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First Human Case of Crimean-Congo Virus Hemorrhagic Fever in the Abobo Health District (Abidjan, Côte d'Ivoire)

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ABSTRACT

Crimean-Congo Haemorrhagic Fever is a serious zoonosis caused by the Crimean-Congo Haemorrhagic Fever Virus (CCHFV). This virus causes outbreaks of severe viral hemorrhagic fever, with a fatality rate of up to 40%. On July 22, 2022, the Institut Pasteur de Côte d'Ivoire received a blood sample on a dry tube from the Service des Maladies Infectieuses et Tropicales (SMIT) for suspected hemorrhagic fever. This blood sample was tested for Yellow Fever, Dengue, Rift Valley fever, West Nile, Chikungunya, Ebola, Lassa and CCHFV. RT-PCR testing for CCHFV was positive, and serology results showed the presence of IgM-type immunoglobulins. Côte d'Ivoire recorded its first human case of Crimean-Congo Hemorrhagic Fever.

Keywords

Côte d'Ivoire, Crimean-Congo Hemorrhagic Fever, First human case.

Introduction

Crimean-Congo Hemorrhagic Fever (CCHF) is a serious disease caused by the Crimean-Congo hemorrhagic fever virus. This virus is transmitted by ticks, with a wide geographical distribution and case-fatality rates ranging from 30% or more [1]. Diagnoses made and human cases already reported demonstrate that the geographical range of the CCHF virus continues to expand, and is endemic in Africa, the Middle East, Southeast Asia and Southern and Eastern Europe [2]. The first human case of Crimean Congo Virus Hemorrhagic Fever (CCHF) was detected in July 2022 in the south of Côte d'Ivoire, in Akeïkoi, a district of the urban commune of Abobo. (Abidjan, Côte d'Ivoire) (Figure 1). Within the framework of interministerial decree N° 393 of June 21, 2006, designating the National Reference Centers (NRC) of the Institut Pasteur de Côte d'Ivoire, in the field of transmissible diseases [3], the NRC for Arboviruses and Haemorrhagic Fever Viruses (based in the Vector-borne Viruses Unit of the Epidemic Viruses Department) was responsible for analyzing the suspected case

of haemorrhagic fever hospitalized in the Service des Maladies Infectieuses et Tropicales (SMIT) at Treichville University Hospital (Abidjan).



Figure 1: Geographical location of the first human case of CCHF in Côte d'Ivoire.

Methods

On Friday, July 22, 2022, the SMIT send a blood sample on a dry tube for suspected hemorrhagic fever to the Institut Pasteur de Côte d'Ivoire. The sample was taken from a 32- year-old male hospitalized for febrile hemorrhagic syndrome in the SMIT at Treichville University Hospital. The information gathered showed that this patient was unemployed and resided in the Abobo Est health district. Molecular techniques using specific primers and probes were performed on this sample, using RT-PCR (reverse transcriptase - polymerase chain reaction) and serological techniques to detect IgM antibodies to arboviruses and viruses responsible for viral haemorrhagic fevers. These included Yellow Fever, Dengue, Rift Valley Fever, West Nile, Chikungunya, Ebola, Lassa and Crimean Congo Haemorrhagic Fever viruses.

Results and Discussion

Serology and RT-PCR results were negative for Yellow Fever, Dengue, Rift Valley Fever, West Nile, Chikungunya, Ebola and Lassa viruses. On the other hand, RT-PCR was positive for Crimean- Congo Hemorrhagic Fever Virus, and serology results showed the presence of IgM immunoglobulins against Crimean-Congo Hemorrhagic Fever Virus. These samples were sent to the supranational laboratories of the Institut Pasteur de Lyon and the Institut Pasteur de Dakar, in accordance with World Health Organization (WHO) quality control procedures. These supranational laboratories confirmed the results of the Institut Pasteur de Côte d'Ivoire, for RT-PCR and serology diagnostics.

Research work carried out at the Institut Pasteur de Côte d'Ivoire had been conducted in five (5) major livestock areas of Côte d'Ivoire to determine the epidemiological situation of CCHF [4]. This study highlighted the circulation of CCHFV in cattle and the presence of this virus in ticks in two (2) regions (Bouaflé and Korhogo) (Figure 2). Before July 2022, no human cases had been detected in Côte d'Ivoire. Investigations into the human case of CCHFV revealed that the infection had been caused by handling the carcasses of two cattle. Information received from the herdsmen revealed that these cattle had been imported from Mali or Burkina Faso, and that, after a brief stay in their pastures, they began to show severe morbidity, followed by death. Infection through contact with contaminated livestock tissues is a known risk factor for some professions. This occupational exposure can be limited by wearing gloves and avoiding skin and mucous membrane exposure to fresh blood and other animal tissues [5]. These measures must be strictly followed by professionals working with potentially infected livestock. Around thirty people are thought to have been in contact with the infected person and/or the carcasses of the two animals. Following RT-PCR detection of CCHFV, these contacts or suspects were confined to their homes and subsequently examined. The National Institut of Public health (NIHP) sent the laboratory blood samples from 32 of the patient's contacts. RT-PCR tests for Crimean Congo Virus in the 32 contacts were negative. As CCHFV causes a severe disease that can be transmitted by exposure to viremic animal and/ or human tissues, and there is no vaccine or specific treatment available, CCHFV is classified as a pathogen with high epidemic potential. This virus is therefore placed in a high biological risk

class. This stipulates that virus culture or experimental animal infections are only permitted in biosafety level laboratories 4 (BSL-4) and (BSL-3 plus) laboratories in endemic countries [6]. To determine the genotype of the patient's isolate, we plan to sequence the isolated strains in order to determine the genotype of the virus in this first human case. The CCHFV virus is highly diverse worldwide, with several distinct lineages. It is therefore the most genetically diverse of all arboviruses. Phylogenetic analysis of the CCHFV S-segment suggests a geographical structuring of genotypes, with strains grouped into seven main clades: clade I (Africa 2), clade II (Africa 1), clade III (Europe 2), clade IV (Africa 3), clade V (Europe 1), clade VI (Asia 1) and clade VII (Asia 2) [7]. Furthermore, this great diversity of CCHFV sequences in one area may increase the likelihood of the emergence of recombinant viral strains, as well as adaptation and circulation in new geographical regions [8]. It should also be noted that CCHFV can productively infect a multitude of animal species, but only humans develop a severe from of the disease.



Figure 2: Areas endemic for CCHFV in ticks in Côte d'Ivoire.

Conclusions

This is the first human case of hemorrhagic fever due to the Crimean Congo Virus in Côte d'Ivoire. The Crimean Congo hemorrhagic fever virus is also a tick-borne arbovirus. In order to assess the level of infestation of potential vectors and estimate the risk of spread, an entomological and epidemiological investigation of the initial case of Crimean-Congo hemorrhagic fever is therefore strongly recommended.

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