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 **ASSIGNMENT**

REPORT OF THE WHO-CHINA JOINT MISSION ON CORONAVIRUS DISEASE

The Virus

The Outbreak

The Virus

On 30 December 2019, three bronchoalveolar lavage samples were collected from a patient with pneumonia of unknown etiology – a surveillance definition established following the SARS outbreak of 2002-2003 – in Wuhan Jinyintan Hospital. Real-time PCR (RT-PCR) assays on these samples were positive for pan-Betacoronavirus. Using Illumina and nanopore sequencing, the whole genome sequences of the virus were acquired. Bioinformatic analyses indicated that the virus had features typical of the coronavirus family and belonged to the Betacoronavirus 2B lineage. Alignment of the full-length genome sequence of the COVID-19 virus and other available genomes of Betacoronavirus showed the closest relationship was with the bat SARS-like coronavirus strain BatCov RaTG13, identity 96%. Virus isolation was conducted with various cell lines, such as human airway epithelial cells, Vero E6, and Huh-7. Cytopathic effects (CPE) were observed 96 hours after inoculation. Typical crown-like particles were observed under transmission electron microscope (TEM) with negative staining. The cellular infectivity of the isolated viruses could be completely neutralized by the sera collected from convalescent patients. Transgenic human ACE2 mice and Rhesus monkey intranasally challenged by this virus isolate induced multifocal pneumonia with interstitial hyperplasia. The COVID-19 virus was subsequently detected and isolated in the lung and intestinal tissues of the challenged animals.Whole genome sequencing analysis of 104 strains of the COVID-19 virus isolated from patients in different localities with symptom onset between the end of December 2019 and mid-February 2020 showed 99.9% homology, without significant mutation.

The Outbreak

As of 20 February 2020, a cumulative total of 75,465 COVID-19 cases were reported in China. Reported cases are based on the National Reporting System (NRS) between the National and Provincial Health Commissions. The NRS issues daily reports of newly recorded confirmed cases, deaths, suspected cases, and contacts. A daily report is provided by each province at 0300hr in which they report cases from the previous day.

Demographic characteristics

Among 55,924 laboratory confirmed cases reported as of 20 February 2020, the median age is 51 years (range 2 days-100 years old; IQR 39-63 years old) with the majority of cases (77.8%) aged between 30–69 years. Among reported cases, 51.1% are male, 77.0% are from Hubei and 21.6% are farmers or laborers by occupation.

Zoonotic origins

COVID-19 is a zoonotic virus. From phylogenetics analyses undertaken with available full genome sequences, bats appear to be the reservoir of COVID-19 virus, but the intermediate host(s) has not yet been identified. However, three important areas of work are already underway in China to inform our understanding of the zoonotic origin this outbreak. These include early investigations of cases with symptom onset in Wuhan throughout December 2019, environmental sampling from the Huanan Wholesale Seafood Market and of other area markets, and the collection of detailed records on the source and type of wildlife species sold at the Huanan market and the destination of those animals after the market was closed.

Routes of transmission

COVID-19 is transmitted via droplets and fomites during close unprotected contact between an infector and infectee. Airborne spread has not been reported for COVID-19 and it is not believed to be a major driver of transmission based on available evidence.