических лихорадок Гвинеи Исследовательского института прикладной биологии Гвинеи, Киндия, Гвинейская Республика, <https://orcid.org/0009-0003-2547-8705>

Ба Мамадю Бандикура — н. с. Исследовательского института прикладной биологии Гвинеи, Киндия, Гвинейская Республика, <https://orcid.org/0000-0002-4565-269X>

Нурдин Ибрагим — к. б. н., н. с. Исследовательского института прикладной биологии Гвинеи, Киндия, Гвинейская Республика; н. с. лаб. вирусных геморрагических лихорадок Гвинеи Исследовательского центра вирусологии, Конакри, Гвинейская Республика, <https://orcid.org/0000-0002-2970-9676>

Токаревич Николай Константинович — д. м. н., профессор, зав. лаб. зооантропонозных инфекций Санкт-Петербургского НИИ им. Пастера, Санкт-Петербург, Россия, <https://orcid.org/0000-0001-6433-3486>

Бумбали Санаба — к. б. н., профессор, консультант Исследовательского института прикладной биологии Гвинеи, Киндия, Гвинейская Республика; директор лаб. вирусных геморрагических лихорадок Гвинеи Исследовательского центра вирусологии, Конакри, Гвинейская Республика, <https://orcid.org/0000-0002-4506-6033>

Сидиме Юсуф — к. вет. н., профессор, директор Института медицинской ветеринарии, Далаба, Гвинейская Республика, <https://orcid.org/0000-0002-0742-0468>

Щербакowa Светлана Анатольевна — д. б. н., зам. директора Российского противочумного института «Микроб», Саратов, Россия, <https://orcid.org/0000-0003-1143-4069>

Кутырев Владимир Викторович — д. м. н., профессор, академик РАН, директор Российского противочумного института «Микроб», Саратов, Россия, <https://orcid.org/0000-0003-3788-3452>

tashov M. Yu. — conducting research, statistical processing of data; *Senichkina A. M.* — conducting research; *Khalilov E. S.* — conducting research, genomic analysis; *Abdoul B. I.* — collection and delivery of biological material samples, conducting research; *Bah M. B.* — collection and delivery of biological material samples; *Nourdin I.* — collection and delivery of biological material samples, conducting research; *Tokarevich N. K.* — literature data analysis; *Bumbaly S.* — organization, collection and delivery of biological material samples; *Sidime Yu.* — organization, collection and delivery of biological material samples; *Shcherbakova S. A.* — research management; *Kutyrev V. V.* — general management. All authors confirm that their authorship meets the ICMJE criteria, made a significant contribution to the search and analytical work and preparation of the article, read and approved the final version before publication.

The article was submitted 24.06.2024;
accepted for publication 08.08.2024;
published 30.10.2024

Участие авторов: *Найденова Е. В.* — планирование, организация и проведение исследований, анализ данных литературы, оформление результатов, написание текста статьи; *Захаров К. С.* — проведение исследований, оформление результатов, статистическая обработка данных, подготовка иллюстраций; *Агафонов Д. А.* — проведение исследований, оформление результатов; *Карташов М. Ю.* — проведение исследований, статистическая обработка данных; *Сеничкина А. М.* — проведение исследований; *Халилов Э. С.* — проведение исследований, геномный анализ; *Абдул Б. И.* — сбор и доставка проб биологического материала, проведение исследований; *Ба М. Б.* — сбор и доставка проб биологического материала, проведение исследований; *Токаревич Н. К.* — анализ данных литературы; *Бумбали С.* — организация, сбор и доставка проб биологического материала; *Сидиме Ю.* — организация, сбор и доставка проб биологического материала; *Щербакова С. А.* — руководство исследованиями; *Кутырев В. В.* — общее руководство. Все авторы подтверждают соответствие своего авторства критериям ICMJE, внесли существенный вклад в проведение поисково-аналитической работы и подготовку статьи, прочли и одобрили финальную версию до публикации.

Статья поступила в редакцию 24.06.2024;
принята к публикации 08.08.2024;
опубликована 30.10.2024