Clinical and virological data of the first cases of COVID-19 in Europe: a case series

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Summary

Background On Dec 31, 2019, China reported a cluster of cases of pneumonia in people at Wuhan, Hubei Province. The responsible pathogen is a novel coronavirus, named severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). We report the relevant features of the first cases in Europe of confirmed infection, named coronavirus disease 2019 (COVID-19), with the first patient diagnosed with the disease on Jan 24, 2020.

Methods In this case series, we followed five patients admitted to Bichat-Claude Bernard University Hospital (Paris, France) and Pellegrin University Hospital (Bordeaux, France) and diagnosed with COVID-19 by semi-quantitative RT-PCR on nasopharyngeal swabs. We assessed patterns of clinical disease and viral load from different samples (nasopharyngeal and blood, urine, and stool samples), which were obtained once daily for 3 days from hospital admission, and once every 2 or 3 days until patient discharge. All samples were refrigerated and shipped to laboratories in the National Reference Center for Respiratory Viruses (The Institut Pasteur, Paris, and Hospices Civils de Lyon, Lyon, France), where RNA extraction, real-time RT-PCR, and virus isolation and titration procedures were done.

Findings The patients were three men (aged 31 years, 48 years, and 80 years) and two women (aged 30 years and 46 years), all of Chinese origin, who had travelled to France from China around mid-January, 2020. Three different clinical evolutions are described: (1) two paucisymptomatic women diagnosed within a day of exhibiting symptoms, with high nasopharyngeal titres of SARS-CoV-2 within the first 24 h of the illness onset (5·2 and 7·4 $\log_{10}$ copies per 1000 cells, respectively) and viral RNA detection in stools; (2) a two-step disease progression in two young men, with a secondary worsening around 10 days after disease onset despite a decreasing viral load in nasopharyngeal samples; and (3) an 80-year-old man with a rapid evolution towards multiple organ failure and a persistent high viral load in lower and upper respiratory tract with systemic virus dissemination and virus detection in plasma. The 80-year-old patient died on day 14 of illness (Feb 14, 2020); all other patients had recovered and been discharged by Feb 19, 2020.

Interpretation We illustrated three different clinical and biological types of evolution in five patients infected with SARS-CoV-2 with detailed and comprehensive viral sampling strategy. We believe that these findings will contribute to a better understanding of the natural history of the disease and will contribute to advances in the implementation of more efficient infection control strategies.

Funding REACTing (Research & Action Emerging Infectious Diseases).

Introduction

The coronavirus disease 2019 (COVID-19) epidemic spread within China, and secondarily also outside China, with a basic reproductive number estimated to be from 2·2[1] to 3·3[2] and a mortality rate of around 2·3%.[3] In the EU (and European Economic Area) and the UK, as of March 6, 2020, 5544 cases have been reported (423 in France), including 159 deaths (seven in France).[4]

So far, several studies have described demographic, clinical, and biological characteristics of patients with COVID-19, and radiological or pathological findings associated with COVID-19. More specifically, these studies have reported the most common symptoms, incubation periods, biological abnormalities, radiographic abnormalities, CT abnormalities, and treatment data. In addition, they have described varying degrees of illness and their severity: mild, severe, or critical. They have reported proportion of complications, including acute respiratory distress syndrome, or case fatality rates, and variables associated with these complications and death.[1,5–9]

In this Article, through a detailed and comprehensive sampling strategy, we report the clinical and biological features of the first five cases of confirmed COVID-19 in Europe, which occurred in France, and their dynamics in parallel with changes in their viral load, based on severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) RNA detection.